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9b_est2:BR0708055103
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9b_gss:CRNS0505SSS
9b_est1:AR9564689
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Query: US-08-973-363-6
Query length: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database sequences: 13736207
Database length: -1841457050
Search time (sec): 4390.400000
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Database: EST:*
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-QB-EST -QFMT=fastap -SUFFIX=p3n.rst -GAPOP=12.000 -GAPEXT=4.000
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-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -TBLOP=6.000
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-MINLEN=0 -MAXLEN=200000000 -USER-VEXUS08973363_eCCN1_1_2938
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3.6e-20
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3e-10

9e-10

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gb_gss:CNS04JPY
gb_gss:CNS02H6W
gb_gss:CNS05R9Z
gb_gss:CNS05HIG
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JOURNAL
COMMENT
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AUTHORS
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VERSION
KEYWORDS
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ORGANISM
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                          Location/Qualifiers
1. .619
               /organism="Mus musculus"
/db_xref="taxon:10090"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 12 (bases 1 to 619)

8 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinayawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y., Saito, R., Saito, 
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
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URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y. Hayatsu.N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu.M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
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watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y., d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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US-08-973-363-6 x BB155356
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TITLE
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         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 660)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Koud, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasak, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                   BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D1300770B13 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="A130024L16"
/clone=lib="RIKEN full-length enriched, 16 days neonate
thymus"
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                                                                                                             Sasaki
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ACCESSION VERSION

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Gaps:

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URL:http://genome.gsc.riken.go.jp,
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
yeagi, K., Fujiwake, S., Inoue, K., Togawa, K., Tanaka, T., Matsuura
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura
, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Laboratory for Genome Exploration Research Group, Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jul 21, 2000 this sequence version replaced gi:9356558 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human Genome Sequences Mamm.
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Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                      211
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                                                                                                                                                                                                                              was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." a 130\ {\rm c} 168\ {\rm g} 151\ {\rm t}
                                                                                                                                                                                                                                                                                                                                                                                                          prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
GAGAGAGAGGGGCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched, 12
spinal ganglion"
208.00
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/dev_stage="12 days embryo"
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/db_xref="taxon:10090"
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URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected coNas to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muzamatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.,
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Contact: Yoshihide Hayashizaki
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BB834922 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) cDNA Mus musculus cDNA clone G930033J21 3′, mRNA
                                                                                        Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. .11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 81-45-503-9222 Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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               Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 438)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,

Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,

Nakamura, M., Sakai, K., Sakazune, N., Sasaki, D., Sato, K.,

Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Makahira, S., Tanaka, T., Tomaru, A., Toya, T.,

Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., 2001)
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu.N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., OkazaKi,Y., Muramatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Fax: 81-45-503-9216
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/db_xref="taxon:10090"
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US-08-973-363-6 x BB830730
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Ratio:
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                              Unpublished (1999)
                                                                                                                                                Bloecker, H.,
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
1 (bases 1 to 430)
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                                                                                    Wiemann,S
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                                             Contact: Bloecker
                                                                                                       EST (Bloecker, H., Boecher, M.,
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Klopferspitz 18a D-82152
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/clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
1 96 c 108 g 96 t
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97.619
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/db_xref="taxon:10090"
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Martinsried,
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                                                                                                         Brandt, P.,
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95.238
                                                                                                       Mewes, H.W.,
Germany
                                                                                                                                                                                         Hominidae;
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                                                                                                                                                Weil,B.
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ACCESSION
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LOCUS AI890775
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US-08-973-363-6 x AL601246
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                                                                                                                               Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone (DKFZp313J1040) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd.
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae.
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No s1 sequence available
                                                                                       Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                            Tissue Procurement: Christopher Moskaluk, M.D.,
                                                                                                                                                                                                                                                                       l (bases 1 to 547)
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cDNA-collection"
a 81 c 86 g 100 t
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/clone_lib="313 (synonym: hlcc2)"
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4.579
92.683
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/db_xref="taxon:9606"
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LOCUS AU125712
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Ratio: 4.579
Percent Similarity: 92.683
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                                                                                                                                                                                                                                                                          TITLE
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                                                 Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                              Isogai,T.
HRI human CDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Verfebrata; Eufeleostomi; Mammalia; Eutheria; Primates; Catarnini; Hominidae; Homo.

(bases 1 to 866)
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Location/Qualifiers
1. .547
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1924 Std Error: 0.00
Seq primer: -40UP from Gibco
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
                                                                                                                                                                                                                                                                                                                                            Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            numan.
Homo sapiens
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AU125712.1 GI:10950428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2443725"
/clone_lib="NCI_CGAP_Ut2"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
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1. (bases 1 to 1028)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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                                                                                                         Plate: LLAM9753 row: h column: 16
High quality sequence stop: 488.
Location/Qualifiers
                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9733 row: h column: 16
                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE895133.1 GI:10358221
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BE895133
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                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .866
/clone="IMAGE:3921087"
/clone_lib="NIH_MGC_72"
                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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4.579
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/cell_line="NT2"
/note="Vector: pME18SFL3; mRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="NT2RM4002061"
/clone_lib="NT2RM4"
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/db_xref="taxon:9606"
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US-08-973-363-6 x BE895133
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LOCUS AL659353
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TITLE
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Ratio:
                                                                                                                                                                                                                                                                                                                                                            Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus trop!calis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu045e20.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                        This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
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AL659353
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           /clone_lib="XGC-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
a 134 c 114 g 226 t
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo |
Average insert size 2 kb. Library constructed by Liftechnologies."
                                                                                                                                                                                     /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="TNeu045e20"
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Gaps: 1
Percent Identity: 90.244
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Library constructed by Life
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US-08-973-363-6 x AL659353/rev
alignment_block:
                                                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 ATTTTACCAGATGATCCAGATAAGAAGCCCCCAAGCCAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 luAlaGlnArgLeu 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLysArgG
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                                   Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCACAAAGACTT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est1:AL644594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Silurana.

1 (bases 1 to 645)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing primer: PIC
This sequence is from a Xenopus
constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL644594 XGC-egg Silurana tropicalis cDNA clone L1E1d12 5', mRNA
                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TROPICALIS_SEQUENCE_ID: L1E1d12.p1c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL644594.1 GI:16796719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                western clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                       Ratio:
                                                                                                                                                                       222
                                                                                                                                                                       Ø
                                                                                                                                                               /lab_host="Escherichia coli XL1-blue"
/lab_host="Escherichia coli XL1-blue"
/lab_host="Escherichia coli XL1-blue"
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was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
125 c 156 g 141 t 1 others
                                 172.00
4.649
97.368
                                                                                                                                                                                                                                                                                  /clone_lib="XGC-egg"
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4.649
97.368
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Gaps: 0
Percent Identity: 86.842
                                     Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB10 1SA, UK
                                                       Length:
Gaps:
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                                     38
0
86.842
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US-08-973-363-6 x AL644594

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REFERENCE
AUTHORS
TITLE
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alignment_block:
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                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506 CAGAGCTGACTACCTCATTAAACTTCTCAATAAAGATCTGCTTAGGAAAG 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 luAlaGlnArgLeu 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLysArgG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov k column: 18 plate: LLCML033 row: k column: 18 High quality sequence stop: 562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF239967 821 bp mRNA linear EST 14-NOV-2000 601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 821)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                            345
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/note="Organ: bone marro
                                                                        147.00
4.455
91.667
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                                                                    Percent Identity: 88.889
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                                                                                                                                             Length:
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TITLE
JOURNAL
COMMENT
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VERSION
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alignment_block:
US-08-973-363-6 x CNS04DVG/rev
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                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-973-363-6 x BF239967
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Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostemi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

Tetraodontidae; Tetraodon.

CE 1 (bases 1 to 856)
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope.

Genoscope.

Direct Submitssion

Direct Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 856)
2 (bases 1 to 856)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetracodon nigroviridis DNA sequence
Unpublished
                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNSO4DVG 856 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 103KOB of library G from Tetraodon nigroviridis, genomic survey sequences
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/note="Genoscope sequence ID : C08G103BF04LP1-end : T7"
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4.294
87.179
                                                                                               Percent Identity: 74.359
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reverse of: CNS04DVG

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alignment_scores:
                                                                                                                                                BASE COUNT
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LOCUS AW996787
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  Ratio:
Percent Similarity:
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Roldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                         Quality:
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AW996787
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-23&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was derived from the FAPE Project. This entry can be seen in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
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Location/Qualifiers
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                                                                                                                                                                                                       /note-"Organ: breast_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector Reverse transcription of
139.50
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94.444
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                                                                                                                                                                                      tissue mRNA and cDNA amplification were performed under
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                                                                                                                                                                                                                                                                                                                                                                                  'organism="Homo sapiens"
                                                                                                                                              stringency conditions."
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US-08-973-363-6 x AW996787/rev
     BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                      Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150 400-152-Co3&t3=2000-04-15&t4=1) Seq primer: puc 18 forward High quality sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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as Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
     165
                                                                                                                                                                                                                                                                                                                      quality sequence start: 19 quality sequence stop: 678 Location/Qualifiers
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                                                                     /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under low stringency conditions."

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US-08-973-363-6 x AW997058/rev
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Al352864.1 GI:8246657
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE TRANSPORT OF THE TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.ft/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 1122)
Roest-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F., Saurin,W. and Weissenbach,J.
Ruman gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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1 (bases 1 to 1122)

1 (bases 1 to 1122)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Direct Submission
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                                                                                                                                                                                                            /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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g 260 c 301 g 246 t 12 others
          Length:
          29
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Database sequences: 1797656
Database length: 1873333701
Search time (sec): 4907.710000
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Query: US-08-973-363-7
Query length: 41
Database: GenEmbl:*
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-USUFT-MEOUT-120 -WARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
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                                                                                                                                                                                                                                                                                                                                                                                                                      out_format : pfs
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5349 | LILOUID NOUSE DIAN-binding prote 153 | A58668 Sequence 2 from Patent W 153 | A58668 Sequence 2 from Patent W 154 | A58663 Sequence 2 from Patent W 154 | A6006513 Homo sapiens chrome 143659 | A6012624 Homo sapiens chrome 145659 | A6012624 Homo sapiens chrome 145659 | A6012631 Homo sapiens chrome 145659 | A6012631 Homo sapiens chrome 145659 | A6012631 Homo sapiens chrome 145639 | A6026718 Homo sapiens chrome 145630 | A6026718 Homo sapiens chrome 1466 | A333351 Sequence 3 from Patent A66 | A760514 Homo sapiens Chrome 1466 | A760514 Homo sapiens Chrome 1466 | A760514 Homo sapiens Chrome 1466 | A7606714 Homo sapiens Chrome 1467 | A6013394 Homo sapiens Chrome 1467 | A7606714 Homo sapiens Chrome 1467 | A7606702 Struthho camelus chrome 1467 | A7606702 Struthho camelus chrome 1467 | A6013394 Homo sapiens ch
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1316 ! A58696 Seque
6608 ! A58691 Seque
6872 ! AF004397 Ga.
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i A58691 Sequence 10 from Patent
i AF004397 Gallus gallus chromo-
A58684 Sequence 3 from Patent v
A58685 Sequence 4 from Patent v
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gb_htg:AC101378
gb_ov:OTU89945
gb_pat:AX286188
gb_pat:TYTCUBS
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            Other publication AU 5906996 961224 
Location/Qualifiers
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Sequence 10 from Patent WO9639505.
A58691
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Other publication AU 5906996 961224.
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Griffiths, R. and Tiw.
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1188 TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG 1237
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Griffiths, and Tiwari B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
Griffiths, R. and Tiwari, B.

AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
Direct Submission
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A CHD1 gene is Z chromosome linked Gene 197 (1-2), 225-229 (1997) 97473516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chicken.
Gallus gallus
                                                                                                                                                                                                                                                                                                                                            Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 800, UK
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 6872)
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/organism="unidentified"
/organism="unidentified"
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1207 c 1459 g 1
DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
                                                                                                        protein"
                                                                                                                                          /gene="CHD-2"
/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain'
/codon_start=1
                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                     /protein_id="AAC60282.1"
/db_xref="GI:2501846"
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                       product="chromo-helicase-DNA-binding on the Z chromosome"
                                                                                                                                                                                                                                    'gene=
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                                                                                                                                                                                                                                                        .6872
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                                                                                                                                                                                                                                     "CHD-Z"
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on the Z chromosome
(CHD-Z) mRNA, comple
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seq_documentation_block:
LOCUS A58684
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US-08-973-363-7 x AF004397
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   Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCACAAAGGCTTGCTGGTGCA 4202
                                                                                                                                                                                                                                                                                                          153 bp
Sequence 3 from Patent W09639505
A58684
                                                       1 (bases 1 to 153)
Griffiths, R. and Tiv
AVIAN GHD GENES AND
                                                                                                                                                                                       unidentified
unidentified
Patent:
                                                                                                                                                   unclassified
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MITTHEWMHPOTKRIKENILLTTYEILLKDKSTLGGLIWAPT TIQTDEAHRLKNIDOSLLY
RTILDFKSNHRLLITGTPLQNSLKELMSLLHFIMPEKFESWEDFEEHGKGREYGYAS
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FLLSTRAGGLGINLASADTYVIEDSDNMPONDLOQAARAHRIGGKKQVNIYKRLTTKG
VEEDILERAKKKMYLDHLYIQRMDTTGKTVLHTGSTPSSSTPFNKEELSAILKFGAEE
LEPERNSRNWEEIIPESORRRIEEEREPGPLTVGDELLSQFKYANFSNMDEDDIE
LEPERNSRNWEEIIPESORRRIEEEREPGPLTVGDELLSQFKYANFSNMDEDDIE
LEPERNSRNWEEIIPESORRRIEEEREPGPLTVGDELKARFIKGSGERSR
SRRYSGSDSDSTTERKRPKKRGRPRTLFRENIKGFSDAEIRRFIKSYKKGFDELERLD
AVARDAELVDKSETDLRRLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPTFRISGV
QVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSNLLVGI
YEYGYGSWEMIKMDPDLSTTQKKICHEDDDFKPQAKGLQTRADYLIKLLNKDLARKEAQ
RLAGACNSKRRTRNKNKMKASKIKEEIKSDSSGQPSEKSDEEDDEEEDNKDEITSVK
HLHKKIKTEKENEEKPEPDIGIKKEAKEENEEKREEKEEKKEKEELKREKKEKEEDKKEILKEK
HLHKKIKTEKENEEKPEPDIGIKKEAKPYNBERSHEKSKKIPLITTATSEPVPISE
ESEELHAKTSTYCKEEKVPEMSENKEEKSKKIPLLDTPVHITATSEPVPISE
ESEELHSKTTSTHUDDSSBOSYSSDRILSGYHDHKOLKKOSGGCHNDONISSNVN
THVIRNPOVERLKETTHUDDSSBOSYSSDRILSGYHDHKOLKKOSDSKKRAPY
SAAFSKKSDHRDMHYKODSRVSOSDSKLSDYNDHESMYKNDSRGKSDSKKRAPY
SAAFSKKSDHRDMHYKODSRVSOSDSKLSDYNDHESMYKNDRGCHSTORKSH
WO 9639505-A 3 12-DEC-1996;
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AHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKD
CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEWGLG
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1223 c 1520 g
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                                                       Tiwari, B.
AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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BASE COUNT ORIGIN

REFERENCE AUTHORS TITLE

JOURNAL

SOURCE ORGANISM

KEYWORDS

VERSION ACCESSION

DEFINITION

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REFERENCE
AUTHORS
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FEATURES
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                                                      alignment_block:
US-08-973-363-7 x A58685
                                                                                                                                        alignment_scores:
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                                                                                               Quality: 190.00
Ratio: 4.634
Percent Similarity: 80.392
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Ratio: 4.634
Percent Similarity: 80.392
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                             Align seg 1/1 to: A58685 from: 1 to: 153
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Other publication AU 5906996 961224.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               unclassified.

1 (bases 1 to 153)

1 (bases 1 to 153)

Griffiths, R. and Tiwari, B.

AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 bp
Sequence 4 from Patent WO9639505.
A58685
                                                                                                                                                                                                                                                                       Other publication AU 5906996 961224
                                                                                                                                                                                                                                                                                      Patent: WO 9639505-A 4 12-DEC-1996; ISIS INNOVATION (GB)
                                                                                                                                                                                                                                                                                                                                                                                           unidentified
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/db_xref="taxon:32644"
1 40 c 31 g 24
                                                                                                                                                                                                 /organism="unidentified"
/db_xref="taxon:32644"
36 c 31.g 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center,
7701 Burholme Avenue, Philadelphia, PA 19111, USA
On Feb 16, 1994 this sequence version replaced gi:293322.
Location/Qualifiers
1. 5349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A mammalian DNA-binding protein that contains a chromodomain and an SNF2/SWI2-like helicase domain Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 5349)
Delmas, V., Stokes, D.G. and Perry, R.P.
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TIKOONWAMKKIDNYKKKODETKWIKNAS PEDVEYYNCOGELTDDLIKQYG IVERI
I AHSNQKSAAGLEDYYCKWOCELYSGESCHEDGALISKKFOTCI IDSYESKNOSKTTEFK
I CHENGKSAAGLEDYYCKWOCELYSGESCHEDGALISKKFOTCI IDSYESKNOSKTTEFK
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RKDPQQAQQAFASSNSGSEDDSSEDDSSSDTSANKYRSRRPQNRSKSNGKKILGGKKRQLDSSEDE
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DCRVGRKGATGATTT I YAV BADGDPNAGFERNKEPGD I QYLI KWKGWSH I HNTWET EE
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/db_xref="taxon:10090"
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    Quality:
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Percent Similarity:
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US-08-973-363-7 x MUSCHD1X
                                                                             alignment_block:
US-08-973-363-7 x A58686
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ORIGIN
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Ratio: 4.561
Percent Similarity: 100.000
                                                 Align seg 1/1 to:
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1 IleLeuProAspAspProAsp...
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5 from Patent WO9639505.
                                                                                                                                                                                                                                                                                                                                      Patent: WO 9639505-A 5 12-DEC-1996; ISIS INNOVATION (GB)
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r publication AU 5906996 961224.
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                                                                                                                              182.00
4.439
80.392
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34 c 31 g
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Percent Identity:
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DEFINITION
ACCESSION
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KEYWORDS
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Quality:
Ratio:
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US-08-973-363-7 x A58683
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Sequence 2 from Patent W09639505
A58683
Homo sapiens CHD1 mRNA, AF006513
AF006513.1 GI:2645428
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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publication AU 5906996 961224
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US-08-973-363-7 x AF006513
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Align seg 1/1 to: AF006513 from: 1 to: 5947
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1 (bases 1 to 5947)

Woodage, T., Basrai, M.A., Baxevanis, A.D., Hietter, P. and Collins, F.S. Characterization of the CHD family of proteins

Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
                                                                                                                                                                                                                                               Quality:
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EGGREFFORDTAFYH
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t Drive, Bethesda, MD 20892-4442,
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KLYKHAIKKRQESQQNSDQNSNLNPHVIRNPDVERLKENTNHDDSSRDSYSSDRHLTQ
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DDDEEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEEEEFETIER
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KKQQQQQQQQQHQASSNSGSEEDSSSSEDSDDSSSEVKRKKHKDEDWQMSGSGSPSQS
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RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWQMDH
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/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                               Percent Identity: 85.366
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US-08-973-363-7 x AC092372/rev
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ACCESSION
                                                                                       Align seg 1/1 to reverse of: AC092372 from: 1 to: 101220
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26932 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 26883
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                        1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACU943/2 101220 bp DNA linear PRI 07-DEC
Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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Mammalla; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 to 101220)

DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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4.359
95.122
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seq_name: gb_htg:AC021449
                                                                                                                                                                                                                                                                                                                    alignment_block:
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|CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAAAAAG
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                                                                        luAlaGlnArgLeuAlaGlyAla 41
                                                                                                              CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAAAAAG 118346
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                                     AAGCT.....CTTTCTGGTGCG 118363
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Submitted (31-OCT 1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mit Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mi
Drive, Wallut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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ne 5 clone CTD-2082I17, complete sequence.
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LOCUS AC021449
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
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McPheeters, R., Meddrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,
Piarre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrella, V., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 143079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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                                                                                                                                        as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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3820: contig of 38820 bp in length
38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
40412 40511: gap of 100 bp
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WORKING DRAFT SEQUENCE, 10 unordered
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seq_name: gb_htg:AC008531
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US-08-973-363-7 x AC021449
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Percent Similarity:
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                                                                                                                                                                                                  116147 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 116196
                                      116247 AAGCT.....CTTTCTGGTGCG 116263
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                                                                            34 luAlaGlnArgLeuAlaGlyAla 41
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43280 43379: gap of 100 bp
43380 46905: contig of 3528 bp in length
46906 47005: gap of 100 bp in length
51831 51930: gap of 100 bp in length
51831 51930: gap of 100 bp
62620 62719: gap of 100 bp
62720 75408: contig of 12689 bp in length
75409 75508: gap of 100 bp
75509 92516: contig of 12689 bp in length
92517 106409: contig of 100 bp
106410 106509: gap of 100 bp
106510 143079: contig of 13793 bp in length
106510 143079: contig of 36570 bp in length
106510 143079: contig of 36570 bp in length
106410 106509: gap of 100 bp
110510 143079: contig of 36570 bp in length
1143079
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43971 a 26246 c 26678 g 45278 t
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4.359
95.122
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clone_end:T7
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clone_end:SP6
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/db_xref="taxon:9606"
/clone="epl-58M12"
/clone_1ib="RPCI-11 Human Male BAC"
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38921. .40411
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92617. .106409
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51931. .62619
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13380. .46905
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10512. .43279
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7006. .51830
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Gaps: 1
Percent Identity: 85.366
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REFERENCE
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LOCUS AC008531
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TITLE
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Consensus quality: 142556 bases at least Q20
Consensus quality: 143744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Bestimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation
Quality coverage: 6.47 in Q20 bases; pulse field gel estimation
Quality coverage: 6.47 in Q20 bases; pulse field gel estimation
Quality coverage: 6.77 in Q20 bases; pulse field gel estimation
Quality coverage: 6.77 in Q20 bases; pulse field gel estimation
Quality coverage: 6.77 in Q20 bases; pulse field gel estimation
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Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
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Center clone name: CIT-HSPC_480B11
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Center: Joint Genome Institute
Center Code: JGI
Quality:
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14565)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                        /chromosome="5"
/clone="CTC-480B11"
/clone="CTC-480B11"
/clone_1lbe="CalTech human BAC library C"
/clone_1be="CalTech human BAC library C"
/clone="CTC-480B1"
/clone=
      170.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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REFERENCE
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SOURCE
ORGANISM
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VERSION
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LOCUS AC091946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_htg:AC091946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                                                              Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q20
Consensus quality: 184175 bases at least Q20
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation
**NOTE: This is a 'working draft' sequence. It currently
**consists of 3 contigs. The true order of the pieces
**is not known and their order in this sequence record is
**arbitrary. Gaps between the contigs are represented as
**runs of N, but the exact sizes of the gaps are unknown.
**This record will be updated with the finished sequence
**as soon as it is available and the accession number will
**be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCT.....CTTTCTGGTGCG 46886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 5 clone RP PROGRESS ***, 33 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 193446)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: RPCI-11_360I2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Project Name: 544799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing of Human Chromosome
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95.122
1358: contig of 1358 bp in length
1458: gap of unknown length
2667: contig of 1209 bp in length
2767: gap of unknown length
3823: contig of 1056 bp in length
3923: gap of unknown length
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                                               alignment_scores:
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9197
10261
10361
12461
12561
14612
14712
                                                                                                                                                                                                  /organism="Homo sapiens"
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35252 c 37061 g 60360 t 3202 others
    170.00
4.359
                                                                                                                                                                                                                                                                                            Location,
                                                                                                                                                                                                                                                                                                                                                                         92891: gap of unknown length
102794: contig of 9903 bp in length
102894: gap of unknown length
110866: contig of 7972 bp in length
110966: gap of unknown length
117571: contig of 6605 bp in length
117671: gap of unknown length
123738: contig of 6067 bp in length
123738: contig of 6067 bp in length
12388: gap of unknown length
130833: gap of unknown length
130833: gap of unknown length
141644: contig of 10861 bp in length
141644: gap of unknown length
                                                                                                                                                                                                                                                                      .193446
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169209: gap of unknown 1
193446: contig of 24237
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f unknown
g of 5563
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f unknown
g of 1670
f unknown
g of 1487
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g of 2366
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g of 1502
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of 1474
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ACU26778

DEFINITION Homo sapiens chromosome 5 clone CTC-428111, complete sequence.

ACCESSION ACU26778

VERSION ACU26778.4 GI:14277282

KEYWORDS Homan.

SOURCE human.

ORGANISM Homo sapiens
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AUTHORS
TITLE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AC091946 from: 1 to: 193446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 95.122
                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
    Quality:
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Source
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US-08-973-363-7 x AC026778/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 195433)

DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission
                                                                                                                                                                                 STS Content:
WI-13675 G23101
SHGC-58345 G38487
SHGC-103595 G57841.
                                                                                                          62762 a
                                                                                                         1..19433
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-428111"
a 37302 c 37040 g 58329 t
                                                                                                                                                              Location/Qualifiers
                                  170.00
4.359
95.122
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                                  Length: 41
Gaps: 1
Percent Identity: 85.366
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Search information block: Query: US-08-973-363-7 Query length: 41
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Database sequences: 1736436
Database length: 858457221
Search time (sec): 523.620000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _p2n.model -DEV-xlh
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                  alignment_block: US-08-973-363-7 \times AAT42754
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Ratio: 5.000
Percent Similarity: 100.000
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                                                                                                                             17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
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167 1.

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seq_documentation_block:
ID AAT42754 standard; cD
XX AAT42754;
XC AAT42754;
XX 12-MAR-1997 (first e
DT 12-DEC-1996:
XX Bird; sex determinati
KW CHD-W; chromodomain-H
XX Gallus sp.
XX W09639505-Al.
XX W09639505-Al.
XX 06-JUN-1996; 956W0-G
PF 05-JUN-1996; 956W0-G
PF 05-JUN-1995; 95GB-0
XX (ISIS-) ISIS INNOVATI
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XX The chicken CHD-W gen
CC The chicken CHD-
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAF90032 + 
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                                                                                                                                                                                                                                                                                                                                                    The chicken CHD-W gene (ANT42754) acting alone or in conjunction with the closely related CHD-1A gene (ANT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a tipe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                         Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT42754 standard; cDNA; 1316 BP.
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Length: 41
Gaps: 0
Percent Identity: 100.000
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94.
73.
131
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luAlaGlnArgLeuAlaGlyAla 41 AAGCACAGAGACTTGCTGGTGCA

1260

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alignment_block:
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                                                                                                                                                                                                       seq_documentation_block:
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                                                   Align seg 1/1
                                                                               US-08-973-363-7 x AAT42751
                                                                                                                       Percent Similarity: 100.000
The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or 2 chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         birds
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Griffiths R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chicken CHD-1A gene
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                                                                                                                                                                                                     Sequence 6608 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex determination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex determination; chromodomain-Helicase-DNA binding chromodomain-Helicase-DNA binding on the W chromoson
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 4129
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17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG

1 IleLeuProAspAspProAsp.....

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alignment_block:
US-08-973-363-7 x AAT42757
                                                                             alignment_scores:
    Quality:
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ID AAT42757 standard;
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Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHB-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW3146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chick CHD-1A gene fragment
                                                                                                                                                                                                                                                                                                                                              Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bird; sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT42757;
                                                                                                                         Sequence 153
                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                           birds
                                                                                                                                                                                                                                                                                                              P-PSDB; AAW08147
                                                                                                                                                                                                                                                                                                                       WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHD-1A; CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCACAAAGGCTTGCTGGTGCA 4202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42757
                                                                                                                                                                                                                                                   8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                          chromodomain-helicase-DNA binding genes - used for sex determn. and to control:
                                                                   Ratio:
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 AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W chromosome; ss.
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and are ignored in a
acid sequence given
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                                                                                                                           31
                                                                                                                          G;
 ë
                                                                                                                          24 T; 0 other;
  153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a repeat of bases in the translated iven in Fig 3"
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                                                                                                                                                                                                                                                                           s determine sex
sex of progeny
                                                                                                                                                                                                                                                                          progeny
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seq_documentation_block:
ID AAT42758 standard; DNA; 153 BP
                         alignment_scores:
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                                                                                           Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rey Location/Qualifiers misc_difference 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                                                                                                                                                                                                                            Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                       Avian chromodomain-helicase-DNA binding genes determine sex in
birds - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                            Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chick CHD-W gene fragment.
                                                                     Sequence 153 BP;
                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bird; sex determination; chromodomain-Helicase-DNA binding 1;
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                                                                                                                                                                                                                                                                                                  1997-043127/04.
DB; AAW08148.
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHD-W; W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                              Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                      95GB-0011439
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190.00
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and are ignored in the translated
acid sequence given in Fig 3"
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seq_documentation_block:
ID AAT42759 standard; DNA; 153 BP
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US-08-973-363-7 x AAT42758
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Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW04164-49. The CHD-IA (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers misc_difference 52..81
                                                                                                                                                                                                                                                                                    Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                 Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Great tit CHD-W gene fragment.
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and are ignored in the translated
acid sequence given in Fig 3"
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to manipulate the

sex of progeny.

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seq_documentation_block:
ID AAT42756 standard; DN
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AC AAT42756;
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US-08-973-363-7 x AAT42759
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P-PSDB; AAW08146.
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                                                        Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                       (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse CHD-1 gene (bases 3855-977).
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     Fig 3; 76pp; English.
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                                                                                                                                                                                                                   Tiwari B;
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US-08-973-363-7 x AAT42756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151
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                                                                                                                                                                                                                                                                                                                Altered telomere repeat binding factor 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 153 BP;
                                                                                                                                                                                                                                                                                      ds; human; telomere repeat binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 AACTACTTAGCAGAGATCTTGCAAAAAGAGAGGCTCAGAGACTTTGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the sex of an embryo, foetus etc. and to manipulate the sex of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 CAAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153
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                                                                                                                                                                                             Location/Qualifiers
1..1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172.00
4.195
80.392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
                                                                                                                                                                                                                                                                        telangeictasia; Down's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 153
                                                                                                                                                                                                                                                                                       factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.588
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                                                                                                                                                                                                                                                                         viral.
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seq_documentation_block:
ID AAK88882 standard; cDNA; 4;
XX
AC AAK88882;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system anti
XX
Human; digestive system anti
XX
KW Human; digestive system anti
XX
KW digestive system disorder;
XX
Human; digestive system disorder;
XX
Cos Homo sapiens.
XX
PN W0200155314-A2.
XX
PN W0200155314-A2.
XX
PN 02-AUG-2001.
XX
PN 04-FEB-2000; 2000US-0180324
XX
AC 31-JAN-2000; 2000US-0180628
PR 04-FEB-2000; 2000US-0186386
PR 04-FEB-2000; 2000US-0186386
PR 16-MAR-2000; 2000US-0186386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality: 129.00
Ratio: 5.160
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-973-363-7 x AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK88882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                      Human, digestive system antigen; gene therapy, cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                     Human digestive system antigen coding sequence SEQ ID NO: 1198.
                                                                                                                                                                                                                                                                                                                                                                                                           05-NOV-2001 (first entry)
                                                                                                                         17-JAN-2001; 2001WO-US01324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998-480769/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW59280.
    2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
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Gaps: 0
Percent Identity: 100,000
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       111-JUL-2000
114-JUL-2000
26-JUL-2000
26-JUL-2000
14-AUG-2000
114-AUG-2000
114-SEP-2000
125-SEP-2000
125-SEP-2000
125-SEP-2000
126-SEP-2000
127-SEP-2000
129-SEP-2000
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18-APR-2000;
  2000US-0199076
2000US-0199173
2000US-0199173
2000US-0191813
2000US-0116807
2000US-0116807
2000US-0116807
2000US-0116807
2000US-0116807
2000US-0116807
2000US-0116807
2000US-0116807
2000US-012963
2000US-0125213
2000US-0125266
2000US-0125267
2000US-0125277
2000US-0125758
2000US-01258447
2000US-01258487
2000US-01258487
2000US-0125888
2000
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17-NOV-2000
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17-NOV-2000
11-NOV-2000
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01-DEC-2000
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05-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
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20-CCT-2000
20-CCT-2000
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20-CCT-2000
20-CCT-2000
20-CCT-2000
01-NOV-2000
08-NOV-2000
08-NOV-2000
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17-NOV-2000
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17-NOV-2000
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17-NOV-2000

17-NOV-2000
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20-OCT-2000;
20-OCT-2000;
                                        digestive
                    Claim
                                                  diagnosing, treating,
                                                            Polynucleotides
                                                                                 WPI; 2001-502630/55
P-PSDB; AAM93109.
                                                                                                                Rosen
                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2000;
17-NOV-2000;
                                                                                                                                   ( HUMA - )
                    ۲,
                                                                                                               CA,
                                                                                                                                    HUMAN
                    SEQ
                                    otides encoding digestive system antigens, useful for g, treating, preventing and/or prognozing disorders o system, particularly cancer and cancer metastases -
                                                                                                               Barash
                                                                                                                                                      2000US-0239937.
2000US-0241785.
2000US-0241786.
2000US-0241808.
2000US-0241808.
2000US-0244617.
2000US-0246474.
2000US-0246475.
2000US-0246476.
2000US-0246524.
2000US-0246524.
2000US-0246524.
2000US-0246524.
2000US-0246528.
2000US-0246528.
2000US-0246528.
2000US-0246511.
2000US-0246611.
2000US-0246611.
2000US-0246611.
2000US-024661.
2000US-0249218.
2000US-024928.
2000US-024928.
2000US-024928.
2000US-024928.
2000US-0251868.
2000US-0251868.
2000US-0251989.
2000US-0254999.
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                                                                                                                                    GENOME
                   NO 1198;
                                                                                                              sc,
                                                                                                                                    SCI INC
                                                                                                               Ruben
                 986pp;
                                                                                                               MS.
                   English.
                                                 ^{\rm of}
                                                  the
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The present invention provides the protein and coding sequences

of.

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                                                                                                                                                                                                                                                                                                                                                                                                         seq_name:
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US-08-973-363-7 x AAK88882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                              Human; colorectal cancer; colorectal cancer antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                            210 GGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 CCGAGCGGATTACTTGTTGAAGCTGCTCAGAAAGGGTCTGGAGAAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 421 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                34 luAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
||||||||||||||||:::|||
                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAI57603
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                                                                                                                                                                                                                                                                                                                                                                                                                             214
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  2000US-0184664.
2000US-018874.
2000US-0199076.
2000US-0199076.
2000US-029515.
2000US-029517.
2000US-0214886.
2000US-0214886.
2000US-0214647.
2000US-0216647.
2000US-0217496.
2000US-0217496.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
2000US-0218290.
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2000US-0180628
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                                                                                                                                                                                                                                                                                                                 cancer antigen cDNA
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4.067
85.714
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                                                                                                                                                                                                                                                                                                                                                                             cDNA;
                                                                                                                                                                                                                                                                                                                                     entry)
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127
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                                                                                                                                                                                                                                                                                                                 SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421
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                                                                                                                                                                                                                                                                                                                 IJ
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0
71.429
                                                                                                                                                                                                                                                                                                                  NO:
                                                                                                                                                                                                                                                                                                                  67.
                                                                                                                                                                                                                                                                                             gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
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14-AUG-2000; 14-AUG-2000; 14-AUG-2000;

2000US-0225213. 2000US-0225214. 2000US-0225266.

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08-NOV-2000:
17-NOV-2000:
17-NO
                                                            The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in the AAI57547-AAI57619 and AAM3859-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2} \left( \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2
Sequence 421 BP; 148 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-457727/49.
P-PSDB; AAM38625.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO: 67; 522pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0246523

2000US-0246524

2000US-0246526

2000US-0246610

2000US-0246610

2000US-0246611

2000US-0246611

2000US-0249201

2000US-0249201

2000US-0249211

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2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249211

2000US-0249214

2000US-0249216

2000US-0255918

2000US-0255918

2000US-0255918

2000US-02551868

2000US-02551868

2000US-02551869

2000US-02551869
78 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM;
         127
G;
61 T; 7
other;
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22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
21-SEP-2000
01-SEP-2000
01-SEP-2000
06-SEP-2000
06-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
14-SEP-2000
15-CCT-2000
15-CCT-2000
15-CCT-2000
15-CCT-2000
15-CCT-2000
16-NOV-2000
16-NOV

2000US -022527 2000US -0225757 2000US -0225757 2000US -0225759 2000US -0225759 2000US -02258661 2000US -022934 2000US -023124 2000US -023124 2000US -023124 2000US -023124 2000US -023141 2000US -02314 2000US -02316 2000US -02318 2000US -02346 2000US -024647 2000US -024647

alignment_scores: Quality: Ratio: 122.00 4.067

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Length: Gaps:

alignment_block:

Percent Similarity:

Quality:

Ratio

88.00 2.839 81.579

Percent Identity:

55.

Gaps:

US-08-973-363-7 x ABL06443

Align seg 1/1 to:

ABL06443

from:

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to: 6240

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seq_documentation_block:
ID ABL06443 standard:
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:ABL06443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAI57603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster expressed
                                                                         insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL06443;
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                                                                                                                                                                                                           interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 luAla 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTCTGCCGGTGGAGACAGATAAAAAGCCTCAGGGGAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGAGCGGATTACTTGTTGAAGCTGCTCAGAAAGGGTCTGGAGAAGAAGG
                                                                                                                                                                                                                                                                         2001-656860/75
                                                                                                                                                                                                                                                                                                                           ) PE
                                                                                                                                                                                SEQ ID NO 13811; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                            CORP NY.
                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology;
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                                                                                                                                                                                                                    detection reagent for detecting 1000 for elucidating cell signalling and o
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С
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Sequence 6240 BP;

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The sequence data for this patent did not form specification, but was obtained in electronic 1

ftp.wipo.int/pub/published_pct_sequences

(ABB57737-ABB72072)

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seq_documentation_block:
ID ABL06442 standard;
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                                                   cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                    The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                       Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                The invention relates to
                                                                                                                                                                                                           genes from Drosophila
                                                                                                                                                                                                                        New isolated nucleic
                                                                                                                                                                                                                                                  P-PSDB; ABB62339
                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                     11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster expressed polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
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                       ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                      'n,
                                                                                                                                  ention relates to an isolated nucleic acid detection of detecting 1000 or more genes from Drosophila. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequences AAS59506-AAS59804 represent DNA molecules encoding Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                                                                                                               Claim 1; SEQ ID No 85; 1069pp; English.
                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic vaccinating against and diagnosing infections, estreating acne vulgaris -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Propionibacterium acnes immunogenic protein encoding DNA #85.
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, Jen S, Carter D;
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seq_documentation_block:
ID AAS96071 standard; cI
XX AAS96071;
XX AAS96071;
XX AC AAS96071;
XX Z6-FEB-2002 (first e
DT 26-FEB-2002 (First e
DT 26-APR-2000) (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmaniasis; Leishmania antigen; immunostimulant; protozoacide; Ldp23; interleukin-15; PCR primer; Lbhsp83; ML5; Lt-1; LbeIF4A; Lmsp1a; Lmsp9a; MAPS-1A; LmgSP1; LmgSP3; LmgSP5; LmgSP8; LmgSP9; LmgSP13; LmgSP19; ss; LcgSP1; LcgSP3; LcgSP4; LcgSP10; ld6-34; lE6-44; 4A5-63; lB11-39; 2A10-37; 4G2-83; 4H6-41; 8G3-100.
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                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-2001; 2001WO-US11254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leishmania antigen 4G2-83 extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
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                                                                            Campos-Neto
Probst P;
                                                                                                                                                                                                                                                      ; 2000US-0551974.
; 2000US-0565501.
; 2000US-0639206.
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                                                                                                              Skeiky YAW,
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Example 2; Fig 1; 87pp; English

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seq_documentation_block:
ID AAZ30163 standard; DN
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AC AAZ30163;
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PAV-3; defective recomplete section in color sect
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US-08-973-363-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acquired immune deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subunit vaccine; nucleic acid immunisation; gene therapy; genetic disease; hemophilia; cystic fibrosis; cancer; vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete nucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccination
New nucleic acids from the genome of porcine adenovirus-3, gene therapy vectors, particularly for immunization
                                                                                                 WPI; 1999-620422/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAV-3; defective recombinant PAV vector; live recombinant virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193pp; English.
                                                                                                                                                             Babiuk
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The present sequence represents the complete nucleotide sequence of the genome of porcine adenovirus-3 (PAV-3). The specification also describes a defective recombinant PAV vector comprising inverted terminal repeats (ITR), packaging sequences and at least one heterologous nucleotide sequence (II), but lacking El functions. The defective vectors replicate innefficiently in cells (other than helper cells) so are unlikely to be immunogenic. Deletion of the El (and optionally other regions) increases the size of heterologous insert that can be packaged. The PAV-3 polynucleotides sequences are used to produce (recombinant or defective) vectors that can express heterologous proteins, e.g. for making live, recombinant virus or subunit vaccines, for nucleic acid immunisation or for gene therapy (e.g. of genetic diseases such as hemophilia or cystic fibrosis, cancer, or viral infections, including acquired immune deficiency syndrome), also for in vitro expression of recombinant therapeutic proteins. They are also used diagnostically to detect PAV antigens and/or nucleic acid. The vectors may be used in human or veterinary medicine, but particularly for expressing protective antigens and/or production, antisense RNA, ribozymes or veterinary medicine, but particularly for expressing protective determinants of porcine pathogens. Regulatory regions may be used to control expression of heterologous genes. Antibodies raised against PAV-3 polypeptides can also be used for diagnosis (to detect PAV-specific antigen).
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seq_documentation_block:
ID AAX39679 standard; DN
XX
AC AAX39679;
XX
Cancer associated ant
XX
Cancer associated ant
XX
KW Cancer associated cancer; colon
KW prostate cancer; ss.
OS Homo sapiens.
XX
PN WO9904265-A2.
XX
PD 28-JAN-1999.
XX
XX
DF 15-JUL-1997; 97US-0-1
XX
DF 17-JUL-1997; 97US-0-1
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US-08-973-363-7 x AAZ30163/rev
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                                                                                                                                                                                                                                                                                                        Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer; prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            Renal cancer associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX39679 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 rLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysGluAlaGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:AAX39679
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  98US-0102322.
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                                                                                                                                                                                                                                                                                                                                     Lung
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alignment_scores: 57.50
Quality: 57.50
Ratio: 2.130
Percent Similarity: 75.000
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US-08-973-363-7 x AAX39679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAX39679 from: 1 to: 2911
                                                                                   1761 GTTTGAGAACCTCTGCAAAATCATG...AAAGACATATTGGAGAAAAAAG 1807
                                                                                                                                                                      10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigen precursors expressed in human breast which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and line cancer.
1808 TGAAAAGG 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2911 BP; 957 A; 519 C; 686 G; 749 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 67; Page 496-497; 787pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-132448/11.
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                                        35 laGlnArg 37
                                                                                                               18 gAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysGluA 35
                                                                                                                                                                                             2 LeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnThrAr 18
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97US-0948705.
97GB-0021697.
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Gaps: 1
Percent Identity: 30.556
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9b_9ss:CNSO54WU
9b_9ss:CNSO5WU
9b_9ss:CNSO2BFS
9b_9ss:CNSO2BFS
9b_9ss:CNSO2BFS
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9b_9ss:CNSO5WU
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9b_est1.AL64594
9b_est1.BL5336
9b_est1.BB61065
9b_est1.BB630922
9b_est1.BB630730
9b_est1.BB630730
9b_est1.BB630730
9b_est1.BB695133
9b_est2.BB695133
9b_gss:CNSS4DVG
9b_est1.BF639967
9b_est2.BF739967
9b_est2.R47903
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9b_est2.R47903
9b_est2.R48556
9b_est2.BG7577172
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Database length: -1841457050
Search time (sec): 4390.400000
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Query: US-08-973-363-7
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-Q-/cgn2_1/USPG0_spool/USO8973363/runat_01082002_080049_18570/app_query.fasta_1.638
-DB-EST -OpmT-fasta_ -SUFIX-P2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -CAPEXT=0.000 -CAPEXT=0.000 -GAPOP=4.500
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1.8e-16
9.3e-15
9.3e-15
1.2e-14
2.7e-14
                                                                                                                                                | N49703 yv23e03.sl Soares fetal | N49703 yv23e03.sl Soares fetal | N49705 EST176834 Colon carcin | A1915135 w150e08.xl NCLCGAP_OV | A1648536 tz55b06.xl NCLCGAP_OV | H53564 y486h11.sl Soares fetal | BG757172 602710541F1 NIH_MGC_48 | NM366889 pm3-pT0037-231299-001 | AL32353 Tetraodon nigroviridis | AL293103 Tetraodon nigroviridis | AL273105 Tetraodon nigroviridis | AL171305 Tetraodon nigroviridis | AL19107 Tetraodon | AL19107 Tetraodon nigroviridis | 
ALJ41950 Tetraodon nigroviridi ALJ36703 Tetraodon nigroviridi ALJ309319 Tetraodon nigroviridi ALJ309319 Tetraodon nigroviridi ALJ309319 Tetraodon nigroviridi ALJ40872 Tetraodon nigroviridi ALJ44872 Tetraodon nigroviridi ALJ97249 Tetraodon nigroviridi ALJ308289 Tetraodon nigroviridi ALJ308287 Tetraodon nigroviridi ALJ37032 Tetraodon nigroviridi ALJ37132 Tetraodon nigroviridi ALJ31668 Tetraodon nigroviridi ALJ308107 Tetraodon nigroviridi
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gb_est2:BM185888
gb_est2:BM070535
gb_est2:BM024825
gb_est2:BM185005
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US-08-973-363-7 x AL659353/rev
                              seq_name: gb_est1:BB155356
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Align seg 1/1 to reverse of: AL659353 from: 1 to: 593
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                                            17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                                                                                                                                                                1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_EQUUNCE_ID: TNeu045e20.sp6
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Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001)

Unpublished (2001)

Contact: Huckle E
Sanger Centre
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibla: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 593)
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This sequence is from a Xenopus Gene Collection (XGC) library
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/clone="TNeu045e20"
/clone="Lagor Type: Vage - Vage 
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/db_xref="taxon:8364"
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Gaps: 0
Percent Identity: 94.872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDMAs to
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MIKEN Mouse ESTs (Arakawa,T., et al. 2001)

Unpublished (2001)

On Jun 29, 2000 this sequence version replaced gi:8811286

Contact: Yoshihide Hayashizaki
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Arakawa,T., Carninci,P., Fukuda,S.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
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Email: genome-res@gs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Genome Sequences Mamm. Genome. 12, 6/3-6/7 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Computational Analysis of Full-Length Mouse cDNAs Compared with luman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
/note="Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                           /tissue_type="thymus"
/dev_stage="16 days ne
                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                  /clone="A130024L16"
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                _lib="RIKEN full-length enriched, 16
                                                                                                                                days neonate"
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                       Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALD44594 XGC-egg Silurana tropicalis cDNA clone LiEld12 5', mRNA
                                                                                                                                                                Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: L1E1d12.plc
                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                        Contact: Huckle E
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                                                                                                            constructed by Aaron M.
                                                                                                                                                 Sequencing primer: P1C
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                                                                                                                                                                                                                                                   Sanger Centre
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                                                                                                                               sequence is from a Xenopus Gene Collection (XGC) library
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/clone="LIEId12"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 660)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,

Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,

Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,

Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B8461065 660 bp mRNA linear EST 25-OCT-2001 B8461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-Dinding protein (CHD-1) mRNA, mRNA sequence.
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
On Jul 21, 2000 this sequence version repla
Bmail: genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carrincl,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-633-9228
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    2000 this sequence version replaced gi:9356558
Yoshihide Hayashizaki

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/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5', end and NotI at 19' end"
a 125 c 156 g 141 t 1 others
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/dev_stage="egg"
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Percent Identity: 94.872
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alignment_block:
US-08-973-363-7 x BB461065
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581 AGGCTCAGAGACTTTGTGGTGCG 603
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                                                                    34 luAlaGlnArgLeuAlaGlyAla 41
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Computer based methods for the mouse full-length cDNA
Computer based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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Ratio: 4.561
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Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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//dev_stage="12 days embryo"
/lab_host="psinal"
/lab_host=
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spinal ganglion"
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/db_xref="taxon:10090"
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., It
Carninci,P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jar
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Jyg-MC(B) CDNA Mus musculus CDNA clone G930033J21 3', mRNA sequence.
                                                        Quality:
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computer-based methods for the mouse full-length cDNA
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182.00
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                                                                                                                                                                                               /tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
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                                                                                                                                                                                                                                                                                                                                                                                 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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Carninci, P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Tanaka,T., Matsuu
%S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                               Computer-based methods for the mouse full-length cDNA
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full-length enriched, mammary gland RCB-0527
Mus musculus cDNA clone G930013K04 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                       German ververs available. No s1 sequence available in This clone (DKFZp313J1040) is available at the RZPD in This clone (DKFZp313J1040) Ressourcenzentrum, Heubnerweg Please contact the RZPD: Ressourcenzentrum, CHEMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                       Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5 sequence of the clone insert
Clone from 5. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz heidelberg.de;
sequenced by GBF (Mational Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL601246 430 bp mRNA linear EST 14-AUG-2001 DKFZp313J1040_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone DKFZp313J1040 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                                                                                     German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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4.195
97.619
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RCB-0527 Jgg-Mc(B) _CDNA"
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_cell_line="RCB-0527 Jyg-MC(B)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 1
Percent Identity: 83.333
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ORIGIN
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AUTHORS
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US-08-973-363-7 x AL601246
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LOCUS A1890775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est1:AI890775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nlh.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html

Insert Length: 1924 Std Error: 0.00
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                                                                                                                                                                                                                                                                          High quality sequence stop: 418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa: Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 547)
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                                                                                                                                                                                                                                                                                                    Seq primer:
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81 c 86 g 100 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170.00
4.359
95.122
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                    -40UP from Gibco
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REFERENCE
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ORGANISM
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US-08-973-363-7 x AI890775/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAAACAGTTGCAGAC
                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                 HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3952
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU125712 NT2RW4 Homo sapiens cDNA clone NT2RW4002061 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                  Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 866)
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                    312
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/cell_line="NY2"
/note="Vector: pME18SFL3; mRNA
precursor cells"
a 149 c 196 g 207 t
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4.359
95.122
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                                                                                                                                                                                                              Location/Qualifiers
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Gaps:
t Identity:
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                  2 others
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                                                       NT2 neuronal
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BASE COUNT
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    Quality:
                                                   alignment_scores:
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US-08-973-363-7 x AU125712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
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Percent Similarity:
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TITLE
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                                                                                                                                                                                                                                                                                                                      source
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM9753 row: h column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BEB95133 1028 bp mRNA linear EST 20-OCT-2000 601436060F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3921087 5',
                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE895133.1 GI:10358221
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BE895133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                         387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU125712
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Site_2: Sall; Cloned unidirectionally. Primer: O
Average insert size 2 kb. Library constructed b;
Technologies."
3 205 c 238 g 198 t
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170.00
4.359
95.122
                                                                                                                                                                                                                                              /clone_lib="NIH_MGC_72"
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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alignment_block:

US-08-973-363-7 x BE895133

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alignment_block:
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                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei,
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 856)
Roest-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNSO4DVG 856 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 103KOB of library G from Tetraodon nigroviridis, genomic survey
                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                              84
                                                                                                                                                                                                                   /organism="Tetraodon nigroviridis"
//db.wef="taxon:99883"
//clone="103068"
/clone=1ib="0"
/note="Genoscope sequence ID : COBG103BF04LP1-end : T7"
a 308 c 252 g 206 t 6 others
                                                                154.00
4.400
89.744
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                                                             Percent Identity: 79.487
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LOCUS BF239967
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                                                                                                                             Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 laGlnArgLeuAlaGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnThrAr 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 821)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                Quality:
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Plate: LLCM1033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                      Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                            /Clone=InMcE:133129"
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/Clone=Lib="NIMCE:4133129"
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/lab_host=Dh10b (T1 phage-resistant)"
/lab_host=D
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4.206
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/db_xref="taxon:9606"
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                                                                                                                             Percent Identity: 83.333
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LOCUS AW996787
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                                                                           alignment_scores:
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             Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 337)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., da Silva, W. Jr., Katsukuma, A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-23&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was derived from the FAPESP/LICR Human Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence start: 2 quality sequence stop: 337
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                                                                                                                                                                                                                            /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORBSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
         133.50
3.926
94.444
                                                                                                                                                                low stringency conditions."
59 c 72 g 123 t
                                                                                                                                                                                                                                                                                                                                               /clone_lib="BN0047"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                            tissue mRNA and cDNA amplification were
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
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Length: 36
Gaps: 2
Percent Identity: 83.333
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BN0047 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer Genome
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alignment_block:
US-08-973-363-7 x AW996787/rev
ORIGIN
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LOCUS AW997058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est1:AW997058
                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 CCGTGCAGACTATCTCATCAATACTT...AGTAGAGATCTTGCAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                                                                                                                                                                                                                                                                                                                                                             This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV3-BN0047-15040-152-c03&t3=2000-04-15&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 686)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Saares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 19 High quality sequence stop: 678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tags
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                      /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                 tissue mRNA and cDNA amplification were performed low stringency conditions."
154 c 126 g 241 t
                                                                                                                                                                                                                /dev_stage="Adult"
                                                                                                                                                                                                                                            /clone_lib="BN0047"
                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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JOURNAL
REFERENCE
AUTHORS
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TITLE
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COMMENT
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
alignment_scores:
Quality: 124.00
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US-08-973-363-7 x AW997058/rev
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Quality: 127.00
Ratio: 3.629
Percent Similarity: 100.000
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ORIGIN
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                                                                                                                                                                                                                                                                                              FEATURES
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Genoscope.

Genoscope.

Birect Submission

Direct Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL352664.1 GI:8246657
GSS; genome survey sequence.
GSS; genome survey sequence.
Tetraodon nigroviridis.
Eukaryota, Meracoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygli; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 1122)
1 (bases 1 to 1122)
1 Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Neissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS05T9J 1122 bp DNA linear GSS 26-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 042M09 of library C from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 1122)
Roest-Crollius,H., Taillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetrackon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1122)
                                                                                                                              303
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/db_xref="taxon:99883"
/clone="042M09"
/clone="11b="C"
/note="Genoscope sequence ID : COBC042AG05C1-end :
a 260 c 301 g 246 t 12 others
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Gaps: 0
Percent Identity: 82.857
     Length:
     29
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Ratio: 4.276 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 79.310
alignment_block: US-08-973-363-7 x CNS05T9J ...
Align seg 1/1 to: CNS05T9J from: 1 to: 1122
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9b_pat: AX333515

9b_pr: AF006514

9b_ht; AC087641

9b_ht; AC074383

9b_ht; AC013394

9b_ov: AF060702

9b_in: CBH06001
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gb_htg:AC099067
gb_htg:AC099350
gb_htg:AC099350
gb_ba:AE006433
gb_ba:AF157835
gb_htg:AC095510
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gb_px:AC026778
gb_px:AC022121
gb_htg:AC092382
gb_ov:D14316
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9b_in:AC007765
9b_in:AC092187
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gb_pr:AC092372
gb_pr:AC012624
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-MODEL-frame+_p2n.model -DEV-xlh
-O-/Cgp2_1/USPTO_SpOOl/US08973363/runat_01082002_080050_18581/app_query.fasta_1.638
-O-/Cgp2_1/USPTO_SpOOl/US08973363/runat_01082002_080050_18581/app_query.fasta_1.638
-DB-GenEmbl -OFWT-fastap -SUFFIX-p2n.rge -GAPOP-12.000
-GAPEXT-4.000 -FINNATCH-0.100 -LOOPCLS-0.000 -XGAPEXT=0.000
-OGAPOP-4.500 -OFAPEXT-7.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTPMT-pfs
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US08973363 @CCN1_1_4551 -MCDU-6 -LCPU-3 -LONGLOG
-DEV_TIMEOUT-120 -MARN_TIMEOUT-30 -NO_XLPXY -MAIT -THREADS-1
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Query: US-08-973-363-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database: GenEmbl:*
Database sequences: 1797656
Database length: 1873333701
Search time (sec): 4907.710000
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Database: GenEmb
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gb_pat:A58686
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       3. 9e-21

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1431 | AC09967 Rattus morvegicus

1422 | AC099950 Rattus morvegicus

1421 | AC099350 Rattus morvegicus

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1450 | AE08510 Rattus morvegicus

1451 | AE06510 Rattus morvegicus

1451 | AE06510 Rattus morvegicus

1451 | AC094708 Rattus morvegicus descriptions
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LOCUS
A58691
DEFINITION Sequence 10 fr.
ACCESSION A58691
VERSION A58691.1 GI:3
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified
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gb_htg:AC101378.
gb_ov:OTU89945
gb_pat:AX286188
gb_htg:LMFLCHR36_25
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AUTHORS
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US-08-973-363-8 x A58696
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Location/Qualifiers
1. .1316
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/db_xref="taxon:32644"
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
Patent: WO 9639505-A 10 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
                                                                                                        1 (bases 1 to 6608)
Griffiths, R, and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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LOCUS AF004397
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1 (bases 1 to 6872)

1 (bases 1 to 6872)

A CHD1 gene 1s Z chromosome linked in the chicken Ga Gene 197 (1-2), 225-229 (1997)

97473516
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AF004397.1
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/db_xref="GI:2501846"
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LKKQQQQQKAAASSDSGSEEDSSSSEDSADDSSSETKKKHKDEDWQMSGSGSVSGTGS
                                                                                                                                                                                                 /gene=
228. .
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1207 c 1459 g 165
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protein"
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1. .6872
                                                                                                                                           /function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
                                                                                                                              /codon_start=1
                                                                                                                                                                                   /gene="CHD-Z"
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                                              1 (bases 1 to 153)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                                                                                                                                                                                Sequence 3 from Patent W09639505
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LHKELEPFELLBRYKKOVEKSLPAKVEQLILMENBALQKOYKWILTRNYKALSKOSKG
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STSGFLNIMMELKKCCNHCYLIKPPDDDEFYNKOBALQHLIRSSGKLILLDKLLIRLR
ERGNRYLIFSQWYMADILAEYLKYROPFFQRLDGSIKGELKQALDHFWABGSEDFC
FLLSTRAGGIGINLASADTVYLFDSDWNPONDLQAQARHTIQKKOVANYYRLYTKGS
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NKEKRENKVKESTQKEEKVNEMKSENKEKKKKIPLLDTPVHITATSEPVDISE
WO 9639505-A 3 12-DEC-1996;
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AHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKD
CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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HRSPFEHSSDHKSTPEHTWSSRKT"
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MIRTHEWMHPQTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGVDEAHRLKNDDSLLY
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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THVIRNPDVERLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKRPY
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101 AATTACTGAATAAAGACCTTGCAAGAAAGAAAGAACAACAAGCACTTCCTGCT 1.50
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Other publication AU 5906996 961224.
Cocation/Qualifiers
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Griffiths, R, and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unidentified
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/db_xref="taxon:32644"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 5349)
Delmas, Y., Stokes, D.G. and Perry, R.P.
A mammalian DNA-binding protein that contains a chromodomain and an SNF2/SWIZ-like helicase domain
Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced g1:293322.
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NNIRTHSWALSKGSKRENGLIST INPEKTSSWEDFEEHGKRERGYGK
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TLEFERNKSKENGEIT DEEGTRKLEEEEERGKELEETYMLFRANKELASLILKFGAB
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SKERYGGSUSDSISERKREKRGRPRTTPRRNIKGFSDAEIRRFKSKAGTKWOTSTROESGERBR
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SDSESEEERDKSSCDGTESDYEPKNKVRSRKPQNRSKSKNGKKILGQKKRQIDSSEDE
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US-08-973-363-8 x MUSCHD1X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_pat:A58686
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Ratio: 4.561
Percent Similarity: 100.000
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                                       Align seg 1/1 to: A58686 from:
                                                              US-08-973-363-8 x A58686
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IleLeuProAspAspProAsp
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Ratio:
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
BIRDS
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Sequence 5 from Patent W09639505.
A58686
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1 1067 c 1319 g 1224 t
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/db_xref="taxon:32644"
34 c 31 g 2
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US-08-973-363-8 x A58683
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                                                                          gb_pr:AF006513
Homo sapiens CHD1 mRNA, AF006513
AF006513.1 GI:2645428
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Sequence 2 from Patent W09639505.
A58683
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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Align seg 1/1 to: AF006513 from: 1 to: 5947
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                                                                                           Quality:
Ratio:
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RASSSGPRSPLDQRSYGSRSPFEHSVEHKSTPEHTWSSRKT"
1 1004 C 1243 G 1570 t
                                                                                                                                                                                                                                     KLYKHAIKKRQESQQNSDQNSNLNPHVIRNPDVERLKENTNHDDSSRDSYSSDRHLTQ
YHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHRDWDHYKQDSRYYSDREKHRKLDDH
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/db_xref="taxon:9606"
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/db_xref="GI:2645429"
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                                                                      Length: 41
Gaps: 1
Percent Identity: 85.366
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26932 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 26883
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                                                                                                                                                                                                                 Quality:
Ratio:
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US;
3 (Dases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624. The number of bases overlapped is 90404.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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DOE Joint Genome Institute.
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/clone="RP11-58M12"
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                                                                            34 luAlaGlnArgLeuAlaGlyAla 41
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                                                                                                                                                    rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
                                        AAGCT.....CTTTCTGGTGCG 118363
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-JUI-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 21, 2001 this sequence version replaced gi:14277267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mit Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 131365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens clone RP11-58M12, V
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                                                                                                                                                                                                                                                                                                                                                                                          * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: project Information
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Center clone name: 58_M_12
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38821 38920: contig of 38820 bp in length
38821 38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
40412 40511: gap of 100 bp
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J., Barna, N., Beckerly, R., Beda, F.,
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alignment_block:
US-08-973-363-8 x AC021449
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seq_name: gb_htg:AC008531
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                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AC021449 from: 1 to: 143079
                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 170.00
Ratio: 4.359
Percent Similarity: 95.122
                                                                                                                                                                                                                       116147 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAACAGTTGCAGAC 116196
                                          116247 AAGCT.....CTTTCTGGTGCG 116263
                                                                                                                                  116197 CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAAAAAG 116246
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                                                                                     34 luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                          17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                                                                                                                                                                                  1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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43280 43379: gap of 100 bp
43380 46905: contig of 3526 bp in length
46906 47005: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment" 75509 ..92516
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1 26246 c 26678 g 45278 t
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/note="assembly_fragment"
/note="assembly_fragment"
106510 .143079
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51931. .62619
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47006. .51830
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43380. .46905
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clone_end:SP6
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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1. .38820
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 41
Gaps: 1
Percent Identity: 85.366
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BASE COUNT
ORIGIN
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AUTHORS
TITLE
JOURNAL
REFERENCE
alignment_scores:
Quality: 170.00
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                      Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q20
Consensus quality: 14374 bases at least Q20
Consensus quality: 14374 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; sum-of-contigs estimation
Quality coverage: 6.4 in Q20 bases; sum-of-contigs estimation
**NOTE: This is a "working draft' sequence. It currently
**consists of 7 contigs. Gaps between the contigs
**are represented as runs of N. The order of the pieces
**is believed to be correct as given, however the sizes
**of the gaps between them are based on estimates that have
**provided by the submittor.

**This sequence will be replaced
**by the finished sequence as soon as it is available and
**the accession number will be preserved.

**56175 56274: gap of unknown length
**100975 110327: contig of 44600 bp in length
**11328 118190: contig of 12153 bp in length
**11328 118190: gap of unknown length
**11328 118190: gap of unknown length
**118291 119694: contig of 4963 bp in length
**118291 119694: contig of 3503 bp in length
**113298 123397: gap of unknown length
**113298 123397: contig of 3503 bp in length
**113298 12397: contig of 3503 bp in length
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 145659)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced gi:7528342.
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Center Code: JGI
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DOE Joint Genome Institute.
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                                                                                                                                                                42561 a
                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="07C-480B11"
/clone="07C-480B11"
/clone="07C-480B1 human BAC library C"
/clone_lib="07B17E6h human BAC 1600 others
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
       Length:
       41
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TITLE
JOURNAL
REFERENCE
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AUTHORS
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ORGANISM
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VERSION
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US-08-973-363-8 x AC008531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_htg:AC091946
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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                                                                                                                                                         Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q30
Consensus quality: 184175 bases at least Q30
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; agarose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC091946 bp DNA 193446 bp DNA Homo sapiens chromosome 5 clone RP11-36012, PROGRESS ***, 33 unordered pieces.
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Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 193446)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: RPCI-11_36012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Project Information
Center Project Name: 544799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                        as soon as it is available and the accession number will be preserved.
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    1359
1459
2668
2768
3824
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95.122
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1358: contig c
1458: gap of c
2667: contig c
2767: gap of c
3823: contig c
3923: gap of c
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79795: contig of 5563 bp in length
79895: gap of unknown length
87511: contig of 7616 bp in length
87611: gap of unknown length
92791: contig of 7818 bp in length
92891: gap of unknown length
102794: contig of 9903 bp in length
102894: gap of unknown length
110866: contig of 7972 bp in length
110966: gap of unknown length
117571: contig of 6605 bp in length
117671: gap of unknown length
117671: gap of unknown length
123738: contig of 6605 bp in length
133838: gap of unknown length
130683: contig of 6745 bp in length
141544: contig of 10861 bp in length
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169109: contig of 7465 bp in length
169209: gap of unknown length
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of 1487
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US-08-973-363-8 x AC026778/rev
                                                          alignment_scores:

Quality: 170.00 Length: 41

Ratio: 4.359 Gaps: 1

Percent Similarity: 95.122 Percent Identity: 85.366
                                                                                                                                                                                     BASE COUNT
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LOCUS AC026778
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US-08-973-363-8 x AC091946
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                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:13677045.
Draft Sequence Produced by DOE Joint Genome Institute
WWW.jg1.doe.gov
Finishing Completed at Stanford Human Genome Center
WWW-Slgc.stanford.edu
Ouality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
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HOMO Sapiens chromosome 5 clone CTC-428I11, complete sequence
AC026778
AC026778.4 GI:14277282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 195433) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 195433)
DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens
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a 37302 c 37040 g 58329 t
                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .195433
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Signal gogdata/hold-genesed/geneseqn-embl/NA1997. DAT:ANT42754 + 205.00 533.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA1997. DAT:ANT42751 + 205.00 537.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA1997. DAT:ANT42757 + 190.00 531.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA1997. DAT:ANT42755 + 190.00 531.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA1997. DAT:ANT42756 + 112.00 531.0
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SIDS1/gogdata/hold-genesed/geneseqn-embl/NA2001A.DAT:ANT42756 + 122.00 330.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA2001A.DAT:ANT59538 + 122.00 330.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA2001A.DAT:ANT59530 + 122.00 330.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA2001A.DAT:ANT59530 + 122.00 330.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA2001A.DAT:ANT59507 + 50.00 141.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA2001A.DAT:ANT59507 + 50.00 142.0
SIDS1/gogdata/hold-genesed/geneseqn-embl/NA2001A.DAT:ANT59507 + 50.00 142.0
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Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 523.620000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search information block:
Query: US-08-973-363-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters:
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-Q-(cgn2_1/USPT0_spool/US08973353/runat_01082002_080050_18606/app_query.fasta_1.638
-Q-(cgn2_1/USPT0_spool/US08973353)runat_01082002_080050_18606/app_query.fasta_1.638
-DB-M_Geneseq_032802 -OFMT-fastap -SUEFIX-p2n.rug -GAPOP=12.000
-GAPEXT-4.000 -MINMATGH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-QGAPOP-4.500 -GAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXY-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40 -Cdi -LIST-45 -DOCALIGN-15 -MODE-LOCAL -OUTFMT-pfs
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-20000000
-USER-US08973363-QCG11_1 186 -NCPU-6 -ICPU-3 -LONGLOG
-USCR-US0873363-QCG11_1 186 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT-120 -WARIN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-973-363-8 to: N_Geneseq_032802:*
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US-08-973-363-8 x AAT42754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 205.00
Ratio: 5.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAT42754 from: 1 to: 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                                                                                                               17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
                                                                                                                                                                                                                                                                                                                              1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                 TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG
                                                                                                                                                                                                                                                                          ATTTTACCTGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGAC
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Length: Gaps: Percent Identity:

41 0 100.000

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seq_documentation_block:
ID AAT42754 standard; cD
XX AAT42754;
XX Chicken CHD-W gene (p
XX Chicken CHD-W gene (p
XX CHD-W; chromodomain-H
XX CHD-W; chromodomain-H
XX CHD-W; chromodomain-H
XX (ISIS-) ISIS INNOVATI
XX (ISIS-) ISIS INNOVATI
XX (ISIS-) ISIS INNOVATI
XX AVIAN Chromodomain-he
PA (ISIS-) used for sex
XX Claim 1; Fig 8; 76pp;
XX
XX The chicken CHD-W gen
CC The chicken CHD-W gen
CC The closely related of
CC The closely related of
CC Temale development in
CC from 2 clones isolate
CC a fragment of the CHD
CC a W chromosome-specif
CC nucleic acids can als
XX Sequence 1316 BP; 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAF90033 - 
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAF90032 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAF86431 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABI26659 + 
/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:AAS74806 +
                                                                        The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate femala development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tiwari B;
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42751

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seq_documentation_block:
ID AAT42751 standard;
                                                                              alignment_block:
US-08-973-363-8 x AAT42751
                                                                                                                                                             alignment_scores:
                                                   Align seg 1/1 to: AAT42751
                                                                                                                     Ratio:
Percent Similarity:
4080
                                                                                                                                                                                                                                       The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo CDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or 2 chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken CHD-1A gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1996;
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                                                                                                                                                                                                   Sequence 6608 BP; 2289 A;
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-043127/04
                                                                                                                                                                                                                             acids can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ISIS-) ISIS
              IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
 ATTTTACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex determination; chromodomain-Helicase-DNA binding
; chromodomain-Helicase-DNA binding on the W chromosor
                                                                                                                                                                                                                                                                                                                                                                                                                       chromodomain-helicase-DNA binding genes determine sex
                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                     used
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                                                                                                                                                                                                                                                                                                                                                                                                                     for sex determn. and
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                                                     from: 1
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                                                                                                                                                                                                                             control the sex of the progeny of a bird
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rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG

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seq_documentation_block:
ID AAT42757 standard;
                                             alignment_block: US-08-973-363-8
                                                                                                                                                       seq_name:
                                                                                                                  alignment_scores:
                      Align seg 1/1
                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW81467-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                    Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHD-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chick CHD-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT42757;
                                                                                                                                                       Sequence 153 BP;
                                                                                                                                                                                                                                                                                                                                                                                  Griffiths
                                                                                                                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS INNOVATION LTD
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1 IleLeuProAspAspProAsp..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42757
                                                                                                                                                                                                                                                                                                                                                         1997-043127/04.
                                                                                                                                                                                                                                                                                                             chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex determination; chr
A; CHD-W; W chromosome;
                                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 153
                                                                                                                                                                                                                                                                                                                                                                                  R,
                       to:
                                               ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                           for sex
                                                                                                                                                                                                                                                                                                                                                                                  Tiwari
                                               AAT42757
                       AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                 95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 52..81
                                                                                190.00
4.634
80.392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                       58 A; 40 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment
                                                                                                                                                                                                                                                                                                           determn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromodomain-Helicase-DNA binding
                       from:
                                                                                Percent
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                                                                                                                                                     31 G;
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                                                                                Gaps:
Identity:
                       to:
                                                                                                                                                       24 T; 0 other;
                       153
                                                                                 80.392
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alignment_scores:
Quality:
Ratio:
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                                                                                  Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW04136-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo,
                                                                                                                                                                                            Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101
                                                                                                                                                                       Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
                                                    Sequence 153 BP; 56 A; 36 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42758
                                                                        to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 52..81
 190.00
4.634
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"bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                      31
                                                     G; 30 T; 0 other;
Length:
Gaps:
 51
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amino
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seq_documentation_block:
ID AAT42759 standard; DN
XX
AC AAT42759; .
XX
AC AAT42759; .
XX
AC AAT42759; .
XX
CHD-1A; CHD-W; W chrc
XX
Bird; sex determinati
KW CHD-1A; CHD-W; W chrc
XX
Parus major.
XX
Parus major.
XX
FT misc_difference 52..
FT wisc_difference 52..
FT wisc_difference 52..
FT woods 9505-A1.
XX
12-DEC-1996.
XX
VO9639505-A1.
XX
12-DEC-1996; 956W0-(
XX
XX
(ISIS-) ISIS INNOVAT
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(ISIS-) ISIS INNOVAT
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(ISIS-) ISIS INNOVAT
XX
PN Griffiths R, Tiwari
XX
PH; 1997-043127/04.
DR P-BSDB; AAW06149.
XX
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CIaim 8; Fig 3; 76pp
XX
Claim 8; Fig 3; 76p
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US-08-973-363-8 x AAT42758
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   Bases 3855-3977 (AAR142756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAR14757), chicken CHD-W (W refers to the W chromosome) gene (AAR142758) and and the great tit CHD-W gene (AAR142759). Translated amino acid sequences of this region are provided in AAW041464-49. The CHD-1A (see also AAR142751) and CHD-W (see also AAR14754) genes determine sex in birds and can be used to identify the sex of an embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird; sex determination; chromodomain-Helicase-DNA CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                              Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                 Claim 8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 Ala 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 IleLeuProAspAspProAsp......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATTTTACCTGATGATCCAGATAAGAAACCCCAGGCTAAGCAGTTACAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                1997-043127/04.
DB; AAW08149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-GB01341
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amino
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Sequence 153

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foetus etc. and

to manipulate the

sex of progeny.; 29 T; 0 other;

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alignment_block:
US-08-973-363-8 x AAT42759
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Quality:
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ID AAT42756 standard;
                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42756
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 Claim
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                                                                            Griffiths R,
                                                                                                                                      05-JUN-1996;
                                                                                                                                                         12-DEC-1996
                                                                                                                                                                            W09639505-A1
                                                                                                                                                                                                                                     misc_difference
                                                                                                                                                                                                                                                                  Mus sp
                                                                                                                                                                                                                                                                                     CHD-1;
                                                                                                                                                                                                                                                                                             Bird; sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                               Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                   12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 AATTACTGAATAAAGACCTTGCAAGAAAAGAAGTGCAAAGACTTACTGGT 150
                                                 P-PSDB;
                                                         WPI; 1997-043127/04.
                                                                                                (ISIS-) ISIS
                                                                                                                   06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity:
                   chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
8; Fig 3;
                                                                                                                                                                                                                                                                                     CHD-W; W chromosome;
                                                 AAW08146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                 INNOVATION LTD
                                                                              Tiwari
                                                                                                                   95GB-0011439
                                                                                                                                     96WO-GB01341
                                                                                                                                                                                                                         Location/Qualifiers 52..81 /*tag= a
76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.392
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4.439
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                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                            "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                         153
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                                                                                                                                                                                                                                                                                     SS.
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t Identity:
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amino
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seq_documentation_block:
ID AAV59280 standard; cDNA;
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US-08-973-363-8 x AAT42756
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                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:AAV59280
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 a Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW408146-49. The CHD-14 (see also AAT42751) and CHD-W (see also AAW42754).
                               04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                                                Homo sapiens Synthetic.
                                                                                                                                                                                                                                ds; human; telomere repeat binding factor; A-TRF; dimerisation domain; telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                                                                                                                                                                                                                                                                             14-DEC-1998
                                                                  13-FEB-1998;
                                                                                          20-AUG-1998
                                                                                                                WO9836066-A1
                                                                                                                                                                                                                                                                   Altered telomere repeat binding factor 1 gene
                                                                                                                                                                                                                                                                                                                    AAV59280;
                                                                                                                                                                                                                                                                                                                                                                                                   151 GCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 153 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the sex of an embryo, foetus etc. and to manipulate the sex of
         (UYRQ ) UNIV ROCKEFELLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL
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                               98US-0018628
97US-0800264
                                                                   98WO-US02765
                                                                                                                                      /*tag= a
/product= "A-TRF"
                                                                                                                                                              Location/Qualifiers
1..1311
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4.195
80.392
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                                                                                                                                                                                                                                                                                           entry)
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Percent Identity:
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70.588
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seq_documentation_block:
ID AAK88882 standard; cD
XX
AC AAK88882;
XX
C5-NOV-2001 (first e
XX
W1 Human digestive syste
XX
W1 Human; digestive syste
XX
W1 digestive system diso
XX
W2-NOV Sapiens.
XX
PN W0200155314-A2.
XX
PD 02-AUG-2001.
XX
PP 17-JAN-2001; 2001W0-U
XX
PP 17-JAN-2000; 2000US-0
PR 04-FEB-2000; 2000US-0
PR 16-MAR-2000; 2000US-0
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US-08-973-363-8 x AAV59280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOX CCCCCCCCCCCXXXIII
                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK88882
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Ratio: 5.160
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1287 CCGTGCAGACTACCTCATCAAACTA 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The altered vertebrate telomere repeat binding protein (A-TRE) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRE, preventing it from binding to the specified repeat sequence. A-TRE, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                   Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; meckel's diverticulum; ss.
                                                                                                                                                                                                                                                                                Human digestive system antigen coding sequence SEQ ID NO: 1198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW59280.
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                                                                                               17-JAN-2001; 2001WO-US01324.
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 2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
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Gaps: 0
Percent Identity: 100.000
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   17-MAR-2000;
18-APR-2000;
2000US-0198076
2000US-0198075
2000US-0205515
2000US-0205515
2000US-0205515
2000US-0216880
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2000US-0217496
2000US-0225215
2000US-0225215
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2000US-0225216
2000US-0225217
2000US-0225275
2000US-0225275
2000US-0225277
2000US-0225277
2000US-0225477
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08-NOV-2000
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08-NOV-2000
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17-NOV-2000
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08-NOV-2000;
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08-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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                                             Claim 1;
                                                                                            digestive system, particularly
                                                                                                              Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders o
                                                                                                                                                                                                                                                                    Rosen
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B; AAM93109.
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2000US-0241785
2000US-0241785
2000US-0241808
2000US-0241808
2000US-0244617
2000US-0246475
2000US-0246476
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2000US-0246476
2000US-0246476
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2000US-0249216
2000US-0249264
2000US-0249264
2000US-0249264
2000US-0251988
2000US-0251989
2000US-0251989
2000US-0254097
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                                          986pp;
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                                                                                            cancer and
                                             English
                                                                                            cancer
                                                                                            metastases
                                                                                                                of
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The present invention provides the protein and coding sequences

of

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alignment_scores:
    Quality:
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ID AAI57603 standard; cDNA; 421 BP
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31-JAN-2000
04-FEB-2000
24-FEB-2000
02-MAR-2000
11-MAR-2000
11-MAR-2000
11-APR-2000
07-JUN-2000
07-JUN-2000
07-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digest.
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2000US-0189874.

2000US-0190076.

2000US-0198123.

2000US-0205515.

2000US-0205467.

2000US-0215135.

2000US-0215135.
2000US-0216880.

2000US-0217487.

2000US-0217496.

2000US-0218290.

2000US-0220963.

2000US-0220964.

2000US-0224518.

2000US-0224519.
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2000US-0184664
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Gaps:
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14 - AUG - 2000; 14 - AUG - 2000;

2000US-0225213 2000US-0225214

2000US-0225266 2000US-0225267 2000US-0225270 2000US-0225477 2000US-0225757 2000US-0225757 2000US-0225759 2000US-0225759 2000US-0225729 2000US-02256881 2000US-02258681 2000US-02258681 2000US-02258681 2000US-02258681 2000US-02258681 2000US-02258681 2000US-0227182 2000US-0227182 2000US-0227183 2000US-02293843

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alignment_scores:
Quality:
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17-NOV-2000
17-NOV-2000
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01-DEC-2000
05-DEC-2000
05-DEC-2000
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05-DEC-2000
06-DEC-2000
08-DEC-2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of a number of colorectal cancer antigens. These are shown in AAAIS7619 and AAM38569-AAM38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or rectum. The present sequence is a colorectal cancer antigen coding sequence of the colon and the diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide for disorders related to the and also for testing and
                                                                                                                                                 The present sequence is a colorectal cancer antigen coding sequence of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08
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                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO: 67; 522pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-NOV-2000;
7-NOV-2000;
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-NOV-2000;
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DB; AAM38625.
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2000US-0246524.
2000US-0246525.
2000US-0246526.
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  Length:
Gaps:
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                                                                                                             other;
    35
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ID ABL06443 standard:
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US-08-973-363-8 x AAI57603
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                                                               capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL018/16-ABL30511), expressed DNA sequences (ABL018/16-ABL30511) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                      Claim 1;
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                                                                                                                                                                                                                                                                P-PSDB;
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11-JUL-2000;
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                                      The sequence data for this patent did not form specification, but was obtained in electronic:
                                                                                                                                                                                                                                                                                                                               (PEKE ) PE CORP NY
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1682 C;
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ID ABL06442 standard; cDNA;
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                                     specification,
                                                                          cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG11), expressed DNA sequences (ABLIG1840-ABLIG175) and the encoded proteins
                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling
                                                                                                                                                                                    Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                          New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                              WPI; 2001-656860/75
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                                                 The sequence data for this patent did not form
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11-JUL-2000;
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Sequences AAS59506-AAS59804 represent DNA molecules encoding propionibacterium acmes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acmes. The disorders include SAPHO syndrome (synovitis, acme, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acmes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acme vulgaris. A method for detecting the presence or absence of P. acmes in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds
                                                                                                                                                                                         Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris -
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                                                                                                                                                            Claim 1; SEQ ID No 85; 1069pp; English.
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, Jen S, Carter D;
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seq_documentation_block:
ID AASS6071 standard; cDNA; 1908 BP.
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26-FEB-2002 (first entry)
XX

DT 26-FEB-2002 (first entry)
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Leishmania antigen 4G2-83 extended:
XX

Leishmaniasis; Leishmania antigen; Lbhsp63
XW MAPS-lA; LmgSP3; LugSP3; LugSP
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leishmaniasis; Leishmania antigen; immunostimulant; protozoacide; Ldp23; interleukin-15; PCR primer; Lbhsp83; M15; Lt-1; LbeIFP4A; Lmsp1a; Lmsp9a; MAPS-1A; LmgSP1; LmgSP3; LmgSP5; LmgSP8; LmgSP9; LmgSP13; LmgSP19; ss; LcgSP1; LcgSP3; LcgSP4; LcgSP8; LcgSP10; IG6-34; 1E6-44; 4A5-63; 1B11-39; 2A10-37; 4G2-83; 4H6-41; 8G3-100.
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Percent Similarity:
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                                                                                                                                                                                                                                                                                         subunit vaccine; nucleic acid immunisation; gene therapy; genetic disease; hemophilia; cystic fibrosis; cancer; viral infection; acquired immune deficiency syndrome; PAV antigen; porcine pathogen; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polypeptides comprising an immunogenic part of a Leishmania antigen. The Leishmania polypeptides and their associated DNA sequences, epitopes and fusion proteins are used in the production of compositions used for inducing a protective immune response against leishmaniasis, for prevention and treatment of the disease. The compositions can also be used generally to treat diseases that respond to interleukin-15 stimulation. In addition, the products may contain an immunostimulant. The sequences represent cDNA molecules encoding Leishmania antigens and PCR primers used to amplify DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402
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New nucleic acids from the genome of porcine adenovirus-3, gene therapy vectors, particularly for immunization
                                                                                                                                                                                                    21-OCT-1999
                                                                                                                                                                                                                                  W09953047-A2
                                                                                                                                                                                                                                                              Porcine adenovirus
                                                                                                                                                                                                                                                                                                                                        PAV-3;
                                                                                                                                                                                                                                                                                                                                                                 Complete nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA230163 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 CTTCCTGATCAACCTGATCGACTCCCCCGGACACGTCGACTTCAGCTCCG
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                                                WPI; 1999-620422/53
                                                                                                                                          15-APR-1998;
                                                                                                                                                                        15-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                               26-JAN-2000 (first entry)
                                                                                                          (UYSA-)
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                                                                                                                                                                                                                                                                                                                                     defective recombinant PAV vector; live recombinant virus;
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                                                                              Babiuk LA;
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seq_documentation_block:
ID AAX39679 standard; DN
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AC AAX39679;
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DT 02-JUL-1999 (first e
XX
Cancer associated ant
XX
Cancer associated ant
XW breast cancer; colon
KW prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN W09904265-A2.
XX
PD 28-JAN-1999;
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PD 28-JAN-1999;
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PF 15-JUL-1998; 98WO-U
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PR 12-JUN-1997; 97US-C
PR 17-JUL-1997; 97US-C
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US-08-973-363-8 x AAZ30163/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a defective recombinant PAV vector comprising inverted terminal repeats (ITR), packaging sequences and at least one heterologous nucleotide sequence (II), but lacking El functions. The defective vectors replicate inefficiently in cells (other than helper cells) so are unlikely to be immunogenic. Deletion of the El (and optionally other regions) increases the size of heterologous insert that can be packaged. The PAV-3
                                                                                                                                                                                                                                                                     Cancer associated antigen; diagnosis; research; treatment; breast cancer; colon cancer; gastric cancer; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the complete nucleotide sequence genome of porcine adenovirus-3 (PAV-3). The specification also degenome of porcine adenovirus-3 (PAV-3).
                                                                                                                                                                                                                                                                                                                                Renal cancer associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX39679 standard; DNA;
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      98US-0102322.
97US-0896164.
97US-0061599.
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alignment_scores:
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US-08-973-363-8 x AAX39679
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Ratio: 2.130
Percent Similarity: 75.000
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                                                                                                                                                                                                                                        The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnostis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
                                                                                                                    1761 GTTTGAGAACCTCTGCAAAATCATG...AAAGACATATTGGAGAAAAAAG 1807
1808 TGAAAAGG 1815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
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                                                                                                                                                     18 gAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysGluA 35
                                                     35 laGlnArg 37
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97US-0948705.
97GB-0021697.
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Percent Identity: 30.556
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J, Stockert E;
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Database length: -1841457050
Search time (sec): 4390.400000
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Query: US-08-973-363-8
Query length: 41
Database: EST:*
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-Co-/cgn2_1/USSP0_spool/US0897363/runat_01082002_080049_18570/app_query.fasta_1.638
-DB-EST -OFM-fasta_ SUFFIX-P2n.rst -GAPOP-12.000 -GAPEXT=4.000
-MINMATCH-0.100 -LOOPEL-0.000 -LOOPEXT=0.000 -GAPDOP-6.000
-GAPEXT=0.050 -XGAPOP-10.000 -XGAPEXT=0.500 -FGAPOP-6.000
-GAPEXT=7.000 -YGAPOP-10.000 -XGAPEXT=0.500 -DELOP-6.000
-BELEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500 -DELOP-6.000
-BELEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500 -DELOP-6.000
-BELEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500 -DELOP-6.000
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-BELEXT=5.000 -YGAPOP-10.000 -YGAPEXT=0.500 -YGAPOP-10.000
-NUNLEN-10.0000000 -USER-US0897365_@CGN1_1_2938
-NCPU-6 -ICPU-3 -LONGLOG -DEV_TIMEOUT-120 -WARR_TIMEOUT-30
-NO_XLPXY -WAIT -THREADS-1
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AL336703 Tetraodon nigroviridi
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gb_est2:BM185888
gb_est2:BM070535
gb_est2:BM024825
gb_est2:BM185005
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alignment_block:
US-08-973-363-8 x AL659353/rev
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246 AAGCACAAAGACTTTCT 230
                                                                                                                                                             296 CAGAGCTGACTACCTCATTAAACTTCTCAATAAAGATCTGCTTAGGAAAG
                 34 luAlaGlnArgLeuAla 39
                                                                                                  17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
                                                                                                                                                                                 1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Silurana tropicalis
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_EEQUENCE_ID: TNeu045e20.sp6
Sequencing primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Huckle E
Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 593)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL659353 XGC-neurula Silurana tropicalis cDNA clone TNeu045e20 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL659353.1 GI:17672995
EST.
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/Ob_wref="taxon:8364"
/Clone="Theu045e20"
/Clone=lib="xGC-neurula"
/Glove_lib="xGC-neurula"
/Gev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/lab_host="Escherichia coli DH10B"
/lab_host="Poctor: PCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into PCS107 with EcoRI at the 5' end and NotI at the 3' end."

BEORI at the 5' end and NotI at the 3' end."
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Gaps: 0
Percent Identity: 94.872
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8 fv74a09.x1 z
5 fu99h05.x1 z
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5 fv16c08.x2 z
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LOCUS BB155356
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                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I., Alzaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp/
Carninci.p., Shibata.Y., Hayatsu.N., Sugahara.Y., Shibata.K., Itoh
M., Konno,H., Okazaki.Y., Muzamatsu.M. and Hayashizaki.Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake.S., Inoue.K., Togawa.Y., Izawa.M., Ohara.E.,
Watahiki.M., Yoneda.Y., Ishikawa.T., Ozawa.K., Tanaka.T., Matsuura
S., Kawai.J., Okazaki.Y., Muramatsu.M., Inoue,Y., Kira.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jaj
Tel: 81-45-503-9222
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On Jun 29, 2000 this sequence version replaced gi:8811286.

Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
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Arakawa,T., Carninci,P., Fukuda,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                            Division of Experimental Animal Research in Riken contributed to
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                                                                                                                                                                                                                                                                                                                                                                         mouse tissues
                                                                                                                                                        thymus
                                                                                                                                                                                                                 /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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   sequenced
                               SalI; Site_2:
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      Mouse
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BamHI; cDNA library was 
use Genome Encyclopedia
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seq_documentation_block:
LOCUS AL644594
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US-08-973-363-8 x BB155356
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                                                                                                                                                                                                                                          Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
                                                                                                                                   Sanger Xenopus tropicalis EST project 2001 TROPICALIS_SEQUENCE_ID: L1E1d12.plc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL644594 XGC-egg Silurana
                                                                                                                    Sequencing primer:
                                                                                                                                                                      Hinxton, Cambridgeshire,
Email: trop@sanger.ac.uk
                                                                                                                                                                                                           Sanger Centre
                                                                                                                                                                                                                             Contact: Huckle E
                                                                                                                                                                                                                                                                                                 Xenopodinae; Silurana.
1 (bases 1 to 645)
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                                                                                                                                                                                                                                                                                                                                                                    Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                                                                      western clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                         AL644594.1 GI:16796719
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                                                                                   constructed by Aaron M.
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                                                                                                 sequence is from a Xenopus Gene Collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
/db_xref="taxon:8364"
/clone=""""
                                                              Location/Qualifiers
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                                                                                                   (XGC) library
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REFERENCE
AUTHORS
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LOCUS BB461065
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US-08-973-363-8 x AL644594
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Ratio: 4.921
Percent Similarity: 97.436
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                                                                                                                                                                                                                                                                                                 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

RIKRN Mouse ESTs (Arakawa, T., et al. 2001)
AL Unpublished (2001)
On Jul 21, 2000 this sequence version replaced gi:9356558.
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Labboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB461065 TIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-thoring protein (CHD-1) mRNA, mRNA sequence.
Email: genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh Carninci,P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y. Muramatsu,M. and Hayashizaki,Y. Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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Arakawa, T., Carninci, P., Fukuda, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB461065.2 GI:16426612
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/note="Vector: pcS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5', end and NotI at by end"
125 c 156 g 141 t l others
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/dev_stage="egg"
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Gaps: 0
Percent Identity: 94.872
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alignment_block:
US-08-973-363-8 x BB461065
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Ratio: 4.561
Percent Similarity: 100.000
581 AGGCTCAGAGACTTTGTGGTGCG 603
                                                                                                                               531 CCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTTGCAAAAAGAG 580
                                                                                                                                                                                                                                                               481 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC 530
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                                                             34 luAlaGlnArgLeuAlaGlyAla 41
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,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Haysshizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Please visit c
further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pBluescript KS(+) after bulk excision from Lambda FLC I." a 130\ c 168\ g 151\ t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Site_1: Sal1; Site_2: BamH1; cDNA library was
/note="site_1: Sal1; Site_2: BamH1; cDNA library was
prepared and seguenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
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/clone_lib="RIKEN full-length enriched, 12 days embryo
spinal ganglion"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 87.805
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FEATURES
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                                                                                            alignment_scores:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., It, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)

wagi, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuu, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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BB834922 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) CDNA Mus musculus CDNA clone G930033J21 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                            Quality:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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URL:http://genome.gsc.riken.go.jp/
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/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
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alignment_block:
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Jyg-MC(B) cDNA N
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encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details. e mouse tissues.
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Normalization and subtraction of cap-trapper-selected cDNAs to
Prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                 Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 rArgAlaAspTyrLeuIleLysLeu.LeuAsnLysAspLeuAlaArgLys 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone inset of Clone from 5. Wateman, Molecular Genome Analysis, German Cancer Research Center (DRF2), Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (Mational Research Center for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Hominidae; Homo.

1 (bases 1 to 430)
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DK72p313J1040_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DK72p313J1040_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                                                                                          No s1 sequence available.
This clone (DKRZp313J1040) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
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RCB-0527 Jyg-MC(B) cDNA"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
generation of the control of the c
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4.195
97.619
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                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-08-973-363-8 x AL601246
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LOCUS AI890775
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                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wm95fil.xl NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHDL HUMAN 014646 CHROMODOMAIN-HELICASE-DNA-BINDING ARB90775
                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/tmage/image.html
Insert Length: 1924 Std Error: 0.00
Seq primer: -40Up from Gibbo
Seq primer: -40Up from Gibbo
Seq primer: -40Up from Gibbo
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
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1 (bases 1 to 547)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                        /Organism="Homo sapiens"
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/clone_lib="NCI_CGAP_Ut2"
/clone_lib="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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cDNA-collection"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                           Location/Qualifiers
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Gaps: 1
Percent Identity: 85.366
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US-08-973-363-8 x AI890775/rev
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LOCUS AU125712
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                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 2
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai,T.
HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai, Y., Sugano,S., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 866)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genomics@hri.co.jp
HRI human cDNA project; 5'-&3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                            /clone_lib="NT2RM4"
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/market
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/market
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/market
/ma
                                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 c
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85.366
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Nagai,T., Suzuki
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alignment_block:
US-08-973-363-8 x AU125712
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alignment_block:
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                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC
                                                                                                                                                                                                                                                                                                                                                                       source
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 1028)
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                        Ratio:
                                                                                                                                                                      387
                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 488.
Location/Qualifiers
                                                                                                                                                              'db_xref="taxon:9606"
'db_xref="taxon:9606"
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/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo c
Average insert size 2 kb. Library constructed by Life
Technologies."
a 205 c 238 g 198 t
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4.359
95.122
                                  170.00
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95.122
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                                                      Gaps:
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1
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US-08-973-363-8 x BE895133

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REFERENCE
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VERSION
alignment_block:
US-08-973-363-8 x CNS04DVG/rev
                                                                                                                                    alignment_scores:
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                                                                                                                                                                                                                                BASE COUNT
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                                                                Percent Similarity:
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostemi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tetraodontidae: Tetraodon.

1 (bases 1 to 856)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS04DVG 956 bp DNA linear GSS 21-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
103K08 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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4.400
89.744
                  Gaps: 0
Percent Identity: 79.487
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REFERENCE
AUTHORS
TITLE
alignment_block:
US-08-973-363-8 x BF239967
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                                                                                                                                                                                                                                                                                    BASE COUNT
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LOCUS BF239967
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                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 821)

NHH-MGC http://mgc.nci.nih.gov.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                            Quality:
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CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lnage.llnl.gov
http://lnage.llnl.gov
Plate: LLCM1033 row: k column: 18
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BF239967
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                                                                                                                                                                                                                                                                              /clone="IMAGE:4133129"
/clone_lib="NIH_MGC_54"
/clone_lib="NIH_MGC_54"
/tlssue_type="from chronic myelogenous leukemia"
/lab_host="DH1DB (Tl phage-resistant);
/nate="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (9gccgcctcggcc); Site_2: SfiI (9gccattaggcc);
); Double-stranded cDNA was prepared from cell line RNA.
); Double-stranded cDNA was prepared from dell line RNA.
); and 3' adaptors were used in cloning as follows: 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTANGGCC-3' and 3' adaptor
sequence: 5'-CACGGCCGATTG-GT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T): Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PGR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
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                                                                                     94.444
                                                                                                             143.00
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/db_xref="taxon:9606"
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                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                              Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=&t2=QV3-BN0047-230 200-102-d03&t3=2000-02-23&t4=1) Seq primer: puc 18 forward High quality secures:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Bilouco,K., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QV3-BN0047-230200-102-d03 BN0047 Homo sapiens cDNA,
                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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                                                                                                                                                                                         /note-*Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                tissue mRNA and cDNA amplification were performed low stringency conditions."
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E., García Correa, R., Verjovski-Almeida, S.,
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                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                               clone_lib="BN0047"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150 400-152-c03&t3=2000-04-15&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dias
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simpson, A.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)
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       165
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                                                                                                                                                                                                /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                     tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
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stringency conditions."
154 c 126 g 241 t
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AUTHORS
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VERSION
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US-08-973-363-8 x AW997058/rev
                         alignment_scores:
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ORGANISM
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                                                                                                                                      BASE COUNT
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Ratio: 3.629
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 ATTCTTCCAGATGATCCCGATAA.AAACCACAAGCAAAACAGTTGCAGAC 79,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 rargalaaspyyleuilelysleuienasniysaspleualaarstysg 34
18 rargalaaspyyleuilelysleuienasniysaspleualaarstysg 34
19 ccgtgcagactacctcatcaaattacttagtagaacatcttgcaaaaagaa 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 GCTCT 24
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AL352864.1 GI:8246657

AL352864.1 GI:8246657

SGS; genome survey sequence.

Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

CE 1 (bases 1 to 1122)

CB Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNSU5T9J 1122 bp DNA linear GSS 26-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 042M09 of library C from Tetraodon nigroviridis, genomic survey sequence
                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 [bbases 1 to 1122]
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J.
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Quality: 124.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 1122)
                                                                                                                                      303 a
                                                                                                            /Clone="042M09"
/Clone_lib="C"
/Clone_lib="C"
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/note="Genoscope sequence ID : C0BC042AG05C1~end : T7"
/note="Genoscope sequence ID : C0BC042AG05C1~end : T7"
                                                                                                                                                                                                                                         /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
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Gaps: 0
Percent Identity: 82.857
Length:
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Percent Similarity: 100.000 Percent Identity: 79.310

alignment_block: US-08-973-363-8 x CNS05T9J ...

Align seg 1/1 to: CNS05T9J from: 1 to: 1122
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- 17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAsp 29 :||||||:::|||||||:::|||||||| 885 CAGAGCTGAGTATCTCCTCAAGCTGCTGAAAAAGGAC 921

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9b_pat:A58696
9b_pat:A58691
9b_ov:AF004397
9b_pat:A58686
9b_pat:A58684
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gb_ro:MUSCHD1X
gb_pat:A58683
gb_pr:AF006513
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Database length: 1873333701
Search time (sec): 4907.710000
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Query: US-08-973-363-9
Query length: 41
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4.8e-15 59
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1316 | ASB896 Sequence 15 from Patent 6802 | APROVANCE 15 From Patent 6872 | AFROVANCE 10 From Patent 6872 | AFROVANCE 153 | ASB868 Sequence 2 from Patent was 153 | ASB868 Sequence 3 from Patent was 153 | ASB868 Sequence 4 from Patent was 153 | ASB868 Sequence 2 from Patent was 153 | ASB868 Sequence 2 from Patent was 154 | AC02174 | Homo sapiens Chromo 13455 | AC02174 | Homo sapiens Chromo 14359 | AC02174 | Homo sapiens Chromo 1543 | AC02173 | Homo sapiens Chromo 1543 | AC02171 | Homo sapiens Chromo 1543 | AC02171 | Homo sapiens Chromo 1546 | AR033515 Sequence 3 from Patent AG022 | AR06514 | Homo sapiens Chromo 1546 | AR033515 Sequence 4024 | From Patent AG029 | AC08764 | Homo sapiens Chromo 18358 | AC08764 | Homo sapiens Chromo 18358 | AC08764 | Homo sapiens Chromo 18358 | AC08764 | Homo sapiens Chromo 18029 | E32270 | Caenorhabditis elegans 16430 | AC01334 | Homo sapiens Chromo 18029 | E32270 | Caenorhabditis elegans 16430 | AC01334 | Homo sapiens Chromo 18036 | AC08764 | Homo sapiens Chromo 18029 | E32270 | Drosophila melanogas 16430 | AC01385 | Drosophila melanogas 16430 | AC01985 | Drosophila melanogas 16430 | AC03510 | Rattus norvegicus Callida | AC03510 | ARtus | AC00510 | ARTUS | ARTUS | ARTUS | ARTUS | ARTUS | ARTUS | ARTU
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gb_htg:AC110387
gb_in:AF139114
gb_ov:AF068773
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AUTHORS
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seq_documentation_block:
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US-08-973-363-9 x A58696
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Ratio: 4.805
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Patent: WO 9639505-A 10 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
                                                                                               1 (bases 1 to 6608)
Griffiths, and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                          unidentified
                                                                                                                                                                                             unidentified.
                                                                                                                                                                                                                                 A58691
A58691.1 GI:3714250
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Sequence 10 from Patent WO9639505.
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Griffiths,R. and Tiwari,B.
AVIAN GHD GERES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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24314 ! AC110387 Rattus norvegious
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2482 ! AF068773 Danio rerio heat s
73128 ! AC101378 Mus musculus clon
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US-08-973-363-9 x A58691
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LOCUS AF004397
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                                                                                                                                                                                                                                                                                                                                                              Archosauria; Aves; Neognathae; Gallii phasianinae; Gallus.
1 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked in Gene 197 (1-2), 225-229 (1997)
97475516
2 (bases 1 to 6872)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF004397 6872 bp mRNA linear VRT 08-OCT-19 Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-Z) mRNA, complete
                                                                                                                                                                                                                                                                                                  Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8QQ, UK
                                                                                                                                                                                                                                                                                                                                                 Griffiths, R. and Korn, R.M.
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/gene="CHD-2"
/function="role in chromatin architecture"
/functe="CHD protein with hydrophilic domain
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1207 c 1459 g 1
                                                                                              protein"
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/db_xref="taxon:9031"
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l. .6872
                                                                                                           /product="chromo-helicase-DNA-binding on the Z
                                                                                                                                                                                                     'gene="CHD-Z"
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                                                                                                                                         domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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                                                                                                            chromosome
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BASE COUNT
ORIGIN
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ORGANISM
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US-08-973-363-9 x AF004397
                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pat:A58686
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Ratio: 4.805
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGTGCAGACTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGCACAAAGGCTTGCTGGTGCA
                                                1 (bases 1 to 153)
Griffiths,R. and Tiwari,
AVIAN GHD GENES AND THEI
                                                                                                                                                                                                                                                                        Sequence 5 from Patent W09639505
A58686
                                                                                                                                                               unidentified unidentified
Patent:
                            BIRDS
                                                                                                                                     unclassified
                                                                                                                                                                                                                                               A58686.1
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WO 9639505-A 5 12-DEC-1996;
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LFKEPEGEEQEPQEMDIDEILKRAETERNEFQFLTVGDELLSQFKVARFSNNDEDDIE
LEPERNSRNWEEIIPESGORRRIEEEERQKELEEITMLFRMRNCAKQISFNGSBGRRS
SRRYSGSDSDSITERKRFKKRGRFTIFRENIKGFSDAEIRRIKSYKKFGGFLERLD
AVARDAELVDKSETDLERLGELVHNGCIKALKDNSSGOERAGGRLGKVKGFTFRISGV
QVNAKLVISHEEELAPLHKSIFSDPEERKRYLTPCHTKAAHFDIDWGKEDDSNLLVGI
YEYGYGSWEMIKNDPDLSLTQKILPDDPDKKFQAKQLOTRADYLIKLLNKDLARKEAQ
RLKKGKGKSKEMIKNDELSTOKKILPDDPDKKFQAKQLOTRADYLIKLLNKDLARKEAQ
RLKKGKGKKRKKKRKKKNKAKKIKELKSDSSPQPSEKSDEDEEDNKDEIVSVK
HLKKIKTKEKENEKEPPDIGIKKASKIKELKEENKKEKEEDKKELKEKD
REKRENKVKESTQKEKEVKEEXVNEMSENKEKSKKIPLLOTPVHITATSEPVPISE
ESEELHQKTFSVCKERMRPVKAALKQLDRPEKGLSBERQLEHTRQCLIKIGHITECL
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AHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKD
CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
                                                                                                                                                                                                                                               GI:3714249
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1223 c
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                                                      AND THEIR USE IN METHODS
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Gaps: 0
Percent Identity: 95.122
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REFERENCE AUTHORS

TITLE JOURNAL

ACCESSION VERSION

DEFINITION

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KEYWORDS

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COMMENT
FEATURES
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AUTHORS
TITLE
                                                                                                                 alignment_scores:
Quality: 182.00 Length: 51
Ratio: 4.439 Gaps: 1
Percent Similarity: 80.392 Percent Identity: 76.471
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US-08-973-363-9 x A58686
                                                                    alignment_block:
US-08-973-363-9 x A58684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
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ORIGIN
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ORIGIN
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LOCUS A58684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pat:A58684
                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: A58686 from: 1 to: 153
                                      Align seg 1/1 to: A58684 from: 1 to: 153
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                                                                                                                                                                                                                                                                                                                source
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101 AATTACTGAATAAAGACTTGCAAGAAAAGAAAGAGTGCAAGACTTACTGCT 150
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1 IleLeuProAspAspProAsp......
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Ratio: 4.659
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Other publication AU 5906996 961224.
                                                                                                                                                                                                                                                                                                                                              Other publication AU 5906996 961224
                                                                                                                                                                                                                                                                                                                                                                  Patent: WO 9639505-A 3 12-DEC-1996; ISIS INNOVATION (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A58684
A58684.1 GI:3714247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unidentified.
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34 c 31 g
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/db_xref="taxon:32644"
/db_x 31 g 2
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1. .153
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REFERENCE
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TITLE
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SOURCE
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US-08-973-363-9 x A58685 , ..
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ORIGIN
DEFINITION Mouse DNA-binding protein (CHD-1) mRNA, complete cds. ACCESSION L10410 x66028
                                                                                         seq_name: gb_ro:MUSCHD1X
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                                          seq_documentation_block:
LOCUS MUSCHD1x
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24 ysteuteuasnlysaspteualaargtysgtuvalginargteurhrcity 40
101 aattaCTGAATAAAGACCTTGCAAGAAAGGAAGGACAGAGACTTGCTGGT 150
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101 AATTACTGAATAAAGACCTTGCTAAGAAAGGAAGCACCACAGGCTTGCTGGT 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other publication AU 5906996 961224.
Location/Qualifiers
1. .153
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A58685
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AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unclassified.

1 (bases 1 to 153)
Griffiths, R. and Ti
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4.439
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36 c 31 g
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                                          ROD 19-SEP-1996
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                           alignment_block:
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US-08-973-363-9 x MUSCHD1X
                                                                                 Percent Similarity:
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L10410.1 GI:455014
DNA binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perry, R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93211972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delmas, V., Stokes, D.G. and Perry, R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unitted (08-APR-1993) Robert Perry, The Fox Chase Cancer 01 Burholme Avenue, Philadelphia, PA 19111, USA Feb 16, 1994 this sequence version replaced gi:293322. Location/Qualifiers
                                                                                                                                                                                                                                                                                             1739
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MNIRTHEWMHPQTKRLKRNILLTTYEILLKDKAFLGGLWWAFIGVDEAHRLKNIDDSLL
YKTLIDFKSHRELLTTGTPLQNSLKELWSLLHFIMPEKFSSWEDPEEHEKGREFXYS
SLHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYKWILTRNYKALSKGSK
                                                                                                                                                                                                                                                                                                                                             QYHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHREWDHYRQDSRYYSDREKHRKLDD
HRSREHRPSLEGGLKDRCHSDHRSHSDHRMHSDHRSSSEHTHHKSSRDYRYLSDWQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK
DRSKKSVVSDAPVHITASGEPVPIAEESEELDQKTFSICKERMRPVKAALKQLDRPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSRRYSGSDSDSISERKRPKKRGRPKTIPRENIKGFSDAEIRREIKSYKKFGGPLERL
DAIARDAELVDKSETDURRLGELVHNGCVKALKDSSSGTERAGGRLIGKVKGPTFRISG
VOVNAKLYLAHEDELIPLHKSIPSDEPERKYTIPCHTKAAHFDIDWGKEDDSNILIG
IYEYGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVEEDILERAKKKWVLDHLVIQRMDTTGKTVLHTGSAPSSSTPFINKEELSAILKFGAE
ELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLSVGDELLSQFKVANFSNMDEDDI
ELEPERNSKNWEEIIPEEQRRRLEEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSTSGFLNIMMELKKCCNHCYLIKPPDNNEFYNKQEALQHLIRSGKLILLDKLLIRL
RERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGSEDF
CFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLKQQNVRGMKKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERI
IAHSNQKSAAGLPDYYCKWQGLPYSECSWEDGALISKKFQTCIDEYFSRNQSKTTPFK
DCKVLKQRPREVALKKQPSYIGGHEGLELRDYQLNGLNWLAHSWCKGNSCILADEMGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDSESEEERDKSSCDGTESDYEPKNKYRSRKPQNRSKSKNGKKILGQKKRQIDSSEDE
DDEDYDNDKRSSRRQATVNYSYKEDEEMKTDSDDLLEVCGEDYPQPEDEEFETIERVM
                                                                                                                                                                                                                                                                                                                     HRAASSGPRSPLDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKT
                                                                                                                                                                                                                                                                                                                                                                                                          KLYKHAIKKRQESQQNSDQNSNVATTHVIRNPDMERLKENTNHDDSSRDSYSSDRHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                         GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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/db_xref="GI:455015"
                                                                              182.00
4.550
97.561
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171. .5306
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1, .5349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MNGHSDEESVRNGSGESSQSGDDCGSASGSGSGSSSSGSSSDGSS/
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                                                                              : 41
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Quality:
Ratio:
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KEYWORDS
              DEFINITION
ACCESSION
                                         seq_documentation_block:
LOCUS AF006513
                                                                             seq_name: gb_pr:AF006513
                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-973-363-9 x A58683
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ORIGIN
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 VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                 101 AACTACTTAGCAGAGATCTTGCAAAAAGGAGGGCTCAGAGAGACTTTGTGGT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                            151 GCG
                                                                                                                                      41 Ala 41
                                                                                                                                                                                 24 ysLeuLeuAsnLysAspLeuAlaArgLysGluValGlnArgLeuThrGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 luValGlnArgLeuThrGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
                                                                                                                                                                                                                      51 CAAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCA 100
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                                                                                                                                                                                                                                    .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL
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Sequence 2 from Patent W09639505
A58683
            Homo sapiens CHD1 mRNA, AF006513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unclassified.
1 (bases 1 to 153)
Griffiths, R. and Tiv
AF006513.1 GI:2645428
                                                                                                            153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: WO 9639505-A 2 12-DEC-1996;
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4.175
78.431
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/db_xref="taxon:32644"
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SOURCE
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US-08-973-363-9 x AF006513
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Align seg 1/1 to: AF006513
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Direct Submission
Submitted (03-UUN-1997) Laboratory of Gene Transfer, National Human
Submitted (03-UUN-1997) Laboratory of Gene Transfer, National Human
Genome Research Institute, National Institutes of Health, 49
Convent Drive, Bethesda, MD 20892-4442, USA
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1 (bases 1 to 5947)

Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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YASIHKELEPFILRPKKNYEKSLPAKYEQIIRWENSALOKQYYWNILTRNYKALSKG
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KGSYEBDILERAKKKWENTI IPROKRADTHENEPGPLTYODELLSQFKYANESNMOED
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DIELEPBRNSKWENTI IPROKRRLEEEERGFLEHKGFSDAEIRREIKSYKKGGFPLE
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EKSKKSSYDAPVHITASGEPVPISEESEELDOKTFSICKERMRPYKAALFODKRESKSOGG
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GGISEREOLEHTROCLIKIGDHTTECLKEYTNPEDKROMRRNAMFYKARTSGEDHTEL
GGISEREOLEHTROCLIKIGDHTTECKENTPREDKROMRNAMFYKSTENBHTAN
GGISEREOLEHTROCLIKIGDHTTECKENTPREDKROMRNAMFYKARTSGENBHTAN
KYLYHAIKKOFSGONANNAMBONANNAMBONTEN KEMPNAMFOSSEDENSTEN
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EETIKQQNVRGMKKLDNYKKKDQETKRWIKNASPEDVETY NCQOEITDDLHKQYQIVG
RILAHSNQSAAQYPDYYCKWQGLPYSECSWEDGALISKKFQACIDEYFSRNQSKTTP
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GLORTIQTISELNYLEHEBOLYGPFLVVPISTITSWQREIQTWASQMNAVYLGDIN
SRNWIRTHEWTHHQTKRLKFNILLTTYEILLKDKAFLGGLNWAFIGVDEAHRLKNDDS
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KKQQQQQQQQAQASSNSGSEEDSSSSEDSDSSEVKRKKHEDDWQMSGSGSPSQS
GSDSESEEEREKKSSCDETESDYEPKNKVKSRKPQNNSKSKSNGKKILAQKKRQLDSSEE
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YHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHRDWDHYKQDSRYYSDREKHRKLDDH
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/product="CHD1"
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/db_xref="taxon:9606"
/chromosome="5"
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Ratio: 4.256
Percent Similarity: 95.122
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26932 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 26883
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624. The number of bases overlapped is 90404.
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Ouality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/chromosome="5"
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gb_htg:AC021449
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Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 M
Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267
Location/Qualifiers
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joi
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitche
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center
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/db_xref="taxon:9606"
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Gaps: 1
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ne 5 clone CTD-2082117, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Forrest, C., Gage, D., Galagan, J., Petreira, P., FitzHugh, M., Forrest, C., Gage, D., Galagan, J., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPhaeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Morman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Diegrie, N., Chara, P., McGur, R., P., McGurt, P., Olivar, T.M., Peterson, K., Diegrie, M., Chara, P., McGurt, P., Olivar, T.M., Peterson, K., Diegrie, N., Chara, P., McGurt, R., P., McGurt, R., P., McGurt, R., P., McGurt, R., P., Chara, P., McGurt, R., P., McGur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassiliv,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                  * as soon as it is available and the accession * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zimmer, A. and Zod
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C. Homo sapiens, clone RP11-58M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC021449 143079 bp DNA linear
Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 143079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 143079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 134743 bases at least Q40 Consensus quality: 139227 bases at least Q30 Consensus quality: 140814 bases at least Q20 Insert size: 144000; agarose-fp Insert size: 142179; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 4.6 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L5154
Center clone name: 58_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
                                  1 38820: contig of 38820 bp in length
38821 38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
40412 40511:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Center
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alignment_block:
US-08-973-363-9 x AC021449
seq_name: gb_htg:AC008531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                              116247 AAGCT.....CTTTCTGGTGCG 116263
                                                                                                                                                                                                                                   116147 ATTCTTCCAGATGATCCCGATAAAAAAACCACAAGCAAAACAGTTGCAGAC 116196
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                                                                                                                                                    34 luValGlnArgLeuThrGlyAla 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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43280 43379: gap of 100 bp
43380 46905: contig of 3526 bp in length
46906 47005: gap of 100 bp
47006 51830: contig of 4825 bp in length
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4.256
95.122
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1 26246 c 26678 g 45278 t
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106510. 143079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment" 62720. .75408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
92617. .106409
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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1. .143079
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REFERENCE
AUTHORS
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AUTHORS
TITLE
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VERSION
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                            alignment_scores:
                                                                                                          ORIGIN
                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q20
Consensus quality: 142744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* but the finished accorders as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE, 7 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
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Center: Joint Genome Institute
Center Code: JGI
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced gi:7528342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 145659)
DOE Joint Genome Institute.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14559)
DOE Joint Genome Institute.
Quality: 166.00
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                                                                                                                             /clone="CTC-480B11"
/clone_lib="CalTech human BAC library C"
a 26309 c 27580 g 48609 t 600 other
                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                            ocation
                                                                                                                                                                                                                                                                                                                                      ssion number will be preserved.
56174: conting of 56174 bp in length
56274: gap of unknown length
100874: conting of 44600 bp in length
100974: gap of unknown length
113127: conting of 12153 bp in length
113127: gap of unknown length
113290: conting of 4963 bp in length
118190: conting of 4963 bp in length
118290: gap of unknown length
118290: gap of unknown length
118594: conting of 1404 bp in length
113397: gap of unknown length
123397: conting of 3503 bp in length
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JOURNAL REFERENCE
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US-08-973-363-9 x AC008531
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Percent Similarity:
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q30
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 33 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC091946 bp DNA 193446 bp DNA 1907 both DNA 1970 by DN
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Center Code: JGI
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1 (bases 1 to 193446)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Summary Statistics
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DOE Joint Genome Institute.
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be preserved
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                                                               alignment_scores:
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31088 36065; contig of 49
36166 40978; contig of 481:
40979 4563; contig of 488:
45764 45763; gap of unknown 1
4564 57745; contig of 5982 b
51746 51845; gap of unknown len
57460 67881; contig of 5982 b
57460 67881; contig of 5982 b
74132; contig of 5151 bp in
74133 74232; gap of unknown length
79896 87511; contig of 5151 bp in
87612 92791; contig of 5653 bp in 1
87612 92791; contig of 7616 bp in 1en
87612 92791; contig of 5180 bp in 1en
92892 102794; contig of 5180 bp in 1en
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102895 110866; contig of 7972 bp in length
10730 123838; gap of unknown length
10731 12338; contig of 6605 bp in length
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163109; contig of 6745 bp in length
16209; gap of unknown length
163109; contig of 27465 bp in length
                                  Quality:
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   Ratio:
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/chromosome="5"
/chromosome="5"
/clone="RP11-36012"
/clone_"RP11-36012"
/clone_lib="RPCI human BAC library 11"
/clone_lib="RPCI human BAC library 11"
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Percent Similarity: 95.122

Percent Identity: 82.927

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AUTHORS
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US-08-973-363-9 x AC026778/rev
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AUTHORS
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TITLE
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LOCUS AC026778
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                                                                                                                                         alignment_scores:
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                                                                      Ouality: 166.00 Length: 41

Ratio: 4.256 Gaps: 1

Percent Similarity: 95.122 Percent Identity: 82.927
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                                                                                                                                                                                                                                                                                                                                                                                                                        submitted (01-JÜN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:13677045.

Draft Sequence Produced by DOE Joint Genome Institute
The Joint Genome Institute
The Joint Genome Center
Thishing Completed at Stanford Human Genome Center
Thishing Completed at Stanford Human Genome Estimated Total Number of Errors is 0.2.

Stimated Total Number of Errors is 0.2.

MI-13675 G23101

NUC-158246 G23407
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Homo sapiens chromosome 5 clone CTC-428I11, complete sequence.
AC026778
AC026778.4 GI:14277282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 (bases 1 to 195433)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19433)
DOB Joint Genome Institute and Stanford Human Genome Center.
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SHGC-103595 G57841.
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DOE Joint Genome Institute.
Direct Submission
                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/cbromosome="5"
/clone="CTC-428111"
62762 a 37302 c 37040 g 58329 t
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-DB-N_Geneseq_032802 -QFMT-fastap -SUFFIX-p2n.rng -GAPOP-12.000
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-DELCP-6.000 -PHR_MIN-0 -ALIGN-120 -HARIX-blosum62
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-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
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Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 523.620000
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Query: US-08-973-363-9
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2.6e-22
2.6e-2
                                                                                                                                                                                                                                     4.6e+0
25.18
82.42
139.97
141.48
2.9e+03
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                                                                                             1188
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seq_documentation_block:
ID AAM42754 standard; cDNA; 1316 BP.
XX
AC AAM42754;

AC AAM42754;

XX
AC AAM42754;

XX
AC AAM42754;

XX
Chicken CHD-W gene (partial sequence continuation; chromodomal feet continuation; chrom
                                                                                                                                                                                                                              alignment_block:
US-08-973-363-9 x AAT42754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:AAD22583 - /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAS46402 - /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAAA60629 + /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:ABL14118 + /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:AAS59590 +
                                                                                                                                                                                                                                                                                                                                                  Quality: 197.00
Ratio: 4.805
Percent Similarity: 100.000
                                                                                                                                                         Align seg 1/1 to: AAT42754 from: 1 to: 1316
    1138 ATTITACCTGATGATCCAGATAAGAAACCCCCAGGCTAAGCAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate femala development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                         1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromodomain-helicase-DNA binding genes determine sex in
  - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 95.122
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
1187
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389
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alignment_block:
US-08-973-363-9 x AAT42751
                                                                                                                                                                                                                                                                                     alignment_scores
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ID AAT42751 standard;
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                                                                                             Align seg 1/1 to: AAT42751
                                                                                                                                                                                                                      Percent Similarity:
4080 ATTTTACCTGATGATCCAGACAAGAAACCCCCAGGCAAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                  The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A - Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progenty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                 Sequence 6608 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09639505-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicken CHD-1A gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT42751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-1997
                         1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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||:::||||||||:::||||||
AAGCACAGAGACTTGCTGGTGCA 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex determination; chromodomain-Helicase-DNA binding chromodomain-Helicase-DNA binding on the \ensuremath{\mathsf{W}} chromosor
                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tiwari B;
                                                                                                                                                                                                                 : 197.00
: 4.805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 228..5390
                                                                                                                                                                                                                                                                                                                                                                 2289 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA; 6608 BP
                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                 1207 C;
                                                                                                                                                                                                                 Length:
Gaps:
Percent Identity:
                                                                                                to: 6608
                                                                                                                                                                                                                                                                                                                                                                 1459 G; 1653 T; 0 other;
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                                                                                                                                                                                                                 41
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17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG

1 IleLeuProAspAspProAsp.....

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seq_documentation_block:
ID AAM42759 standard; DN
XX
AC AAM42759;
XX
DT 12-MAR-1997 (first 6
XX Bird; sex determinat;
XX Bird; sex determinat;
XX CHD-1A; CHD-W; W chrx
OS Parus major.
XX
FH Key Locat
FT misc_difference 52...(
FT //not.
FT MO9639505-A1.
XX
PN W09639505-A1.
XX
PN W09639505-A1.
XX
12-DEC-1996.
XX
12-DEC-1996.
XX
PN W09639505-A1.
XX
PN W09639505-A1.
XX
PN G-JUN-1995; 95GB-
XX
PN G-JUN-1995; 95GB-
XX
PN G-JUN-1995; 95GB-
XX
PN G-JUN-1995; 95GB-
XX
PN O6-JUN-1995; 95GB-
XX
PF O5-JUN-1995; 95GB-
XX
PF O5-JUN-1995; 95GB-
XX
PF O5-JUN-1995; 95GB-
XX
PF O5-JUN-1997; 95GB-
XX
PF O5-JUN-1996; 96WO--
XX
PN O5-JUN-1996
                                                          alignment_block:
US-08-973-363-9
                                                                                                                                                                                                                                        alignment_scores:
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Align seg 1/1
                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                              Sequence 153 BP; 60 A; 33 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 luValGlnArgLeuThrGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCACAAAGGCTTGCTGGTGCA 4202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromodomain-helicase-DNA binding genes determine sex
- used for sex determn. and to control sex of progeny
                                                                                                                                                                                                         Quality:
                                                                                                                                                                                 Ratio:
   to:
                                                             x AAT42759
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   AAT42759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 52..81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /notem "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                            191.00
4.659
80.392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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   from:
                                                                                                                                                  Percent
                                                                                                                                                                                                                                                                                                                              31 G; 29 T; 0 other;
   μ,
                                                                                                                                            Length:
Gaps:
Identity:
   :01
      153
                                                                                                                                            51
1
80.392
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alignment_scores:
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                                                                     Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AA742758) and the great tit CHD-W gene (see also AA742759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AA742751) and CHD-W (see also AA742751) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 Ala 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42757
 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 52..81
182.00
4.439
                                                                                                                                                                                                                                                                                                                                                                           "bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
                                                  G;
                                                  24 T; 0 other;
Length:
Gaps:
  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
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amino
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seq_documentation_block:
ID AAT42758 standard; DNA; 153 BP
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US-08-973-363-9 x AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759): Translated amino acid sequences of this region are provided in AAW041464-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chick CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151
                                                                                                            Claim 8; Fig 3; 76pp; English.
                                                                                                                                     Avian chromodomain-helicase-DNA binding genes determine birds - used for sex determn. and to control sex of prog
                                                                                                                                                                             WPI; 1997-043127/04.
P-PSDB; AAW08148.
                                                                                                                                                                                                                      Griffiths R,
                                                                                                                                                                                                                                                  (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                      05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                 12-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                             WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHD-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 AATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 CAAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IleLeuProAspAspProAsp......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATTITACCTGATGATCCAGACAAGAAACCCCCAGGCAAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ysLeuLeuAsnLysAspLeuAlaArgLysGluValGlnArgLeuThrGly 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp.
                                                                                                                                                                                                                      Tiwari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Σ
                                                                                                                                                                                                                                                                             95GB-0011439
                                                                                                                                                                                                                                                                                                      96WO-GB01341.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.392
                                                                                                                                                                                                                                                                                                                                                                                  /note "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome;
                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 76
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                                                                                                                                                   sex
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amino
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SXC

Sequence 153

ВP;

56 A;

36

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31

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30

T; 0 other;

foetus etc.

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to manipulate the sex of progeny.

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PXXXX 
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ID AAT42756 standard; DNA; 153
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US-08-973-363-9 x AAT42758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAT42758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird; s
CHD-1;
                                                                                 Avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
     Claim
                                                                                                                                                                            WPI; 1997-043127/04.
                                                                                                                                                                                                                              Griffiths R,
                                                                                                                                                                                                                                                                                                                                             06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT42756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101
                                                                                                                                               P-PSDB; AAW08146
                                                                                                                                                                                                                                                                                     (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTTACCTGATGATCCAGATAAGAAACCCCCAGGCTAAGCAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex determination; chromodomain-Helicase-DNA binding
; CHD-W; W chromosome; ss.
                                                 chromodomain-helicase-DNA binding genes determine sex — used for sex determn. and to control sex of progeny
     8;
Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                        INNOVATION LTD
                                                                                                                                                                                                                                 Tiwari
                                                                                                                                                                                                                                                                                                                                             95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                    96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 52..81
76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182.00
4.439
80.392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from:
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Gaps: 1
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
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amino
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seq_documentation_block:
ID AAV59280 standard; cDNA; 1311 BP
XX
AC AAV59280;
XX
DT 14-DEC-1998 (first entry)
XX
DE Altered telomere repeat binding
XX
KW ds; human; telomere repeat binding
XW
KW telomere; ageing; ataxia telange
XX
KW telomere; ageing; ataxia telange
XX
KW telomere; ageing; ataxia telange
XX
CS Synthetic.
XX
FH Key Location/Qualifi
FT CDS 1..1311
FT CDS 1..1311
FT CDS 1..1311
FT CDS 20-AUG-1998.
XX
PD 20-AUG-1998.
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PD 20-AUG-1998.
XX
PD 20-AUG-1998.
XX
PD 13-FEB-1998; 98WO-US02765.
XX
PR 13-FEB-1998; 98US-0018628.
PR 13-FEB-1997; 97US-0800264.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
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US-08-973-363-9 x AAT42756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:AAV59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW427549. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify AAW42754-55) genes determine sex in birds and can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                 ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Altered telomere repeat binding factor 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 GCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 153 BP; 61 A; 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 Ala 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
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                                                                                                                                                                                                                               /*tag= a
/product= "A-TRF
                                                                                                                                                                                                                                                                    Location/Qualifiers
1..1311
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4.175
78.431
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
1
68.627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
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                                                                                                                                                                                                                                                                                                                                                                                   viral.
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alignment_block:
US-08-973-363-9 x AAV59280
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Quality:
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ID AAK88882 standard; cDNA; 421
                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK888882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 129.00
Ratio: 5.160
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAV59280 from: 1 to: 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                           1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atmophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g. for expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                                              AAK88882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
 31-JAN-2000; 2000US-0179065.
04-FEB-2000; 2000US-0130628.
24-FEB-2000; 2000US-0184664.
02-MAR-2000; 2000US-0186350.
16-MAR-2000; 2000US-0189874.
                                                                                                                                                                                   Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                       Human digestive system antigen coding sequence SEQ ID NO: 1198.
                                                                                                                                                                                                                                                                  05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW59280.
                                                                              17-JAN-2001; 2001WO-US01324
                                                                                                                                    WO200155314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  17
                                                                                                                                                                                                                                                                                                                                                                                     1998-480769/41.
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Gaps: 0
Percent Identity: 100.000
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   18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

31-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

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08-SEP-2000

08-SEP-2000

11-SEP-2000

11-SEP-2000

11-SEP-2000

11-SEP-2000

11-SEP-2000

11-SEP-2000
14-SEP-2000
21-SEP-2000
25-SEP-2000
25-SEP-2000
26-SEP-2000
27-SEP-2000
27-SEP-2000
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2000US-0198123.
2000US-0205515.
2000US-0209467.
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20 - OCT - 2000;
01 - NOV - 2000;
08 - NOV - 2000;
The present invention provides the protein and coding sequences
                    Claim
                                    Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of digestive system, particularly cancer and cancer metastases -
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DF 19-CCT-2001 (first e
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Human; colorectal canc
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Human; colorectal canc
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Human; colorectal canc
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XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colorectal cancer antigen
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                                                              2000US-0189074
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2000US-0225214. 2000US-0225266. 2000US-0225267.

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                         Isolated polypeptide disorders related to and also for testing
                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                               Sequence 421 BP; 148 A;
                                                                                                                                                                                                                                                                                                                                             P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                       for treating, preventing and/ or prognosing the colon and rectum including colorectal cancers and detection e.g. diagnosis
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AAI57603

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Align seg 1/1
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                                                                                                                                                                                                                     capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                   The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical; gene;
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                                                                                         Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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2000US-0614150
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DR WP1; 2001-656860/75.
alignment_block:
US-08-973-363-9 x ABL06442
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                                                                                                                                                                                                                                                                                                                                                                                                                insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                  The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic a
genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster expressed polynucleotide SEQ
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2000US-0614150
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                                                                                                                                                                                                                                                        2468 C;
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                                                                                     Percent Identity:
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Align seg 1/1 to:

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9933

1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh

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ID AAA95315 standard; DNA; 2595 BP
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                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAA95315 from: 1 to: 2595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6771 GCGTGCCGAGTACCTGCTCAAGATCATCAAGAAGAACGTG 6810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a number of methods which can be used to detect the presence of bovine Neospora infection. The infection leads to neosporosis in cattle, and can cause abortion of foetuses. The present sequence comprises a vector coding sequence. The sequence, and the protein it encodes, can also be used to produce vaccines against the infection and in protein isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2595 BP; 609 A; 796 C; 637 G; 553 T; 0 other;
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                                                                                                                                                          328 CCACAAGATCCAGACCGGAGTCTCAAGTATCCTGTACGGCTGCTGATTGT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 71-72; 75pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel immunodominant Neospora antigens, N54 and N57, useful for protecting bovine Neospora and protection by bovine Neospora and detecting the presence of antibodies specifically immunoreactive with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAB26153
                                   378 AGACAAGCCTGCGGGGGATGAAGAGGAGACTAGACCATCATTTGTGCAGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neospora antigens -
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                                                                                         9 ....LysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleL 24
                                                                                                                                                                                                     3 ProAspAspProAspLys.....
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US-08-973-363-9 x AAX39679
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seq_documentation_block:
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XX Cancer associated ant
XX Cancer associated ant
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XX prostate cancer; ss.
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XX CANCT-1997; 9705-0
PR 11-0CT-1997; 976B-0
XX (LUDW-) LUDWIG INST C
XX Chen Y, Gout I, Gur
PI Tureci O;
XX Chen Y, Gout I, Gur
PI Ficundachuh M, Sahi
PI Tureci O;
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                                                                                                    The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
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        Sequence 2911 BP; 957 A; 519 C; 686 G; 749 T; 0 other;
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Scanlan MJ,
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alignment_scores:
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AAZ80575 standard;
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                                                                                                                AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .808
                                                                                                       dysplasia or hyperplasia.
                                                                                                                                                                                                                                                   Claim 15; Page 393; 469pp; English.
                                                                                                                                                                                                                                                                            Novel nucleic acids, used to develop products for the diagnosis treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer
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Carroll E,
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colorectal adenocarcinoma; cell line SW480; cell proliferation;
                                                                               Sequence
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Catino TJ,
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Identity:
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            Length:
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d DM, Lewis
                                                                              142 T;
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                                                                              other;
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alignment_block:
US-08-973-363-9 x AAZ80575
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ID ABI99578 standard;
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                                                               The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia) or vasospastic ischaemia) by measuring expression levels of particular genes (AB199202 to AB19912, encoding the profein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression profile of a gene group comprising these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which we consider the condition of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes
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                                                  which are
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 1516-1517; 2690pp; English
                                                  used
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                                                  exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takahashi
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                                               present invention
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Sequence 826 BP;

270 A;

161 C;

206 G;

189 T;

0 other

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gb_estl:BB15336
gb_estl:BB34922
gb_estl:BB339273
gb_estl:BB339273
gb_estl:BB339273
gb_estl:BB339273
gb_estl:BB339273
gb_estl:BB395133
gb_gss:CNS04DVG
gb_estl:BB395133
gb_gss:CNS04JPY
gb_gss:CNS04JPY
gb_gss:CNS05DSJ
gb_gss:CNS05DSJ
gb_gss:CNS05DSJ
gb_gss:CNS05DSJ
gb_gss:CNS05DSJ
gb_gss:CNS05DSJ
gb_gss:CNS05DSV
gb_gss:CNS05DSV
gb_gss:CNS05DSV
gb_gss:CNS05DSV
gb_gss:CNS05BVS
gb_gss:
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Database: EST: *
Database sequences: 13736207
Database length: -184157050
Search time (sec): 4390.400000
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Query: US-08-973-363-9
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-Q-/cgn2_1/USPF0_spool/US08973363/runat_01082002_080049_18570/app_query.fasta_1.638
-DB-EST -OpmT-fasta_ -SUFTX*p2n.rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH+0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPOEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPOEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPOXT=0.500 -DELOP=5.000
-NINLEN=0.0000000 -USER=US08973363_CCM1_1_2938
-NOPU=6 -LOPU=3 -LOUGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1
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            | AL332012 Tetraodon nigroviridis | AL32335 Tetraodon nigroviridis | AL123303 Tetraodon nigroviridis | AL123303 Tetraodon nigroviridis | AL123105 Tetraodon nigroviridis | AL18973 Tetraodon nigroviridis | AL18973 Tetraodon nigroviridis | AL18973 Tetraodon nigroviridis | AL336703 Tetraodon nigroviridis | AL303019 Tetraodon nigroviridis | AL302041 Tetraodon nigroviridis | AL302047 Tetraodon nigroviridis | AL302088 Tetraodon nigroviridis | AL346289 Tetraodon nigroviridis | AL317122 Tetraodon nigroviridis | AL317123 Tetraodon nigroviridis | AL317123 Tetraodon nigroviridis | AL317123 Tetraodon nigroviridis | AL317127 Tetraodon nigroviridis | AL317128 Tetraodon nigroviridis | AL3171283 Tetraodon nigroviridis | AL3171383 Tetraodon nigroviridis | AL310958 Tetraodon nigroviridis | AL310958 Tetraodon nigroviridis | AL310958 Tetraodon nigroviridis | AL317135 Tetraodon nigroviridis | AL317135 Tetraodon nigroviridis | AL317135 Tetraodon nigroviridis | AL317575 EST17684 Colon carcin | A19703 yv23e03 sl Soares fetal | A3195135 wi50e08.xl NCI_CGAP_Ov
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A1644594 A1644594 XGC-egg Silur

BB155356 BB155356 RIKEN full-le

BB461065 BB461065 RIKEN full-le

BB484922 BB334922 RIKEN full-le

BB8304790 BB8304790 RIKEN full-le

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BB830770 BB830730 RIKEN full-le

A1601246 DKFZp313V1040_r1 313

A1690775 wm95fil.xl WCI_CGAP_Ut

A1125712 AU125712 WTZR44 HOMO s

1 BB895133 G01436060F1 NIH_MCC_7
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BF239967 601905170F1 NIH_MGC_54
AW996787 QV3-BN0047-230200-102-
AW997058 QV3-BN0047-150400-152-
I AL293839 Tetraodon nigroviridi
AL352864 Tetraodon nigroviridi
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gb_est2:BG757172
gb_est1:AW364689
gb_est1:AL658477
gb_gss:CNS03IQ2
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
                           seq_name: gb_est1:AL644594
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US-08-973-363-9 x AL659353/rev
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ORIGIN
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LOCUS AL659353
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Percent Similarity:
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                                                                       246 AAGCACAAAGACTTTCT 230
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Silurana tropicalis
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Sanger Centre
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Align seg 1/1 to reverse of: AL659353 from: 1 to: 593
296 CAGAGCTGACTACCTCATTAAACTTCTCAATAAAGATCTGCTTAGGAAAG
                                                                                              1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: trop@sanger.ac.uk
Sanger Xenopus tropicalls EST project 2001
TROPICALIE_SEQUENCE_ID: TNeu045e20.sp6
Sequencing primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 593)

Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="Tuku045e20"
/clone=lib="xGc-neurula"
/dev_stage="neurula"
/lab_host="Escherichia coli DH10B"
/lab_host="Escherichia coli DH10B"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from neurula.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."
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Percent Identity: 92.308
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RM3-DT0037-231299-0
AL658477 AL658477 XGC-neurul
AL245891 Tetraodon nigroviri
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REFERENCE
AUTHORS
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ORGANISM
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US-08-973-363-9 x AL644594
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                                                                                                                                                                                                          luValGlnArgLeuThr 39
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                                                                                                                                                                                        AAGCACAAAGACTTTCT
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                            619 bp mRNA linear EST 18-OCT-. BB155356 RIKEN full-length enriched, 16 days neonate thymus Mus musculus cDNA clone A130024L16 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence. BB155356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
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BB155356.2
EST.
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/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
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/dev_stage="egg"
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/clone="L1E1d12"
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length cDNA libraries for rapid discovery of new grapare full-length g
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1 (bases 1 to 619)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Har Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., K., M., KOya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sa,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
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wagi.K., Fujiwake,S., Inoue,K., Togawa,Y., Zawa,M., Ohara,E.,
wathiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsu,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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On Jun 29, 2000 this sequence version replaced gi:8811286.
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Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
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Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Rike
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/db_xref="taxon:10090"
/clone="A130024L16"
prepared by using trehalose thermo-activated transcriptase and subsequently enriched for :
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/dev_stage="16 days neonate"
/lab_host="DH10B"
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I., Kouda
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US-08-973-363-9 x BB155356
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LOCUS BB461065
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

El (bases 1 to 660)

RS Arakawa, T., Carninci, P., Fükuda, S., Füruno, M., Hanagaki, T., Hara, A.,

M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,

Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki

D., Shibata, K., Shinagawa, A., Tshiraki, T., Sogabe, Y., Suzuki, H.,

Tagani, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,

Muramatsu, M. and Hayashizaki, Y. et al. 2001)

On Jul 21, 2000 this sequence version replaced gi:9356558.

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

11-72 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9216

Frax: 81-45-503-9216
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Bmail: genome-reségsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.
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us-08-973-363-9 x BB461065
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
DIVISION of Experimental Animal Research in Riken contributed to
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Computational Analysis of Full-Length Mouse cDNAs Compared with Computational Sequences Mamm. Genome. 12, 673-677 (2001)
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,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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//dev_stage="12 days embryo"

//dev_stage="12 days
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/db_xref="taxon:10090"
/clone="p130070B13"
/clone_lib="RIKEN full-length enriched, 12 days embryo spinal ganglion"
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                                                        Quality:
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
wagehiari
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The Institute of Physical and Chemical Research (RIKEN)
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e mouse tissues.
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Computer-based methods for the mouse full-length cDNA
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,
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watah,Ki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Contact: Yoshihide Hayashizaki
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGCTCAGAGACTTTGTGGTGCG 423
                                                                                                                                                                     Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DRFZ); Email s. wiemann@dkfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp313J1040) is available at the RZPD in Berlin.
Tlease contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 430)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Bloecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL601246.1 GI:15164752
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95.238
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108 g 96 t
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/clone="DkFZp313J1040"
/clone_lib="313 (synonym: hlcc2)"
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Gaps: 1
Percent Identity: 80.952
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cDNA clone
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COMMENT
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alignment_block:
US-08-973-363-9 x AL601246
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LOCUS AI890775
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Lumbut Serie Linea

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Capabs-femail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.linl.gov/bbrp/image/image.html

Insert Length: 1924 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wm95f11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHDL_HUMAN O14646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1;, mkNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 547)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
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4.256
95.122
                                                                                                                                                                                      /organism="Homo sapiens"
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
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Gaps: 1
Percent Identity: 82.927
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US-08-973-363-9 x AI890775/rev
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LOCUS AU125712
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                                                                                                                                                                                                          Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                    Saito,K., Yamamoto,J., Nak
,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; L (Bases 1 to 866)
                                                                                                                                                                                                                                                                                                                                                                                                                                         HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU125712.1 GI:10950428
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a 118 c 85 g 230 t
   precursor cells"
149 c 196 ~
                                                                                     /cell_type="teratocarcinoma"
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                                                                                                                        /clone="NT2RM4002061"
                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                2 others
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; Homo.
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1 5', mRNA
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US-08-973-363-9 x AU125712
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 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Conso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE895133 1028 bp mRNA linear EST 20-OCT-2000 601436060F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3921087 5',
                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov lolumn: 16
High quality sequence stop: 488.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1028)
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                                  Quality:
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                                                                                                                    387
                                                                                                               /clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host="DHNOB (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Si
Site_2: Sall; Cloned unidirectionally. Pri
Average insert size 2 kb. Library constru
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7 a 205 c 238 g 198 t
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4.256
95.122
                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/clone="IMAGE:3921087"
166.00
4.256
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Tetraodon nigroviridis.
Tetraodonis.
Tetraodonis.
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodonis.
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Charaterization and repeat analysis of the compact genome of the Charaterization and Tereshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J. Saurin, W. and Weissenbach, J. Brottler, Brown wide analysis using Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                              Submitted (10-APR-2000) to the EMBL/GenBank/DDBJ databases submitted (10-APR-2000) to the EMBL/GenBank/DDBJ databases this sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope.
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4.286
89.744
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                                                            Gaps: 0
Percent Identity: 76.923
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seq_name: gb_est2:BF239967
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alignment_block:
US-08-973-363-9 x BF239967
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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//db_xref="raxon:9606"
//db_xref="raxon:9606"
//dlone=lib="RHAGE:4133129"
//clone=lib="NHH_MGC_54"
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//note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
//note="Organ: bone marrow; Vector: pDNR-LIB (Glontech);
//note="Organ: bone marrow; Vector: pDNR-LIB (Glonte RNA);
//note="Organ: bone marrow; Vector: pDNR-LIB (Glonte RNA);
//note="Organ: bone marrow; Vector: pDNR-LIB (Glonte RNA);
//note="Organ: bone marrow; Vector: pDNR-LIB (Glontech);
//note="Organ: bone marrow; Vector: pDNR-LIB (Glont
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4.088
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Gaps: 1
Percent Identity: 80.556
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                                                                     alignment_scores:
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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200-102-d03&t3=2000-02-23&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
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                         Ratio:
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Location/Qualifiers
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  129.50
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)

1 (bases 1 to 686)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Costa,F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150 400-152-c03&t3=2000-04-15&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                           /note="Organ: breast_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed low stringency conditions."
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/db_xref="taxon:9606"
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alignment_block:
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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/db_xref="taxon:99883"
/clone="114P18"
/clone="114P18"
/clone_1ib="G"
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Search information block:
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Copyright (c) 1993-2000 Compugen
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seq_documentation_block:
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Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked in the chicken Gallus domesticu Gene 197 (1-2), 225-229 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-MAY-1997) Zoology, Molecular Glasgow G12 8QQ, UK
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Griffiths,R. and Korn,R.M.
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| PIOCETI
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NKEKRENKVKESTOXEKEVKEEKVNEMKSENKEKSKKIPLLDTPVHITATSEPVPISE
ESBELHOATFSVCKEHARPVWAALKQLORPEKGLSEREOLEHTROCLIKIGHITEGL
                                                                                                       YEYGYGSWEMIKMDPDLSLTQKILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQ
RLAGAGNSKRRKTRNKKNKMKASKIKEEIKSDSSPQPSEKSDEDDEEEDNKDEIVSVK
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/gene="CHD-Z"
/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
/codon_start=1
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1 Homo sapiens of
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Griffiths, R. and Tiwari, B.
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Sequence 12 from Patent WO9639505.
A58693
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                                                                                                                                                                               unclassified
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                                                                                                                                                                                                          unidentified
                                                                                                                                                                                                                                     A58693.1 GI:3714251
                                                                                 Other
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                                                                               publication AU 5906996 961224
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THVIRNPDVERLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHGDAYKKSDSRKRPY
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SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
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alignment_scores:

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                                                       Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624. The number of bases overlapped is 90404.
                                                                                                                                                                                  Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 ND Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                          Location/Qualifiers
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/chromosome="5" /clone="RP11-58M12" 34122 a 18862 c 17827 g 30409 t

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Homo sapiens chromosome 5 clone CTD-2082I17, complete sequence.
AC012624
AC012624.6 GI:14993679
Direct Submission
Submitted (21-7UL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Maint Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.

Location/Qualifiers
                                                                                                                                                                                                                                                                 Direct Submission
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
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                                                                                                                           Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 13456)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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US-08-973-363-11 x AC012624
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavky, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeAreilano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McBeus, L., Morrow, J., Naylor, J., Nacheus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC021449 DNA linear HTO HOMO Sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-58M12
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AC021449.3 GI:10047806
HTG; HTGS_PHASE1; HTGS_DRAFT.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 24497 c 25503 g 43951 t
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/db_xref="taxon:9606"
/chromosome="5"
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ICE, 10 unordered
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COMMENT

JOURNAL TITLE

> Direct Submission Zimmer, A. and Zody, M.

Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as i
be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 144000; agarose-fp Insert size: 142179; sum-of-contigs
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106510 14307
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38821 38920: gap of 100 bp

38921 40411: contig of 1491 bp in length

40412 40511: gap of 100 bp

40512 43279: contig of 2768 bp in length

43280 43379: gap of 100 bp

43280 43695: contig of 3526 bp in length
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38921. .40411
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/clone="RP11-58M12"
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/note="assembly_fragment"
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AUTHORS

DOE Joint Genome Institute

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REFERENCE
AUTHORS
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LOCUS AC008531
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 REFERENCE
                                                                                                                     SOURCE
                                                                                                                                     KEYWORDS
                                                                                                                                                  VERSION
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                                                                                                                                                                                                                                                      seq_name: gb_htg:AC008531
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                               TITLE
                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                      117919 TAAAGGAAGAAAG
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                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                              AC008531 145659 bp
Homo sapiens chromosome 5 clone
                            Sequencing of Human Chromosome
                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                       Homo sapiens
                                                                                                                                  HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                  AC008531.3 GI:12830078
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                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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BASE COUNT
ORIGIN
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US-08-973-363-11 x AC008531
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source
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48336 AGACAGTGAAGAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG 48385
                                                                                                                   48286 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG 48335
                                      17 sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG 34
                                                                                                                                                      1 AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGluLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 139128 bases at least 040
Consensus quality: 142556 bases at least 020
Consensus quality: 142744 bases at least 020
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in 020 bases; pulse field gel estimation
Quality coverage: 6.4 in 020 bases; pulse field gel estimation
**NOTE: This is a 'working draft' sequence. It currently
**consists of 7 contigs. Gaps between the contigs
**are represented as runs of N. The order of the pieces
**is believed to be correct as given, however the sizes
**of the gaps between them are based on estimates that have
**provided by the submittor.**

**This sequence will be replaced
**by the finished sequence as soon as it is available and
**th. **arcaraia** **marker** will he preserved
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced gi:7528342.
------Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
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/db_wref="taxon:9606"
/chromosome="5"
/clone="CTC-480B11"
/clone="CTC-480B11"
/clone_lib="cal?ech human BAC library C"
/clone_1b="cal?ech human BAC 1600 others
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56174: contig of 56174 bp in length
56274: gap of unknown length
100874: contig of 44600 bp in length
100874: contig of 44600 bp in length
100974: gap of unknown length
113127: contig of 12153 bp in length
113127: gap of unknown length
118190: contig of 4963 bp in length
118290: gap of unknown length
118290: gap of unknown length
119594: contig of 1404 bp in length
123397: gap of unknown length
123397: contig of 303 bp in length
123397: gap of unknown length
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Gaps: 0
Percent Identity: 78.409
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                               Estimated insert size: 20450; agarose-fp estimation
Datimated insert size: 190246; sum-of-contigs estimation
Ouality coverage: 5.38 in 020 bases; agarose-fp estimation
Quality coverage: 5.79 in 020 bases; sum-of-contigs estimation
Quality coverage: 5.79 in 020 bases; sum-of-contigs estimation
NOTE: This is a 'working draft' sequence. It currently
consists of 31 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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1 (bases 1 to 19346)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
------Genome Center
Center: Joint Genome Institute
Center Code: JGI
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Center Project Name: 544799
Center clone name: RPCI-11_360I2
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DOE Joint Genome Institute.
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1459
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8: contig of 1358 bp in length
8: gap of unknown length
7: contig of 1209 bp in length
7: gap of unknown length
3: contig of 1056 bp in length
0: contig of 1957 bp in length
0: contig of 1997 bp in length
0: gap of unknown length
0: gap of unknown length
4: contig of 1474 bp in length
4: gap of unknown length
4: contig of 1502 bp in length
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BASE COUNT
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                        alignment_block:
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/clone_lib="RPCI hu
35252 c 37061 g
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/db_xref="taxon:9606"
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g of 7616 bp in 14
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WI-13675 G23101
                                                                                                                                                                                                            www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of
Estimated Total Number of Errors is
                                                                                                                                                                                                                                                                              Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:13677045.
Draft Sequence Produced by DOE Joint Genome Institute
Www.jgi.doe.gov
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Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia; Eutheria; Primates; C
1 (bases 1 to 19543)
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            /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-08-973-363-11 x AC026778/rev
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www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
STS Content:
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Homo sapiens chromosome 5 clone CTD-2007H13, complete sequence.
ACUZZ121
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                                                                                                                                              Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                              Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US 3 (bases 1 to 21258)

DOE Joint Genome Institute and Stanford Human Genome Center.
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DOB Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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          Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
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DOE Joint Genome Institute.
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SHGC-103595 G57841
  Center Code: JGI
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DOE Joint Genome Institute.
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WI-13675 G23101
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                                                                                                                                                                                                                     Sequencing of Human Chromosome 5
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/chromosome="5"
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Gaps: 0
Percent Identity: 78.409
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HTG 03-JUL-2001

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Consensus quality: 229677 bases at least Q40
Consensus quality: 256163 bases at least Q30
Consensus quality: 256163 bases at least Q20
Consensus quality: 260799 bases at least Q20
Estimated insert size: 174820; agarose-fp estimation
Estimated insert size: 271581; sum-of-contigs estimation
Quality coverage: 8.62 in Q20 bases; agarose-fp estimation
Quality coverage: 5.55 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 47 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project Information
Center Project Name: 435334
Center clone name: RPCI-11_75H1
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/db_xref="taxon:9606"
/chromosome="5"
/clone="RP11-75H1"
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a 51769 c 50026 g 82854
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                                                                                                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GluLysLysGluLysGluAspLysLysGluLeuLysGluLysAspAsnLy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 alLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 18A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:17384104.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; Sw.,
SWISSPROT: Tr., TREMEL, Mp., WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-202F3 is
from the RPC1-23 Mouse PAC Library
constructed by the group of Pleter de Jong.

PEGTOR: PBACE3 6

The STATES ACCES 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                          OR: pBACe3.6
sequence is the entire insert of clone RP23-202F3 The true end of clone RP23-171015 is at 179956 in this sequence. The right end of clone RP23-153B6 is at 117857 in this sequence. Location/Qualifiers
                                                                                                                                                                                                            /organism**Mus musculus*
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/chromosome="13"
/clone="RP23-202F3"
/clone_lib="RPCI-23"
3942. 4127
                     /note="Single clone region. Sequence from clone PCR only." 29783. 30099
/note-"Single clone region. Sequence from reads from a short insert library derived from a clone PCR. Restriction digest data confirm the assembly." a 46963 c 46966 g 61646 t
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AUTHORS
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US-08-973-363-11 x AL589701/rev
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LOCUS AL645746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_htg:AL645746
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Ratio: 2.961
Percent Similarity: 81.013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LysLysIleLysThrGluLysGluAsnGluGluLysProGluProAspIl 27
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                                                                                 Direct Submission Submitted (11-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 28, 2001 this sequence version replaced g1:17017892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL645746 282611 bp DNA 1:
Mus musculus chromosome 13 clone RP23-153B6,
PROGRESS ***, in unordered pieces.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: mouseg@har.mrc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: UK Medical Research Council Center code: UK-MRC
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Project Information
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Percent Identity: 55.696
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HTG 12-JAN-2002

Murinae; Mus

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SEQUENCING HTG

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10-JAN-2002

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alignment_block:
US-08-973-363-11 x AL645746
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Quality:
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Percent Similarity:
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71289. .2
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51151. .
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fragment_chain:2"
219160 . .250487
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60936 c 60357 g 80189 t
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fragment_chain:2"
cfain
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/chromosome="13"
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Gaps: 3
Percent Identity: 55.696
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SOURCE
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LOCUS AL645990
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 201289 bases at least Q40
Consensus quality: 201587 bases at least Q30
Consensus quality: 201880 bases at least Q20
Insert size: 202406; sum-of-configs
Insert size: 202406; sum-of-configs
Quality coverage: 13.87x in Q20 bases; sum-of-configs
Coverage: 13.39x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 11, 2002 this sequence version replaced gi:17529594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: bM403CIz
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL645990 203606 bp DNA linear Mus musculus chromosome 11 clone RP23-403C12, *** PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL645990.7 GI:18135245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL645990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (sites)
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                                                                                                                                                                                                                                                                                                                                                                           vector_side:left"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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alignment_scores:

BASE COUNT

57271 a

misc_feature misc_feature misc_feature misc_feature

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seq_documentation_block:
LOCUS A58694
DEFINITION Sequence 13 fr
ACCESSION A58694
VERSION A58694.1 GI:3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-973-363-11 x AL645990/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 187.00
Ratio: 2.791
Percent Similarity: 80.723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96762 GAAGGAGAAGAAGGAGAAGAAGGAGAAGAAGGAGGAAGAAG 96714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL 40
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                                                                                                                                                                                                                                                                                                                                                      137 bp
Sequence 13 from Patent WO9639505.
A58694
                                                                                                      Other publication AU 5906996 961224.
                                                                                                                                                                                   1 (bases 1 to 137)
Griffiths, R, and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                      unidentified
                                                                                                                                                                                                                                                                                                                                A58694.1 GI:3714252
                                                                                                                         Patent: WO 9639505-A 13 12-DEC-1996; ISIS INNOVATION (GB)
                                                                                                                                                                                                                                                                                       unidentified.
                                                                                                                                                                                                                                                inclassified
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44361 c 43131 g
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    18 t
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                                                                                                                                                                                                                                                                                                                                                                                             PAT 06-MAR-1998
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MEDLINE
REFERENCE
AUTHORS
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AUTHORS
TITLE
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SOURCE
ORGANISM
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ACCESSION
VERSION
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US-08-973-363-11 x A58694
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                CDS
                                                                                  polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 GGAGAAAAAGAGAGACAAAAGAAAAGGAAAATAAG 136
                                                                                                                                        polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 GluGluLysArgGluThrLysGluLysGluAsnLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 ysGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAla 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATGGGATTGTTTCAGTGAAACATCCACATAAAAAAATAAAAGCAGAAAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGlu.L 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ensser,A., Pflanz,R. and Fleckenstein,B. Direct Submission Submitted (27-MAY-1997) Institut fuer Klinische und Molekulare Virologie, Friedrich-Alexander-Universitaet Erlangen-Nuernberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFUU5370 130608 bp DNA linear Alcelaphine herpesvirus 1 L-DNA, complete sequence. AF005370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alcelaphine herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlossgarten 4, Erlangen 91054, Germany Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ensser,A., Pflanz,R. and Fleckenstein,B. Primary structure of the alcelaphine herpesvirus 1 genome J. Virol. 71 (9), 6517-6525 (1997) 97404659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wildebeest herpesvirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gammaherpesvirinae; Rh
1 (bases 1 to 130608)
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89.130
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                                                                                                                                                                                                                                                                                                          'note="putative ORF"
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VRL 19-OCT-2001

COMMENT FEATURES

REFERENCE

ORGANISM

AUTHORS TITLE

JOURNAL

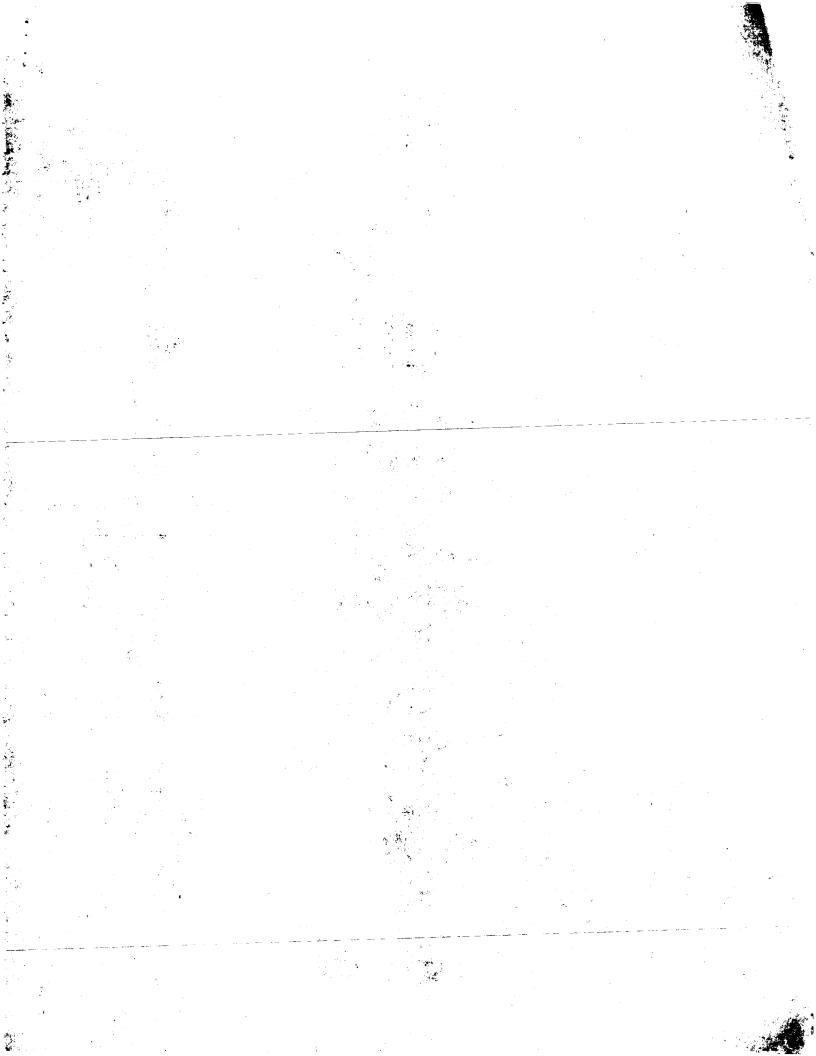
EYWORDS

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BASE COUNT

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CDS
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                                                 polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                       QYKMHMPKQPSEGTEDTPLAPDMSNIQLFKNLDVTEDLLLQVLRHPTVGCKAHIVHHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLYOPFRNELFNSSLDFYATIYPPRFLKDKVRHYVHGDINLNITGAASNYNWASPHT
AVTDSEIFRIPYTHVVRFIDRWEIRVRYPDVGFHGSRGVRFRGJGGAAKMCSTLASTT
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GYMEKYTMFKLAKACGUGLGLSMSAFSLPAHTLRLLKKWHFRULMYNHRZIKUSMSKLVD
SAAALLVIADNEYQDYSKKMDIALSGNGCPFHILGNLTPNSNTIVISDKNQYGEIVDI
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LTTIKGTIHIYVRYEDSNSTTALNILEINPFQKPAPIQNILLDNTNLKLYVNSEWEVS
EVPLDLCSVYGNDCFSGFMSRDPLCTWYNNTCSFKQRVSVETGGPANRTLSEMGGDHY
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                                                                                                                                                                                                                                         DTFTVEHQNTQLLSVPVSRLKHNWTLFSKSVDLLIVKEDQVLPEETSYGNTEVHLTVD
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                                                                                                   HYRSLLRTNLRHTFNFETQQLDFPHADRRGAVPHDNPQYIPMDAMDPSQ'
                                                                                                                                           VLPCWVQGTHLGFSHNNITFFGDLETRQQVAATFNGPLVQSGPAREYPLNPTEAEHPY
AGLCSEDGRHLALLFDPCLAFNTWQWQHNQTGPGQGELPVSPWKLMFYRLYNWSKFHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTSQSNELTAILQTRDAREKVFNVERIQHCRLLFFSGPGSEQLNHTHYALLREILCGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENSWEETLIYGLFLSPWNFSAVCVFTVKDIDHVFKTSKLKNYHHKLPTPRPGQCMKNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC58055.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAC58053.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                    polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                          TNGGLLLVWQPLVQQKLLDAKGLLDAVKKQQNTTTTTTTTTSRRQRRSVSSGIDDVYTAESTILLTQIQFAYDTLRAQINNVLEELSRAWCREQHRASLMWNELSKINPTSVMSSIYGRPVSAKRIGDVISVSHCVVVDQDSVSLHRSMRVPGRDKTHECYSRPPVTFKFINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SREYLSTLRLHFFALITGPLITQEGLFPSPPNVQLAHCLEAAHFMPHQKMLLNEMIKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLRGISPVPRTDIYITSSSCLECVLETSVVPNQGETLNELLLNHNCHHLVERVPPEPIKGLFESELQNLGLKVHIATDTIEQSVGKHEAVLQESLAYLKAHTIFNNTPKQVLELSNLLYMNSGQNQPSDSGVKCSELSKIWSRENELQKYRPKLNNGEPPGHFFDLHSPQGTEL
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CDLHKKLNVQFYNECGIEVNLTLINDIERFLSRLNCVFYCLSSSSALLALKEALTFLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLKIWGSVVYKQSATLLNHFLFRQSWVTQASLPPSVNGSPEQFENSKFIKSSLYVKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFCGGIFSSTHDTITALKQDCSNTFMKQTRLTGVAKRQNELFMRLSNILYGEEVPTKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQFVAFEEEQVKLTSMDHSGKVVGGKKRKIATMFDDLDL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKYAEAGAFSLPLLHGVTVEEAFVPNVKAVYKKIDMTTVSVKLSTFYNRAIIFHNVEK
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FKERLHLGKLIYLKSQMHSVMINKTEVYRIPLYDEDLFTKKSSLRRLYLPAVSEYLYY
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/note="ORFO9; similar to EBV BALF5, CMV UL54, HSV UL30"
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Sequence

| Strick | Strick | Orlg | ZScore | Escore | Len | Documentation | Side | Strick | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database: N. Geneseq_ 032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 523.620000
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Query: US-08-973-363-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-973-363-11 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              858457221
): 523.620000
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343.55
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8.6e-1
                                                                                                                                         us-08-973-363-11 x AAT42752
                                                                             Align seg 1/1 to: AAT42752
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seq_documentation_block:
ID AAM42752 standard; cDNA; 265 BP.
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AC AAM42752;
XX
T12-MAR-1997 (first entry)
DT 12-MAR-1997 (first entry)
DX
Chicken CHD-1A insert motif.
XX
Bird; sex determination; chromodomic KW CHD-W; chromodomain-Helicase-DNA bird;
XX
Gallus sp.
XX
Gallus sp.
XX
Key Location/Qualifiers fr misc_difference 52
FT misc_difference 62
FT 
                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42752
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    Percent Similarity:
                                                                                                                                                                                                                                                                       A composite nucleotide sequence (AAT42752) and putative translation (AAW08144) sequence are provided of a motif that is found spliced to a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the complete motif. There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of the CHD-W clone CC14 (see also AAT42753).
                                                                                                                                                                                                             Sequence 265 BP; 158 A; 16 C; 61 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key Location/Qualifiers
misc_difference 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                          Quality:
432.00
4.909
98.876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/note= "base 52 disrupts the reading frame for
the translated amino acid sequence given
    Length: 89
Gaps: 1
Percent Identity: 98.876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153.50
153.50
153.50
153.50
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from:

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seq_name:
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A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CC14 (see also AAT42754). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found as an insert in some CHD-1A clones (see also AAT42752).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
                                                                                                                                                                     Griffiths R,
                                                                                                                                                                                                               06-JUN-1995;
                                                                                                                                                                                                                                    05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                          Gallus
                                                                                                                                                                                                                                                                                                                                                                                              CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT42753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                   Disclosure; Fig
                                                                                                                  Avian
                                                                                                                                                                                                                                                        12-DEC-1996
                                                                                                                                                                                                                                                                             WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT42753
                                                                                                                                                                                          (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValLysGluGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGluLysArgGluThrLysGluLysGluAsnLysArgGluLeuLysAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gGluLysCluLysGluAspLysCyuSGluLeuLysGluLysAspAsnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGAAAAAAGAGAGACAAAAGAGAAAGGAAAATAAAAGGGAATTGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGAAGGAAGAAG
                                                                                                                                               1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42753
                                                                                                       chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of process.
                                                                                                                                                                                                                                                                                                                                                                                                        sex determination;
                                                                                                                                                                                                                                                                                                                                                                        sp.
                                                                                                                                                                                                                                                                                                                                                                                            chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                             CHD-W clone CC14 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; cDNA;
                                                                                                                                                                                          INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                     Tiwari
                                                                                                                                                                                                               95GB-0011439
                                                                                                                                                                                                                                   96WO-GB01341
                                                                                   7; 76pp;
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                      В;
                                                                                                                                                                                                                                                                                                          "base 52 disrupts the reading frame
the translated amino acid sequence
                                                                                                                                                                                                                                                                                                  in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137
                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                             chromodomain-Helicase-DNA binding case-DNA binding on the W chromoson
                                                                                                                                                                                                                                                                                                  Fig
                                                                                                                                                                                                                                                                                                                                                                                                                          motif.
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                                                                                                                                                                                                                                                                                                                                                                                             chromosome;
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                                                                                                                                                                                                                                                                                                                                                                                                       1 Avian;
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alignment_block: US-08-973-363-11 x
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:AAS90688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
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XX
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                                                                                                                                                                                   WPI; 200
P-PSDB;
polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCN) primers, oligomers, and for chromosome polymerase and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                      diagnostics, for responsible for
                                                                              The
                                                                                                                                                                                                                                                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS90688 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101
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                                                                                                     Claim
                                                                                                                                                             New isolated
                                                                                                                                                                                                                                          (HYSE-)
                                                                                                                                                                                                                                                                                                    30-MAR-2001;
                                                                                                                                                                                                                                                                                                                          11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                 WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluGluLysArgGluThrLysGluLysGluAsnLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ysGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGGGATTGTTTCAGTGAAAACATCCACATAAAAAAATAAAAGCAGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGlu.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity:
                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGAAAAAAGAGAGACAAAAGAGAAAGGAAAATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-639362/73
DB; ABG26501.
                                                                                                                                                                                                                                                                                                                                                                                            supplement;
                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                       chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                      RT,
                                                                                                                                                                                                                                           HYSEQ
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                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to:
                                                                                                                                      polynucleotide and encoded polypeptides, useful forensics, gene mapping, identification of mutator genetic disorders or other traits and to assumptions.
                                                                                                                                                                                                                      Liu
                                                                                                     Ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                 2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                    2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                               novel
                                                                                                                                                                                                                                           INC.
                                                                              relates to isolated
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4.390
89.130
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                                                                                                                                                                                                                                                                                                                                                                                           e mapping; gene mapping; gene therapy; forensic
medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                              human diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA;
                                                                                                     26492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 10
                                                                                                                                                                                                                     Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   621
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                                                                                                   103pp;
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                                                                                                    English.
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Identity:
                                                                              polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ço:
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                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137
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                                                                                                                                                                                                                                                                                                                                                                                                        forensic;
                                                                                                                                        mutations
o assess
                       techniques
                                                                                                                                                                                                                                                                                                                                                                                             SS
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Sequence 621 BP; 324 A; 36 C;

227 G;

34 T; 0 other;

quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fifth. Wipo.int/pub/published_pct_sequences.

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seq_documentation_block:
ID AAS46691 standard; DN
XX
AC AAS46691;
XC AAS46691;
XX

THEORY SUPPRESSOR GET
XX

THOOUR SUPPRESSOR GET
XX

WHUMAN; tumour suppres
KW Cancer; tumour; CpG o
KW Cytosine methylation;
XX

Gytosine methylation;
XX

PD WO200168912-A2.
XX

PD 20-SEP-2001.
XX

PF 15-MAR-2001; 2001DC-1
PR 06-APR-2000; 2000DE-1
PR 07-APR-2000; 2000DE-1
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US-08-973-363-11 x AAS90688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
    Quality:
    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAS46691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAS90688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                            294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194
                                                                   15-MAR-2001; 2001WO-EP02955
                                                                                                                                                                                                                                                           Tumour suppressor gene derived chemically modified sequence #414.
                                                                                                                                                                                                                                                                                                                                                            AAS46691 standard; DNA; 24259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 GGAG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu
||||||||||||:::|||:::::||||::::|||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspLysCluLeuLysGluLysAspAsnLysGluLysArgGluAsnLy
                                                                                                                                                                                                                                                                                                                                                                                                                                        sValLysGluSerThrGlnLysGluLysGluValLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000DE-1013847.
; 2000DE-1019058.
; 2000DE-1019173.
                                                                                                                                                                                                                                                                                          (first entry)
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2.573
75.610
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Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                             ВP
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1
41.463
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11996

sGluLysArgGluAsnLysValLysGluSerThrGlnLysGluLysGluV 84

51

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alignment_block:
US-08-973-363-11 x AAS46691/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (CS) and sequences complementary to (SS). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may be a complementary to (SS). The nucleic acid may be a periode for a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cc ancers and tumours. The probes can also be used in a method for a carray for analysing diseases associated with CpG dinucleotides e.g. cc ancers and tumours. The probes can also be used in a method for accertaining genetic and/or epigenetic parameters may be compared to another set of genetic and/or epigenetic parameters, the cc diseases, by analysing cytosine methylations. The parameters may be cc compared to another set of genetic and/or epigenetic parameters, the cc differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the complementary sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. IB and ID). ID 536 and ID 535, except for those whose partner sequence cc cis missing).
                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AAS46691 from: 1 to: 24259
                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                 Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 24259 BP; 6392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-602752/68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is missing).
17 sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG 34
                                                                                                                                                                                    l AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGluLy 17
                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                157.00
2.343
76.136
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                                                                                                                                                                                                                                                                                                                                                                Length:
Gaps:
Percent Identity: 35.
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alignment_scores:
    Quality:
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                                                                                                                      CC polypeptide (II) sequences. (I) is useful as hybrilisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The production of (II) are therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (III). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical company of sites expressing (II). (I) and (II) are useful in medical company of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed confirmation but was obtained in electronic format directly from WIPO at free wine intention, but was obtained in electronic format directly from WIPO at first wine intention but was obtained and accounts of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                            ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder; ss.
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No 5345;
   156
                                                                           191
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                                                                         c;
                                                                       149
                                                                         <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein #5345
 Length:
                                                                         36 T; 0 other;
 75
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:AAS74240
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ID AAS74240 standard;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCD) primers, oligomers, and for chromos and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence for identifying expressed genes. (I) is useful in gene therapy tech
                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodyversity
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                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel
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                                                                                         Claim 1;
                                                                                                                 biodiversity
                                                                                                                                                                                                                                                                         31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                  P-PSDB;
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                                                                                                                                                                                               2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome mapping;
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                                                                                        SEQ
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2000US-0649167
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77.333
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medical imaging; diagnostic; genetic (
                                                                                     10044; 103pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     human diagnostic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA;
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                                                                                        English
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                                                                                                                                                                                                                                                                                                                                                                                                                             forensic;
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chromosome

techniques

9999999999999998% 99999999999999

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alignment_block:
US-08-973-363-11 x AAS74240
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ID AAS90715 standard; cDNA; 693 BP
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 AGAAG 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 AAGAAGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGAGGAGGA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 693 BP; 296 A; 79 C; 234 G; 84 T; 0 other;
WO200175067-A2
                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #26519.
                                                                                                                                                                                                                                                                                                13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 gGluAsnLysValLysGluSerThrGlnLysGluLysGluValLysGluG 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LeuLys......GluLysAspAsnLysGluLysAr 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 snLysArgGluLeuLysArgGluLysLysGluLysGluAspLysLysGlu 60
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75.294
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Gaps: 2
Percent Identity: 41.176
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alignment_block:
US-08-973-363-11 x AAS90715
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Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at fig. at tip. wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAS90715 from: 1 to: 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
387 GGAGGAGGAGAAGAAGAAGAAGGAGGAGAAGGAGAAGGTGAAGGAGA 436
                                                                                      190 AAGAAGAATAAGGAGGAGAAAGAGGAGAAGGAAGAAGGAGAAGGAG.. 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 693 BP; 296 A; 79 C; 234 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 26519; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                     61 LeuLys......GluLysAspAsnLysGluLysAr 70
                                                                                                                                                                                                                          44 snLysArgGluLeuLysArgGluLysGluLysGluAspLysLysGlu 60
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                                                                                                                                                                                                                                                                                                                 eGlyIleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluA 44
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Ratio:
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2.438
75.294
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Gaps: 2
Percent Identity: 41.176
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AGAAG 441

87

luLys

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alignment_block:
US-08-973-363-11 x
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                                                   Align seg 1/1
                                                                                                                        Percent Similarity:
 2299
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                                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatoryvulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
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01-SEP-2000;
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antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic;
                                                                                                                                                                                                       Sequence 14006 BP;
                                                                                                                                                                                                                                                                                                                                                         Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                         LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:ABL33958
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                                                                                                                                                   Quality:
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                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                                                                                                                                                                                                                                                                 methylation
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2000DE-1043826
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                                                    reverse of: ABL33958
                                                                               ABL33958/rev
                                                                                                                     156.00
2.438
78.049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin
                                                                                                                       Gaps:
Percent Identity:
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                                                                                                                                                                                                      3257 G;
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seq_name:
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polymerase chain reaction (PCR) primers, oligomers, and for chromosome cand gene mapping, and in recombinant production of (II). The complete sare also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques concentration (II) is useful in gene therapy techniques (II). (II) is useful in gene therapy techniques (II). (II) is useful for generating annibodies against it, detecting or quantitating a polymeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating concers involving aborrant protein expression or biological activity. The polymeptide and polynucleotide sequences have applications in changings in the sequences of data and products dependent on DNA and concers involved and polynucleotide sequences have applications in consider the produce other types of data and products dependent on DNA and consider sequences. AAS64197-AAS94564 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2099
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                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding
                                                                                                                                                                                                                                                                                    Claim 1;
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                                                                                                                                                                                                                                                     invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        supplement;
                                                                                                                                                                                                                                                                                                                                                                                            2001-639362/73
DB; ABG26538.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome mapping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYSEQ
                                                                                                                                                                                                                                                                                    SEQ
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                                                                                                                                                                                                                                                                                    IJ
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2000US-0649167.
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medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                26529; 103pp; English
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SSSSSSS

diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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seq_documentation_block:
ID ABA58819 standard; DNA; 475
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US-08-973-363-11 x AAS90725
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Quality:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAS90725
               WPI;
                                                                                                                           30-JUN-2000;
03-AUG-2000;
                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 297 BP; 153 A; 12 C; 112 G; 20 T; 0 other;
                                       Penn
                                                                                                                                                                                        30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                             WO200157277-A2
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                              Human; foetal liver; gene expression; single exon nucleic acid
                                                                                                                                                                                                                                                                                                                     Human foetal liver single exon nucleic acid probe #7124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197
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                                                               (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GluLysLysGluLysGluAspLysLysGluLeuLysGluLysAspAsnLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 HisLeuHisLysLys......IleLysThrGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sGluLysArgGluAsnLysValLysGluSerThrGlnLysGlu 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-483447/52
                                       SG,
                                                               MOLECULAR DYNAMICS INC.
                                       Hanzel DK,
                                                                                      2000US-0180312

2000US-0207456

2000US-0608408

2000US-0632366

2000US-0632368

2000US-0234587

2000US-023635

2000US-023635

2000US-023635
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71.605
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44.444
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                                                                                                                                                                                                                                                                                              probe;
                                                                                                                                                                                                                                                                                              SS
 04-FEB-2000; 2000US-0180312
26-MAY-2000; 2000US-0207456
                                                                                                                                       Human, gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                      276
                                    30-JAN-2001; 2001WO-US00666
                                                               09-AUG-2001
                                                                                       WO200157274-A2
                                                                                                                 Homo sapiens.
                                                                                                                                                                                      Probe #6203 for gene expression analysis in human heart cell sample
                                                                                                                                                                                                                 23-JAN-2002
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(first entry)

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alignment_block:
US-08-973-363-11 x ABA58819/rev
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ID ABA27737 standard;
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                                                          seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:ABA27737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 7124; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver - \,
                                                                                                      Sequence 475 BP; 38 A; 198 C; 45 G; 194 T; 0 other;
                                                                                                                                                                                                                  57 AspLysGluLeuLysGluLys...AspAsnLysGluLysArgGluAs 72
                                                                                                                                                                                                                                                                                                                                                                                  23 oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL 40
                                                                                                                                           72 nLysValLysGluSerThrGlnLysGluLysGluValLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr 23
                                                                                                                                                                                                                                                                      ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu 56
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Ratio:
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2.430
77.108
DNA; 475
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Gaps: 2
Percent Identity: 42.169
  ВP
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Seq.
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US-08-973-363-11 x
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                                                                                                                                                                                        seq_name:
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                               documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the propertication, but was obtained in electronic format directly from the properties of the content of the properties of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the
                                                                                                                                                                                                                                                                                                                                                                                                  276
  Human brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr
                                                                                                                                                                                                                               AGAGGAG
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                                                                                                                                                                                    /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK06973
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                                                                                                                            standard;
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
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    expressed
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                                                                                                                            DNA;
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probe
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alignment_block:
US-08-973-363-11 x AAK06973/rev
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                               brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; brain expressed exon; microarray; Alzheimer's dise; epilepsy; cancer; ss.
                                                                                   276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
176
                                         226
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27-SEP-2000;
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                    72
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oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL
                                                                                                                                                                                 LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr
                 nLysValLysGluSerThrGlnLysGluLysGluValLysGluGluLys
                                          AspLysLysGluLeuLysGluLys...AspAsnLysGluLysArgGluAs 72
                                                                                  ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu
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2000US-0234687.
2000US-0236359.
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2000US-0608408.
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Identity:
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42.169
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                    88
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                                         177
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alignment_block:
US-08-973-363-11 x AAK32709/rev
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ID AAK32709 standard; DNA; 475 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
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                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AAK32709 from: 1 to: 475
                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000; 2000US-0180312.
26-MAY 2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                        Sequence 475 BP; 38 A; 198 C; 45 G; 194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone {\tt marrow} -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00668.
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                                                                                                                  Example 4; SEQ ID NO: 7266; 658pp + Sequence Listing; English.
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                                                                 40 ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu 56
                                                                                                                                             23 oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL 40
                                                                                                                                                                                                                                                    7 LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr 23
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US-08-973-363-11 x AAI38524/rev
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                                                                                                                                                                                                                                                    Ratio: 2.430
Percent Similarity: 77.108
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26-MAY-2000; 2000US-0207456.

30-UUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-023559.

04-OCT-2000; 2000GB-0024263.
                                              364 AAACAGAAGAAGAAGGAAGAAGGAGGAGGAGGAGGAGGAAGGA 315
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 475 BP; 38 A; 198 C; 45 G; 194 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producting a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; SEQ ID No 7210; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53.
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23 oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 nLysValLysGluSerThrGlnLysGluLysGluValLysGluGluLys 88
                                                                            7 LysHisLeuHisLysLysIleLysThrGluLysGluAsnGluGluLysPr 23
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Ratio:
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seq_documentation_block:
ID ABA71159 standard; DN
XX
AC ABA71159;
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DT 01-FEB-2002 (first e
XX
DT 01-FEB-2002 (200005-0
PR 20-AUG-2001; 2001W0-U
XX
DP 09-AUG-2001; 2001W0-U
XX
AC 04-FEB-2000; 2000US-(
PR 21-SEP-2000; 2000US-(
PR 21-SEP
alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; SEQ ID NO 19464; 639pp + sequence listing; English.
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alignment_block:
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                 72 nLysValLysGluSerThrGlnLysGluLysGluValLysGluGluLys
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 AAGAAGAAGAAGAAGAAGAAGAAGAGGAGAAAGAGAGGAGGAGGA
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                                                                                       AspLysGluLeuLysGluLys...AspAsnLysGluLysArgGluAs 72
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Query: US-08-973-363-11
Query length: 88
Database: EST:*
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Search time (sec): 4390.400000
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-MODEL-frame+_p2n.model -DEV=x1h
-MODEL-frame+_p2n.model -DEV=x1h
-MODEL-frame+_p2n.model -DEV=x1n
-MODEL-frame+_p2n.model -DEV=x1-000 -GAPEXT=4.000
-MODEL-frame+_p2n.model -SUPFIX-p2n.rst -GAPOP=12.000 -GAPEXT=4.000
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-NOPU-6 -LOPU-3 -LONGLOG -DEV_TIMEOUT-120 -MARN_TIMEOUT-30
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Copyright (c) 1993-2000 Compugen
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gb_gss:AG061359
gb_est2:BG533694
gb_est2:BG539033
gb_est2:BM168323
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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US-08-973-363-11 x BM015597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS BM015597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: BM015597
                                                                                                                                                                                                      140 AGACAGTGAAGAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                          34 luGluLysArgGluThrLysGluLysGluAsnLysArgGluLeuLysArg
                                                                                                                                                                                                                                                                              17
                                                                                                                                                                                                                                                                                                                                                           90 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                               1 AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 677)

RS NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12066 row: g column: 08
High quality sequence stop: 674.

S Location/Qualifiers
                                                                                                                                                                                                                                               sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est2:BM015597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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//db_xref="taxon:9666"
//clone=lib="NHI_MGC.87"
//clone_lib="NHI_MGC.87"
//clone_lib="NHI_MGC.87"
//lab_host="DH10B (phage-resistant)"
//note="Organ: breast; Vector: pCWV-SPORT6; Site_1: Not1;
//note=
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766 i AG061359 Pan troglodytes DNA
900 i BG533694 602562348F1 NIH_MGC
1119 i BG539033 602568396F1 NIH_MG
233 i BM168323 EST570846 PyBS Plas
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                       alignment_scores:
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AA748563
AA748563
AA769.51 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309072 3' similar to SW:CHDL_MOUSE P40201 CHROMODOWAIN-HELICASE-DNA-BINDING PROTEIN CHD-1. [1] ;contains element L1 repetitive element ;, mrNA
  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allma
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome

DNA Sequencing by: Washington Colone distribution

Clone distribution: NCI-CGAP Clone distribution
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
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1 (bases 1 to 343)
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                                                                                                                                                                                                                                        j. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTPT3 vector. Library went through one round of normalization, and was
                                                                                                         constructed by Bento Soares and M. Fatima Bonaldo." 69 c 35 g 177 t
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/db_xref="taxon:9606"
  272.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1309072"
/clone_lib="NCI_CGAP_GCB1"
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430 bp mRNA linear EST 01-DEC-1991 qh81f02.x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:1851099 3' similar to contains element LTR5 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
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Unpublished (1997)
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(Pharmacia), digested with Fac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library
                                                                  /note="Organ: Liver and Spleen; Vector: pT/TT3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen lNFIS library 1st strand chamausa refund
                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1851099"
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91.304
                                                                                                                                                                                                                                              /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                            /sex="male"
                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
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                                                                                                                                                                                                                                                                     /dev_stage="20 week-post conception fetus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 GAGATAAAAGAAAAAGAGATAAGAAAGATATAAAGGAAAAAGATTTTAA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGluLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AGAA 3
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 456)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
Mhite,Y., Wylie,T., Waterston,R. and Wilson,R.
MashU-NCI human EST project
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA699918 456 bp mRNA linear EST 19-DEC-1997 z161f12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:435311 3', mRNA sequence.
                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40mil frd. ET from Amersham
High quality sequence stop: 420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA699918.1 GI:2702881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111
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4.371
91.176
/organism."Homo sapiens"
//db_xref="GDB:1335080"
//db_xref="taxon:9606"
//db_xref="taxon:9606"
/clone="IMACE:435311"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
                                                                                                                                                                  Location/Qualifiers
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Gaps: 0
Percent Identity: 77.941
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REFERENCE
AUTHORS
TITLE
JOURNAL
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
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US-08-973-363-11 x AA699918/rev
                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS BF239967
                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est2:BF239967
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: AA699918 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 AAGAAAAGAGGAAAGGAAAAAGGAGAATAAAAAAGAACTTAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 AGACAGTGAAGAAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GluLysLysGluLysGluAspLysLysGluLeuLysGluLysAspAsnLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 GAGATAAAAGAAAAGAGGATAAGAAAGATATAAAGGAAAAAGATTTTAA
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 821)

E 1 (bases 1 to 821)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BF239967
                                                                                                                                                                                                                                                                                                                                                                   BF239967 821 bp mRNA linear EST 14-NOV-2000 651995170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5',
                                                                                                                                                                                                                                                                                                    BF239967.1 GI:11153890 EST.
                                                                                                                                                                                                                                                                 Homo sapiens
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4.361
91.045
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Gaps: 0
Percent Identity: 77.612
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BASE COUNT
ORIGIN
                                                                                                                                                                                                         seq_documentation_block:
LOCUS BM168938
                                                                                                                                                                                                                                                                seq_name: gb_est2:BM168938
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                    REFERENCE
                                                                               SOURCE
                                                                                                                                                                                    DEFINITION
                                                                                                  KEYWORDS
                                                                                                                         VERSION
                                                                                                                                            ACCESSION
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    AUTHORS
                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGluLy 17
                                                                                                                                                                                                                                                                                                                                                                                                            LysGluLysArgGluAsnLysValLysGluSerThrGlnLysGluLysGl 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluGluLysArgGluThrLysGluLysGluAsnLysArgGluLeuLysAr
                                                                                                                                                                                                                                                                                                                                               uValLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGAGATAAAAGAAAAGAGGATAAGAAAGATAT . AAGGAACAAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGAAAAGAGGGAAGCAAAAGAAAAGGAGGAATAAAAAAAGAACTTAAAAG
                                                                                                                                                                                                                                                                                                                                                                                       AAAGAAAAACGAGAAAACCAAAGTAAAAGAAGCTATACAGAACGAAAAAG
                                                                                                                                                                                                                                                                                                          ACTAAAGGACGAAAAG 498
                                                                                                                                                                   EST571461 PyBS Plasmodium yoelii yoelii cDNA clone PYCPJ56 5' end, mRNA sequence
                  Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 660)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                           mRNA sequence.
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Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
                                                                                                                       BM168938.1 GI:17302170
                                                                                                                                            BM168938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type_from chronic myelogenous leukemia"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DH108 (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: Sfii (ggccgctcaggcc); Site_2: Sfii (ggccattatggcc);
Doubbe-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
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3.367
87.778
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/clone="IMAGE:4133129"
/clone_lib="NIH_MGC_54"
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Gaps: 2
Percent Identity: 68.889
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6
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JOURNAL
COMMENT
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                                                                                                                                                             104
                                                                                                                                                                                                     44
                                       77
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AAAAGAAGAAAAAAGAAGAAAAGGAAGAAAAG
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alignment_block:
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                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 AGAAGAAAAAAGGATGAAAAGGAAGAAAAGGAAAAAAGAAAAAGAAA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LysLysIleLysThrGluLysGluAsnGluGluLysProGluProAspIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CGCGAGTTGAAAACTGAGAAAGTGGAAGAAAAGGAAAAGGAAAAGGAAAA 53
rThrGlnLysGluLysGluValLysGluGluLys
                                                                                                                                                                                                                                                                                                                              eGlyIleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluA 44
                                                                                                                                                                                         LeuLysGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fraser, C.M. and Carucci, D.J. Plasmodium yoelii EST project at TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: ADF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          //lab_host="E. coli xI.1 Blue"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     After packaging, the phagemid vector (pAD-GAL4) excised from the HybriZAP vector and plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195.00
3.047
82.051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="PyBS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Plasmodium yoelii yoelii"
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Gaps: 0
Percent Identity: 48.718
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                                  88
                                                                                                                                                                                                                                                                                   153
                                                                                                               203
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TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                      alignment_block:
US-08-973-363-11 x BM161742
                                                                                                                                                                                                                                                                                                                                                alignment_scores
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LOCUS BM161742
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                                                                                                                  Align seg 1/1 to: BM161742
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contact: Jane Cariton

Parasite Genomics Group

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium yoelii yoelii.
Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 605)
Carlton,J.M., Daly.T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.W. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
Contact: Jane Carlton
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BM161742
BM161742.1 GI:17307423
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             //dev_stage="Asexwal blood stages"
//dev_stages="Asexwal blood stages"
//dev_stages="Asexwal blood stages="Asexwal blood stages"
//dev_stages="Asexwal blood stages="Asexwal blood sta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carlton@tigr.org
                                                                                                                                                                                                                                                             193.00
3.063
81.818
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37 c
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/clone="PYCKI49"
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/strain="17XL"
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                                                                                                                  from: 1
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Gaps: 0
Percent Identity: 49.351
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AUTHORS
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SOURCE
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
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LOCUS BM167712
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 640)
Carlton, J.M., Daly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST.
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                           358
                        isolated."
a 34 c
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1. .640
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                        144 g
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62 LysGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSerTh 78
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Plasmodium yoelii EST project at TIGR
Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-338-0208
Fax: 301-388-0208
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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EST570235 PyBS Plasmodium yoelii yoelii cDNA clone PYCOP51 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cariton@tigr.org
Email: cariton@tigr.org
For clone info, please contact the Malaria Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reagent Resource Center, ATCC http://www.malaria.mr4.org/mr4pages/index.html
                                           /dev_stage "Asgual blood stages"
//lab_host="E. coli XL-I Blue"
//lab_host="E. coli XL-I Blue"
//lab_host="E. pah-GALA, At 20-25% parasitemia, blood was collected from BALB/CByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystaline cellulose collumns. Total RNA was isolated using the guanddinium isothiocyanate method, and mRNA isolated using the guanddinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl 5-500 column.
Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pbb-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Plasmodium yoelii yoelli"
/strain="17xL"
/db_xref="taxon 73239"
/clone="PYCOP51"
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104 t
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REFERENCE
AUTHORS
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ORGANISM
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LOCUS AZ009894
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US-08-973-363-11 x BM167712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 LysIleLysThrGluLysGluAsnGluGluLysProGluProAspIleGl
                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (Pieteredejong med.buffalo.edu). Clones may be purchased from RACPAC Resources (http://bacpac.med.buffalo.edu). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 348 row: I column: 8
Seq primer: SP6
Class: BAC ends.
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse BAC End Sequences from Library RPCI-23 
Unpublished (1999) 
Other_GSSs: RPCI-23-348I8.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 600)
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3.063
81.818
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-34818"
                                                                                               Location/Qualifiers
                                                                               . 600
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Gaps: 0
Percent Identity: 49.351
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US-08-973-363-11 x AZ009894
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/note-*Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "a 121 c 167 g 104 t
190.50
2.977
81.013
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-23"
/sex="Female"
/lab_host="DH10B"
                              Length:
Gaps:
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from: 1
                  :
                                                Percent Identity: 54.430
;
0:
600
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11	LysLysIleLysThrGluLysGluAsnGluGluLysProGluProAspIl 27	
371	AAGAAGAAGAAGAAGAAGAAGGAGAAGAAGGAAGAAGGAG	
27	27 eGlyIleLysLysGluAlaGluCluLysArgGluThrLysGluLysGluA 44	
413	AAGAAGGAGAAGGAGAAGAAGAAGAAGAAGAAGAA	
44	snLysArgGluLeuLysArgGluLysGluLysGluAspLysLysGlu 60	
456	456 AGAAGAAGGAGAAGAAGGAGAAGAAGGAGAAGAAGAA	
61	LeuLysGluLysAspAsnLysGluLysArgGluAsnLysValLysGl 76	
503	AAGAAGGAGGAAGAAGGAAGGAAGGAAGGAAGGAAGGA	
76	76 uSerThrGlnLysGluLysGluValLysGluGluLys 88	
553	553 GGAGACGAAGGAAGAAGGAAGAAGGAAGAAG 589	

BASE COUNT

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alignment_block:
US-08-973-363-11 x AL628267
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LOCUS AI890775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   497 AAAAA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    303 AGAAAATGAGGACCGAACAGAGTTAGATGTCAGTGTTAACAAAGAGCCAG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 GAGGAAACTGTACCCCTCAGAACAAATAATAAAAGG...AGAGCAGAGAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 AAGAAAAGAAAGAGATA.....AAAGAAAATAAAAAGGACCCTAAGAAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 alLys 85
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A1890775 A1890775 GI:5595939
                                  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 547)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
cDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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2.828
78.824
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/note="Vector: pCS107; Site_2: NotI; CDNA
/note="Vector: pCS107; Site_2: DNA
/note="Vector: pCS107; Site_2: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 c
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Gaps: 2
Percent Identity: 44.706
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VERSION
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REFERENCE AUTHORS TITLE

SOURCE ORGANISM

ACCESSION VERSION

KEYWORDS

DEFINITION

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alignment_block:
US-08-973-363-11 x AI890775/rev
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Ratio: 4.375 Gaps: 0
Percent Similarity: 90.909 Percent Identity: 77.273
                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 luGluLysArgGluThrLysGluLysGluAsn 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 AGACAGTGAAGAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 sGluAsnGluGluLysProGluProAspIleGlyIleLysLysGluAlaG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspGluIleValSerValLysHisLeuHisLysLysIleLysThrGluLy 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.lnl.gov/bbrp/lmage/lmage.html
Insert Length: 1924 Std Error: 0.00

Seq primer: -40UP from Giboo
Seq primer: -40UP from Giboo
Seq primer: -40UP from Giboo
                                  9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                           Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 634)
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret Jao,S., Nierman,W., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ008814 634 bp DNA linear GSS 25-FEB-2000 RPCI-23-38903.TJ RPCI-23 Mus musculus genomic clone RPCI-23-38903,
                                                                                                                                                                                                                                                   and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ008814.1 GI:7084198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 a
szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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VERSION
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US-08-973-363-11 x AZ008814
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ORIGIN
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SOURCE
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                                                                                                                               seq_documentation_block:
LOCUS AZ330985
                                                                                                                                                                                          seq_name:
                                                             ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                               211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161
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                                                                                                                                                                                                                                                                                                                           258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AAGCATCATCACCAGTTCTTTTGATGGAAAAAGAAGAAGAAGAAGGAGGAGGA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 LysHisLeuHis......LysLysIleLysThrGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgGluLeuLysArgGluLysGluLysGluAspLysGluLeuLy 62
                                                                                                                                                                                                                                                                                                                           lnLysGluLys.....GluValLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                                  sGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSerThrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....AlaGluGluLysArgGluThrLysGluLysGluAsnLys 45
                                                                                                                                                                                                                                   AGGAGGAGAAGGAGGAGGAGGAGGAGGAG
                                                                                                                                                                                       gb_gss:AZ330985
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Ratio:
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                                                                             AZ330985 743 bp DNA linear GSS 29-SEP-20
1M0056C22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0056C22 R, DNA sequence.
                                      AZ330985.1 GI:10393428
                                                             AZ330985
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house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " a 73 c 219 g 63 t 1 others
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2.703
67.368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RPCI-23"
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Gaps: 4
Percent Identity: 47.368
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alignment_block:
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                                                                                                                                                                                             Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                 743
869
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                                                                                                                                       11 LysLysIleLysThrGluLysGluAsnGluGluLysProGluProAspIl 27
                                           27 eGlyIleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluA 44
                                                                                              Mus musculus
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
1 (bases 1 to 743)
                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0056 row: C column: 22
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606 Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 743
                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                             ţ
  107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114|gblAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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                                                                                                                                                                                             reverse of: AZ330985
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2.730
80.769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, I
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jaci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0056C22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weiss
                                                                                                                                                                                                                                                                                                                Gaps: 3
Percent Identity: 51.282
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Rodentia;
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656
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seq_name: gb_gss:AZ952930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LeuLysGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSe 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 571)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Welss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0217 row: N column: 19
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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2M0217N19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0217N19 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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801 585 7177
/abb_nst="E. coli strain XL10-Gold, T1-resistant, F-"
/labb_nst="E. coli strain XL10-Gold, Form the Jackson
musculus C57BL/GJ (female) was obtained from the Jackson
Laboratory Mouse DNA Resources
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil 4732114 (gb)AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC2M library"
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MEDLINE
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COMMENT

REFERENCE

AUTHORS

ORGANISM KEYWORDS VERSION ACCESSION DEFINITION

FEATURES

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alignment_block:
US-08-973-363-11 x AZ952930
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Ratio: 2.664
Percent Similarity: 78.049
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MEDLINE
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                                                               JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 sValLysGluSerThrGlnLysGluLysGluValLysGluGluLys 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 AspLysLysGluLeuLysGluLysAspAsnLysGluLysArgGluAsnLy 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 ysGluLysGluAsnLysArgGluLeuLysArgGluLysLysGluLysGlu 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 oGluProAspIleGlyIleLysLysGluAlaGluGluLysArgGluThrL 40
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                                                                                                                                                                                        Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottlier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuveglise, C., Ozker-Kalogeropoulos, O., Potter, S.,
Saurin, W., Pekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEBS, Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lepingle, A., Casaregola, S., Neuveglise, C., Bon, E., Nguyen, H., Artiguenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemlascomycetous yeasts: 14. Debaryomyces hansenii var. hansenii FEBS Lett. 487 (1), 82-86 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Debaryomyces hansenii.
Debaryomyces hansenii
Direct Submission

Direct Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex - FRANCE (E-mail :
seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS07B7L 981 bp DNA linear GSS 08-JUL-2001
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                                                                                                                  Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 981)
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46 c 194 g 48 t
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Gaps: 1
Percent Identity: 43.902
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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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US-08-973-363-11 x CNS07B7L
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                  840 AAGARAGAT...AAGAACGAGAAGAAGAAGAAGAAAGATAAGAACGAGAA 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
931 AGAAAGAAGAAGAAGAAGAAAGAAA 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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                                                                                 78 hrGlnLysGluLysGluValLysGluGluLys 88
                                                                                                                                                                                                                                                   61 uLysGluLysAspAsnLysGluLysArgGluAsnLysValLysGluSerT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 lyIleLysLysGluAlaGluGluLysArgGluThrLysGluLysGluAsn 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                               LysArgGluLeuLysArgGluLysLysGluLysGluAspLysLysGluLe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....LysThrGluLysGluAsnGluGluLysProGluProAspIleG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. unarum, Saccharomyces exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to 8 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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gb_ov:AF004397
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137 ! A58694 Seque
6872 ! AF004397 Ga
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AUTHORS
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                                                                                                                                     ACCESSION
VERSION
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US-08-973-363-14 x A58694
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                                                                                                                                                                                                                                                                       DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                               101 GGAGAAAAAGAGAGAGAAAGGAAAAGAAATAAG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                     34 GlyGluLysArgGluThrLysGluLysGluAsnLys 45
    Archosauria; Aves; Neognathae; Gall
Phasianinae; Gallus.
1 (bases 1 to 6872)
Griffiths,R. and Korn,R.M.
A CHP1 gene is Z chromosome linked
Gene 197 (1-2), 225-229 (1997)
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Sequence 13 from Patent W09639505.
A58694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: WO 9639505-A 13 12-DEC-1996; ISIS INNOVATION (GB) Other publication AU 5906996 961224.
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Griffiths,R. and Ti
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unidentified
                                                                                                                                       Gallus gallus
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                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                        chicken.
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97.826
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1 AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGlu.L 17
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                                                                                                                                                                                                                                                                    AF004397 MRNA linear VRT 08-OC
AF004397 MRNA linear VRT 08-OC
Gallus gallus chromo-helicase-DNA-binding on the Z chromosome
protein, variant with hydrophilic domain, (CHD-2) mRNA, compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffiths,R. and Tiwari,B.
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Gaps: 1
Percent Identity: 97.826
                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae;
in
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201978 : AC079533 Mus musculus clo
49221 : At450106 Human DNA sequenc
132755 : AC092536 Homo sapiens BAC
147541 : AC097032 Rattus norvegicu
chicken Gallus
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US-08-973-363-14 x AF004397
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4341 GATGAGATTGTTTCAGTGAAACATCTACATAAAAAATAAAAAAACAGAAAA 4390
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SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
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LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERII
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DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
DDDEDYDKRGSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTEEDEFETIEKFMD
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/note="CHD protein with hydrophilic domain"
/codon_start=1
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/db_xref="GI:2501846"
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/db_xref="taxon:9031"
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US-08-973-363-14 x A58693
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Sequence 12 from Patent W09639505.
A58693
                          1 (bases 1 to 101220) DOE Joint Genome Institute and Stanford Human Genome Center
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 101220)
                                                                                                                     AC092372
AC092372.3 GI:17402768
HTG.
                                                                                                                                                                Homo sapiens chromosome 5 clone RP11-58M12, complete sequence
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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              Direct Submission
                                                                                       Homo sapiens
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US-08-973-363-14 x AC092372/rev
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Ratio: 4.077
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Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
Location/Qualifiers
Direct Submission
Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Submitted Intitute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                     Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 134365)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (03-UUI-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US3 (bases I to 101220)
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Homo sapiens chromosome 5 clone CTD-2082I17,
AC012624
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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/db_xref="taxon:9606"
/chromosome="5"
/clone="RPil-58M12"
34122 a 18862 c 17827 g 30409 t
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LOCUS AC021440
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Align seg 1/1 to: AC012624 from: 1 to: 134365
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Ballwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearrichano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., McGotald, P., Marquis, N., McGwan, P., McGurk, A., McKernan, K., McCheeters, R., Meldim, J., Meneus, L., Morrow, J., Naylor, J., Morman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,
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Homo sapiens clone RP11-58M12, W
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On JUL 72001 this sequence version replaced g1:14277267.
Location/Qualifiers
1. .134365
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Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Unpublished
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DOE Joint Genome Institute and Stanford Human Genome Center.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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1 (bases 1 to 143079)
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/db_xref="taxon:9806"
/chromosome="5"
/clone="crb-2082117"
40414 a 24497 c 25503 g 43951 t
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Gaps: 0
Percent Identity: 68.889
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Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,

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FEATURES
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Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center clone name: 58_M_12
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Contact: sequence_submissions@genome.wi.mit.edu
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38821 38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
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/note="assembly_fragment"
                                                                                              /note="assembly_fragment"
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JOURNAL REFERENCE
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SOURCE
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US-08-973-363-14 x AC021449
                                                                                                                                  COMMENT
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                                                                                                                                                                                       TITLE
                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                    Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:7528342.
                                                                                -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                   2 (bases 1 to 145659)
DOE Joint Genome Institute
                                                                                                                                                                                                                                                                     DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 145659)
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Homo sapiens chromosome 5 clone
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Center clone name: CIT-HSPC_480B11
               Center Project Name: 369535
                               Project Information
                                                                Web site:
                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                      Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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/note="assembly_fragment
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62720. .75408
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51931. .62619
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4.077
                                                                http://www.jgi.doe.gov
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Gaps: 0
Percent Identity: 68.889
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alignment_block:
US-08-973-363-14 x AC008531
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LOCUS AC091946
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Consensus quality: 14256 bases at least Q40

Consensus quality: 14256 bases at least Q30

Consensus quality: 143744 bases at least Q20

Estimated insert size: 148000; pulse field gel estimation

Estimated insert size: 145059; sum-of-contigs estimation

Quality coverage: 6.27 in Q20 bases; pulse field gel estimation

Quality coverage: 6.27 in Q20 bases; pulse field gel estimation

NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 10875 100974: gap of unknown length

* 10875 100974: contig of 56174 bp in length

* 10875 100974: gap of unknown length

* 11328 11829: contig of 1253 bp in length

* 118291 11829: gap of unknown length

* 118191 11829: gap of unknown length

* 118191 11829: contig of 4040 bp in length

* 118291 119694: contig of 4040 bp in length

* 113298 12339: gap of unknown length

* 113298 12339: contig of 3503 bp in length

* 123298 12339: contig of 3503 bp in length

* 123298 12339: contig of 3503 bp in length

* 123298 12359: contig of 5503 bp in length

* 12359 1250: contig of 5503 bp in length
193446 bp DNA linear HTG 09-JUN-2001 Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.
AC091946 AC091946.1 GI:14333882
HTG; HTGS_PHASE1.
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/clone_lib="CalTech human BAC library C"
26309 c 27580 g 48609 t 600 other
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/db_xref="taxon:9606"
/chromosome="5"
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Gaps: 0
Percent Identity: 68.889
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Consensus quality: 180259 bases at least Q20
Consensus quality: 184715 bases at least Q20
Consensus quality: 184715 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.
** NOTE: This is a 'working draft' sequence. It currently
** consists of 33 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
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Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 193446)
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Center Project Name: 544799
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DOE Joint Genome Institute.
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         18: contig of 1358 bp in length
18: gap of unknown length
17: concil of 1209 bp in length
18: gap of unknown length
18: contig of 1957 bp in length
18: contig of 1502 bp in length
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18: contig of 1502 bp in length
18: gap of unknown length
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19: gap of unknown length
19: gap of unknown length
19: gap of unknown length
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19: gap of unknown length
19: contig of 2366 bp in length
19: contig of 3324 bp in length
19: gap of unknown length
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FEATURES

BASE COUNT

KEYWORDS ACCESSION DEFINITION

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SOURCE
ORGANISM
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US-08-973-363-14 x AC091946
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Quality:
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                                                                                             seq_documentation_block:
                                                                                                                     seq_name: gb_pr:AC026778
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                                                                 Homo sapiens chromosome 5
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                                        AC026778.4 GI:14277282
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/clone_lib="RPCI human BAC library
35252 c 37061 g 60360 t 3202
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Location/Qualifiers
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110866: contig
110966: gap of
117571: contig
117671: gap of
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130583: contig of 6745 bp in length
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BASE COUNT
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LOCUS AC022121
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                 Homo sapiens chromosome AC022121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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WI-13675 G23101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 1, 2001 this sequence version replaced gi:13677045. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
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Direct Submission
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Mammalia; Eutheria; Primates;
1 (bases 1 to 195433)
DOE Joint Genome Institute and
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-428I11"
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CTD-2007H13,
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                                                                                                                                                                  complete sequence
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LOCUS AC092382
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ORIGIN
                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                       seq_name: gb_htg:AC092382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AC022121 from: 1 to: 219258
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                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                     17 sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG 34
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Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 219258)
                                                                                                                       276181 bp DNA linear HTG 03-JUL-200 Homo sapiens chromosome 5 clone RP11-75H1, WORKING DRAFT SEQUENCE, 47 unordered pieces.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHGC-103595 G57841
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SHGC-58345 G38487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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Unpublished
                                                              AC092382.1 GI:14589571
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                            uman.
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/chromosome="5"
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71954 a 42062 c 40933 g 64309 t
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4.077 Gaps: 0
86.667 Percent Identity: 68.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 229677 bases at least Q40.
Consensus quality: 256163 bases at least Q20
Consensus quality: 256163 bases at least Q20
Consensus quality: 25699 bases at least Q20
Estimated insert size: 174820; agarose-fp estimation
Quality coverage: 8.62 in Q20 bases; agarose-fp estimation
Quality coverage: 5.55 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary, Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Center Code: JGI
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Center clone name: RPCI-11_75H1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalla: Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 276181)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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1161: gap of unknown length
2827: contig of 1666 bp in length
2927: gap of unknown length
4227: contig of 1300 bp in length
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alignment_block:
US-08-973-363-14 x AC092382/rev
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9 276181: contig of 44813 bp in
Location/Qualifiers
                                     159.00
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157894: contig of 11081 bp in 1
157994: gap of unknown length
171752: contig of 13758 bp in 1
171852: gap of unknown length
201687: contig of 29835 bp in 1
201787: gap of unknown length
231268: contig of 29481 bp in 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group. Further Information Comp. Further Information Comp. The Amount of the Amount of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on Jul 14, 2000 this sequence version replaced gi:8919096. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; TT:, TRENBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 104780)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence is the entire insert of clone RP5-1185H19 The true t end of clone RP5-1039L11 is at 65940 in this sequence.
/clone_lib="RPCI-5"
26. .677
/note="L1M4 repeat:
                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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                                                                                                                                            /map="p13.1-13.3"
/clone="RP5-1185H19"
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	/note="L2 repeat: matches 26942737 of consensus" 1567515802	at: matches 57286155	S	מונים ביים מונים ביים מונים ביים מונים ביים ביים ביים ביים ביים ביים ביים ב	tches 2698 2750 of	repeat	/note="match: GSS: Em:AQ253971"	b .	/note="ILM4 repeat: matches 47875048 of consensus"		" .	,	. 3	/note="L2 repeat: matches 15011795 of consensus" 1068310798		/note="L2 repeat: matches 17942359 of consensus" 94939774	eat: matches 587361	/note="12 copies 2 mer ta 95% conserved" · 76547923	. !	/note="20 copies 2 mer gt 92% conserved" 7363. 7408	L1MC/D repeat: matches 7353	/note="MER58 repeat: matches 2106 of consensus" 71557307	er ta 65% conserv	5: EM:H	eat: m	: Em:AQ752096"	cepeat	/note="match: GSS: Em:AQ629810" 51625542	n : AQ04		/note="match: GSS: Em:AQ282331 match: STS: Em:G55257"	/note-"Alub repeat: matches 1296 of consensus"	/note="LIM4 repeat: matches -11498 of consensus" 2638 2932	in in	· (D	678967 /note="AluSx repeat: matches 1293 of consensus"
repeat_region	repeat_region	repeat_region	repeat_region	mild Carato		misc feature	repeat_region	misc_feature	misc_feature	misc_feature	misc_feature	repeat_region	<pre>repeat_region</pre>	misc_feature	repeat_region	misc_feature	repeat_region	misc_feature	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region
	835295 e="L2 repeat: matches 24582595 of	3499435150 /note="L2 repeat: matches 25712710 of consensus"	₹.	`e, "≡°	10	<pre>/note="MER47A repeat: matches 1365 of consensus" 3291833452</pre>			132173	532225	0. 32079 0. 32079	10	7 12	complement(3121531789) note="match: GSS: Em:AO375764"			2857428814 /note="AluJb repeat: matches 83311 of consensus"	lement(2842528881) e="match: GSS: Em:AQ455754"	2792828137 /note="L2 repeat: matches 25282750 of consensus"	2728327406 /note="FLAM_C repeat: matches 11134 of consensus"	826748 e="L2 repeat	onserved"	<pre>026431 e="L2 repeat: matches 24312596 of</pre>	:e="t		φ. ω	1. e="A	e .	79. 23226 Te="24 copies 2 mer ta 89%	Ε	73.	20593. 20648 matches 2641 2696 of consensus "	, 0		18900. 19082 Inote="MIR reneat: matches 3 208 of consensus"	/note="AluY repeat: matches 86296 of consensus" 1789617983

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                                                                                                                                                                                                                                                                                                                                               Submitted (05-APR-2001) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave Bronx, NY 10461, USA
On Apr 5, 2001 this sequence version replaced gi:13194207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-APR-2000) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Han,J., Montgomery,K.T., Grills,G., Lee,E., Lor Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Gordon,M., Goltz,J.S. and Kucherlapati,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Han, J., Montgomery, K.T., Grills, G., Lee, E., Long, J., Pome Ioshikhes, I.P., Shim, C., Decker, J., Thomas, E., Perera, A., Gordon, M., Goltz, J.S. and Kucherlapati, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC067964 219769 bp DNA linear ROD 05-APR-Mus Musculus Strain C57BL6/J Chromosome 5 RP23-337K7, complete
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ANNOTATION OF FEATURES: STSs are identified using ePCR (Genome Res. 7:541-550).
                                                                                                                   CLONE LENGIH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Han,J., Montgomery,K.T., Grills,G., Lee,E., Long,J., Pomerantz,R., Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A., Gordon,M., Goltz,J.S. and Kucherlapati,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High Throughput Mouse Sequencing
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                                                                                                     overlaps
                                                                                                                                                                                          Contact: gnktm@capecod.bwh.harvard.edu
                                                                                                                                                                                                                                                                                                           Harvard Partners Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ouse mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 219769)
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76.316
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Gaps: 0
Percent Identity: 50.000
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                                                                                                   Features
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST and CDNA sequences in Unique. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Attempts are made to complete double stranded sequence for all regions. All sequence is completed to a standard of coverage with a manimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the annotation as Low Coverage. Low coverage linkages are verified by PCR product size verification or verification of forward and reverse reads from clones which span the low coverage area.

bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality. QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than 1 per 10,000

Assembly program: Phrap version 0.990319 Contig length: 219769 Fraction of Phrap value < 40: 0.00293 Error Rate in Consed: 0.07 per 10,000 bases Number of N's in consensus: 0 Center project name: ACS Sequencing vector: pUC18; L08752 Chemistry: Dye-terminator Big Dye; 100% Summary Statistics

Distribution of Quality < 40 Bases:

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misc_feature
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FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="(TTTTC)n"
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|Lement(7927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              __family="B4A"
lement(7610
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._.3772
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10882
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AUTHORS
TITLE
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-08-973-363-14 x AC067964
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LOCUS AL589701
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AL Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (30-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Feb 1, 2002 this sequence version replaced gi:17384104. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw., SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at hit private and the sequence of places are uk/Projects/C_elegans/wormpep RP23-202F3 is from the RPC1-3 Mouse PAC Library constructed by the group of Pieter de Jong.

FOR further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3 is the entire insert of clone RP23-202F3 The true right end of clone RP23-171015 is at 179556 in this sequence. The true right end of clone RP23-153B6 is at 117857 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1. (bases 1 to 219200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALD89701 219200 bp DNA linear ROD 30-JAN-2002 Mouse DNA sequence from clone RP23-202F3 on chromosome 13. AL589701
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Gaps: 1
Percent Identity: 44.444
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US-08-973-363-14 x AL589701/rev
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ORIGIN
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LOCUS AC098600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LysLysleLysAlaGluLysGluAsnGluGluLysAspGluProGluI1 27
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E Nachus.

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Adio-Oduola, B., Ali-osman, F.R., Allen, C., Are, J.R., Banks, T., Barbaria, J., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burcell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, M., Gill, R., Gorrell, J.H., Guerra, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jackson, E., Kellv, S., Khan, U., Kins, L., Korvah, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231947 bp DNA linear
Rattus norvegicus chromosome Rf1 clone CH230-95C8,
SEQUENCE, 62 unordered pieces.
AC098600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC098600.4 GI:17973757
HTG; HTGS_PHASE1; HTGS_I
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29783. .30099
/note="Single clone region. Sequence from reads from a short insert library derived from a clone PCR. Restriction digest data confirm the assembly." a 46953 c 46966 g 61646 t
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Gaps: 0
Percent Identity: 57.143
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Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced g1:17064593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                             findPhrapList
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 231947)
Consensus quality: 191710 bases at least Q40 consensus quality: 199153 bases at least Q30 consensus quality: 203798 bases at least Q30 Estimated insert size: 197288; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 3.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: GIKD Center clone name: CH230-95C8 Center Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Phrap; version 0.990329First call to
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REFERENCE AUTHORS

JOURNAL TITLE TITLE

JOURNAL

COMMENT

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
consists of 62 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved. 11491 11591 21784 64420 64520 71197 40487 40587 47307 47407 56517 56617 21884 30103 30203 21783: 21883: 64519: 21883: gap of unknown length 30102: contig of 8219 bp in length 56616: 56516: 11490: 11590: gap of unknown length contig of 10284 bp in 1 gap of unknown length contig of 6720 bp in le contig of 6720 bp in le gap of unknown length contig of 9110 bp in le gap of unknown length contig of 7803 bp in le gap of gap of contig contig of 11490 bp in length gap of unknown length contig of 10193 bp in length f unknown g of 6677 length bp in length bp in length bp in length bp in length in length length

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length

178991 18179991 18179991 181802 1818102 1818102 183912 183912 187992 197996 1930299 193129 194129 195142 19514 195142 19514			71297 77297 78027 84373 84473 90430 94570 94570 110581 110583 110583 110583 1109843 1109843 1118635
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	36 ysArgGluThrIysGluLysGluSnIys 45 56 :::: ::: ::: ::::: 37	ACO98600/rev ACO98600/rev illysHisProHisLysLysIleLysAlamillill ::: TAAACATACCAAAAAAAAAAAGAAGAAGAAGAAGAAGAAGAAGAAGA	* 206063 206162 * 207721 * 207722 207821 207822 210574 * 210575 212688 * 212699 217288 * 212789 217288 * 21289 21730 213802 21544 * 213702 213801 213702 21544 * 215548 21754 * 215548 217054 * 215648 217054 * 215648 217054 * 21648 217054 * 217154 218335 * 217154 218335 217154 218335 217154 218335 219343 210531 219343 200551 229343 200551 22943 20051 220551 220551 220650 220651 220650 220751 220751 220752 220751 220752 220751 220753 220751

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               About: Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: Aug 3, 2002 4:34 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MODEL-frame+_p2n.model -DEV+x1h
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-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT42753;
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seq_documentation_block:
ID AAT42753 standard; cDNA; 137 BP
                                                                                                                                                              alignment_block:
US-08-973-363-14 x AAT42753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:ABL21448 - 
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Ratio: 4.889
Percent Similarity: 97.826
                                                                                                              Align seg 1/1 to: AAT42753
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CCl4 (see also AAT42754). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found as an insert in some CHD-lA clones (see also AAT42752).
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 137 BP; 75 A; 10 C; 34 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW08145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers misc_difference 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD^-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken CHD-W clone CC14 3' motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1997 (first entry)
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96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a /note= "base 52 disrupts the reading frame for the translated amino acid sequence giv in Fig 7" \,
                                                                                                              from:
                                                                                                                                                                                                                                                  Length: 46
Gaps: 1
Percent Identity: 97.826
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0
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158.95
163.24
161.47
172.30
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alignment_scores:
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    Ratio:
    Percent Similarity:
                                                                                                  alignment_block:
US-08-973-363-14 x
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AAT42752 standard;
                                                                                                                      A composite nucleotide sequence (AAT42752) and putative transla (AAW08144) sequence are provided of a motif that is found splic a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the complete motif. There are no splice donor or acceptor sites withe motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of CHD-W clone CC14 (see also AAT42753).
                                                                                                                                                                                                                                                                       Avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus
                                                                                                                                                                                                                                     Disclosure; Fig
                                                                                                                                                                                                                                                                                                                             Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken CHD-1A insert motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                   Sequence 265 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                          W09639505-A1
                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGAAAAAGAGAGAAAGAGAAAGAGAAATAAG
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                                                                                                                                                                                                                                                                                                        1997-043127/04.
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                                                                                                                                                                                                                                                         chromodomain-helicase-DNA binding genes determine sex – used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex determination; chromodomain-Helicase-DNA binding; chromodomain-Helicase-DNA binding on the \overline{W} chromoson
                                                                                                                                                                                                                                                                                             AAW08144.
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AAT42752
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                                                                                                                                                                                                                                                                                                                                                                                               96WO-GB01341
                                                                                                                                                                                                                                    7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 52
                               180.00
4.390
89.130
                                                                                                   158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA;
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                                                                                                  A; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                           "base 52 disrupts the reading frame the translated amino acid sequence in Fig 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265
                                  Percent
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                              Identity:
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84.783
                                                                                                  other;
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                                                                                                                                   end of the
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alignment_block:
US-08-973-363-14 x
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Quality:
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ID AAA64139 standard:
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                                     Percent Similarity:
                                                                                                                        an antigen of the membranous structure or the membranous structure of the membranous structure or the maxing Meniere's disease. Is a chronic ear disease with unknown etiology. Serum from patients suffering from this disease contain autoantibodies against a 30 kDa cochlear protein antigen. The disease is believed to an autoimmune disease. The beta-tubulin antigen is useful as a target substance in diagnosing or detecting Meniere's disease and in distinguishing this disease from other autoimmune ear diseases.
                                                                                                                                                                                                                                                                                                autoimmune ear diseases
                                                                                                                                                                                                                                                                                                         New beta-tubulin antigen in the membranous structure of the inner reactive with antibodies of patients with Meniere's disease, for diagnosing Meniere's disease and distinguishing this disease from
                                                                                                                Sequence
                                                                                                                                                                                                                                             The present
                                                                                                                                                                                                                                                                        Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-558400/51.
                                                                                                                                                                                                                                                                                                                                                                                                                (UYTE-) UNIV TENNESSEE RES CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chronic ear disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beta-tubulin antigen; inner ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGlu.L
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                                                                                                                50000 BP;
                                                                                                                                                                                                                                                                    Page 51-74; 115pp; English.
                                                    Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: AAT42752
                                                                                                                                                                                                                              sequence encodes a beta-tubulin antigen. The protein of the membranous structure of the inner ear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US04795
AAA64139
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                                     3.154
66.667
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Identity:
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                                                                                                                  other;
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                                                                                                                                                                                                                                                                                                                                    ear,
                                                                                                                                                                                                                                                                                                              other
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Align seg 1/1

to:

AAA64139

from:

9

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Seq_documentation_block:
ID AAK70780 standard; DNA; 37783 BP.
XX

AC AAK70780;
XY

AC AAK70780;
XY

AC AAK70780;
XY

DT 06-NOV-2001 (first entry)
XX

Human immune/haematopoietic; immur (cytostatic; gene therapy; vaccine; n XX

Homo sapiens.
XX

HOMO sapiens.
XX

D9-AUG-2001:
XX

PN W0200157182-A2.
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5449 AGGAGAAGGAGAAGAAG 5465
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cytostatic; gene therapy; vaccine; metastasis; ds.
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       14 - SEP 2000
114 - SEP 2000
114 - SEP 2000
21 - SEP 2000
25 - SEP 2000
26 - SEP 2000
27 - SEP 2000
29 - SEP 2000
29 - SEP 2000
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08-SEP-2000
  2000US-0229344
2000US-0229344
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2000US-0231413
2000US-0231413
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2000US-0246476
2000US-0246613
2000US-02469213
2000US-0249213
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alignment_scores:
Quality:
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US-08-973-363-14 x AAK70780/rev
                                                                                                                                                                                                                                                             CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK5950 and AAM82169
                                                           Align seg 1/1
                                                                                                                                  Percent Similarity:
    16327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2000

01-DEC-2000

05-DEC-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen useful for preventing, diagnosing and/or treating cancers metastasis -
                                                                                                                                                                                                                       Sequence 37783 BP; 9418 A; 9546 C; 9545 G; 9274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metastasis
                                                                                                                                                                                                                                                    represent sequences used in
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               7 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs
CA,
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2000US-0249215
2000US-0249217
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2000US-0249245
2000US-0249264
2000US-0249297
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2000US-0251988
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2000US-0251856
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46.154
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seq_documentation_block:
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
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07-JUN-2000;
28-JUN-2000;
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04-FEB-2000;
24-FEB-2000;
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22-AUG-2000;
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17-MAR-2000;
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                                                                                                                  14-AUG-2000;
18-AUG-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                          14-AUG-2000;
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2000US-0225758
2000US-0225759
2000US-0226879
2000US-022681
2000US-0226868
2000US-022709
2000US-022709
2000US-022709
2000US-0229287
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2000US-0217487
2000US-0217487
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2000US-0224519.
2000US-0225213.
2000US-0225214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; vaccine; metastasis;
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06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;

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2000US-0246526
                                                                                                                                                             alignment_block:
US-08-973-363-14 x AAK76625/rev
                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                CC anino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cartivity, and can be used in gene therapy and vaccine production. (I) cytostantic content of diseases associated with inappropriate (I) expression. For cx example, they may be used to treat disorders associated with decreased cx expression by rectifying mutations or deletions in a patient's genome cx that affect the activity of (I) by expressing inactive proteins or to cylonicated vith patients own production of (I). Additionally, (I) proteins and be used to produce the secreted (I), by inserting cx the nucleic acids into a host cell and culturing the cell to express the creations and polynucleotides may be used to produce the secreted (I), by inserting cx the nucleic acids into a host cell and culturing the cell to express the cx diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic concerns and cancer metastases of haematopoietic antigen genomic concerns the present invention. AAK84942 to AAK8950 and AAM82169 cx represent sequences used in the exemplification of the present invention.
                                                                                                                              Align seg 1/1 to reverse of: AAK76625 from: 1
                                                                                                                                                                                                                Percent Similarity:
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01-DEC-2000;
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08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                              Sequence 37783 BP; 9418 A; 9546 C; 9545 G; 9274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 31437; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483426/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                             23 pGluProGluIleGlyIleLysLysGluAlaGlyGluLysArgGluThrL 40
                                                                                             7 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA,
                                                                                                                                                                                                                            Quality:
Ratio:
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; 2000US-0251990.
; 2000US-0254097.
; 2001US-0259678.
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2000US-0249245
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2.793
74.359
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                                                                                                                                                                                                            Length: 39
Gaps: 0
Percent Identity: 46.154
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to: 37783

11 4 SEP 2000
21 SEP 2000
21 SEP 2000
25 SEP 2000
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XC AAK80913;

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XX O9-AUG-2001; 2001WO-1
XX O9-AUG-2001; 2000US-1
PR 14-FEB-2000; 2000US-1
PR 24-FEB-2000; 2000US-1
PR 24-FEB-2000; 2000US-1
PR 17-MAR-2000; 2000US-1
PR 18-MG-2000; 2000US-1
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AGGAGAAGGAGGAG 16211
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14-SEP-2000;
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2000US-0249216

2000US-0249216

2000US-0249297
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Ratio:
Percent Similarity:
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US-08-973-363-14 x AAK80913/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) genome the secret of the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, and include any be used to prevent. The nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, and cancer metastases of haematopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: AAK80913 from: 1 to: 37783
16227 AGGAGAAGGAGAAGGAG 16211
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17-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 35725; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37783 BP; 9418 A; 9546 C; 9545 G; 9274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483426/52.
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                                       40
                                                                                                                  23 pGluProGluIleGlyIleLysLysGluAlaGlyGluLysArgGluThrL 40
                                                                                                                                                                               7 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23
                                       ysGluLysGluAsnLys 45
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2000US-0251997
2000US-0259678
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2.793
74.359
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                                                                                                                                                                                                                                                                                                                               Length: 39
Gaps: 0
Percent Identity: 46.154
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA46373

4 ValSerValLysHisProHis.....LysLysIleLysAlaGluLy

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ABA46373 standard; DNA; 420 BP XX

ABA46373; STANDART; DNA; 420 BP XX

ABA46373;

XC ABA46373;

XX ABA46373;

XX OFFER-2002 (first entry)

DT 01-FEB-2002 (first entry)

DT 01-FEB-2002 (first entry)

DE Human breast cell single exon XX

Human; microarray; single exon XX

Human; microarray; single exon XX

OS Homo sapiens.

XX OFFER-2000; 2000US-0180312.

PR 09-AUG-2001; 2001WO-US00662.

XX OFFER-2000; 2000US-0180312.

PR 26-MAY-2000; 200US-0180312.

PR 26-MAY-2000; 20
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US-08-973-363-14 x ABA46373
                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a spatially-addressable set of single exon concleic acid probes for measuring gene expression in a sample derived from human breast and BY 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical conjugate on cells. The microarray of this invention presents a far greater than expressed sequence tag microarrays. The method is suitable for than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. On the sequence of the invention printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Align seg 1/1 to: ABA46373
                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 5068; 327pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human breast cell single exon nucleic acid probe #5068
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                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                      79.00
2.469
71.111
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from:
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Gaps: 2
Percent Identity: 42.222
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to: 420
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alignment_block:
US-08-973-363-14 x
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Align seg 1/1
                                                         Percent Similarity:
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                                                                                                                                                 Note: The sequence data for this patent did not form part printed specification, but was obtained in electronic form from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                     fetal liver. The present probe of the invention.
                                                                                                                                                                                                           The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human
                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver;
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                                                                                                                             Sequence 420
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                                                                                                                                                                                                                                                                                                                                                      SG,
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                                                                                                                                                                                                                                                                       ۲.
                                                                                                                                                                                                                                                                                            genome-derived single exon nucleic acid |
zing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               foetal liver single exon nucleic acid probe #5244.
                                                                               Quality:
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                                                                                                                                                                                                                                                                       SEQ
                                                                     Ratio:
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; 2000US-0207456.
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; 2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
 ABA56939
                       ABA56939
                                                                                                                                                                                                                                                                      NO 5244; 639pp + sequence listing;
                                                        79.00
2.469
71.111
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                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                             42 C;
                                                                                                                                                                                                 sequence is a single exon nucleic acid
 from:
                                                         Percent
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42.222
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seq_documentation_block:
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                                             e.g. cardiovascular disease, congenital heart disease. Note: The sequence data for t
                                                                               The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular systems.
Sequence
                                    specification,
                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                     Single
                                                                                                                                                                                                                                             WPI; 2001-488899/53
                                                                                                                                                                                                                                                                     Penn
                                                                                                                                                                                                                                                                                                                                                      30-JUN-2000;
03-AUG-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              congenital heart disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; gene expression; heart; microaccardiovascular disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #5017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABA26551;
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                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                              21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157274-A2
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                       ftp.wipo.int/pub/published_pct_sequences
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 420 BP;
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2000US-0236359.
2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                      2000US-0608408
2000US-0632366
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2000US-0207456
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                                                                                                                                                                                 ID No
                                   but was obtained in electronic
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42
                                               for this patent did not form
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ension; cardiac
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 0 other;
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iac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human heart cell sample
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                                   part of the printed directly from WIPO
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                                                                       and
                                                                                                                                                                                                                     human
                                                                                  system
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alignment_scores:

Quality:

79

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Length:

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seq_documentation_block:
ID AAK05034 standard; DN
XX
AC AAK05034;
XZ
AC AAK05034;
XY
C5-NOV-2001 (first e
DT 05-NOV-2001 (first e
DT 05-NOV-2000 (firs
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US-08-973-363-14 x ABA26551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name:
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                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzhaimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; microarray; Alzheimer's disease; multiple sclerosis; seepilepsy; cancer; ss.
          Sequence 420 BP; 157
                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 5025; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 lyGluLysArgGluThrLysGluLysGluAsnLys 45
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2000US-0207456.
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Identity: 42.222
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      99 T; 0 other;
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schizophrenia;
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seq_documentation_block:
IID AAK30564 standard; DNA; 420 BP.
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AC AAK30564;
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Human bone marrow expressed exon microarray; cancer; leukaemia; ly XX
Human; bone marrow expressed exon KW
Human; bone marrow expressed exon XX
OS Homo sapiens
XX

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MO200157276-A2:
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VOS HOMO sapiens
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US-08-973-363-14 x AAK05034
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Ratio:
Percent Similarity:
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                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bone marrow expressed exon; gene expression analysis; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes analyzing gene expression in human bone marrow - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              278 GGAGGAGAAGGAAGGATGAGAAGAA.....AACAAGAAGAGGA 318
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                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO: 5121; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed single exon
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Gaps:
Percent Identity: 42.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353
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A; 42 C; 122 G;

99 Η,

0 other;

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seq_documentation_block:
ID AAII5181 standard; DN
XX
AC AAII5181;
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DT 12-OCT-2001 (first 6
XX
Probe #5114 for gene
XX
Probe; human; microal
KW Probe; human; microal
XX
Probe; human; microal
XX
OS Homo sapiens.
XX
OS Homo sapiens.
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OS Homo sapiens.
XX

09-AUG-2001; 2000US-1
PR 20-MAY-2000; 2000US-1
PR 26-MAY-2000; 20
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US-08-973-363-14 x AAK30564
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Percent Similarity:
                                                                                                                                         The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                              expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319
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      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValSerValLysHisProHis.....LysLysIleLysAlaGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGGAGAAGGAAGGAAGAAA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-488901/53.
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                                                                                                                                                                                                                                                                                                                                                                                         genome-derived single exon nucleic acid probes useful : zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                 SEQ ID No 5114; 487pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to:
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from:
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Gaps: 2
Percent Identity: 42.222
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                                                                                                                                                                                                                                                                                                                                 English.
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6
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alignment_block:
US-08-973-363-14 x
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XX
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAI15181
                                                                                                                                                            03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                    WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                        genetic
                                                                                                                                                                                                                                                                                                                                                                                                             319
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                                                                                   Human
                                                                                                                                                    04-OCT-2000;
                                                                                                                                                                                                                       30-JAN-2001;
                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                       WO200157272-A2
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                 Probe #5195
                                                                                                                                                                                                                                                                                                                                 17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                   AAI36509
                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                               Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGGAGAAGGAAGGATGAGAAGAAA......AACAAGAAGAGGA
                                                                        genome-derived single exon nucleic ac
zing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                        disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420
                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                         SEQ
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                                                                                                                                                                                                                                                                                                                 used
                                                                                                                                                            2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                 (first entry)
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2.469
71.111
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                                                         No 5195;
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                                                                                                                                                                                                                                                                                                human;
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                                                                                                                    Rank
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                                                        English.
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: Identity:
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                                                                                                                    DR.
                                                                                                                                                                                                                                                                                                antenatal diagnosis;
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                                                                            acid
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                                                                                                                                                                                                                                                                                                                 in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                 probes
                                                                                   useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277
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The present invention relates to single exon nucleic acid probes (The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying ge expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders.

gene

useful

(SENP)

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alignment_block:
US-08-973-363-14 x AAI36509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AA104921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAI36509 from: 1 to: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                    04-FBB-2000; 2000US-0180312
26-MAY-2000; 2000US-0207456
30-JUN-2000; 2000US-0608408
03-AUG-2000; 2000US-052366
21-SEP-2000; 2000US-0234667
27-SEP-2000; 2000US-0236359
The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe; human; breast disease; breast cancer; development disorder; ss;
inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                          Claim 25; SEQ ID No 4912; 322pp; English.
                                                                                                                                     Novel single exon nucleic acid probe used to measuring gene expression in a human breast -
                                                                                                                                                                             WPI; 2001-476286/51.
                                                                                                                                                                                                        Penn
                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2001; 2001WO-US00661.
                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #4912 used to measure gene expression in human breast sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAI04921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI04921 standard; DNA; 420 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 AGGAGAAGGAGGAGGAAAATGAGAAGGAGAAGAAG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 228 ATAAACTTACGTGATCCTCATTTCAAGGAGAAGAAGGAGAAGTTGAAGAA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 lyGluLysArgGluThrLysGluLysGluAsnLys 45
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                                                                                                                                                                                                                                                         2000GB-0024263.
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71.111
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Gaps: 2
Percent Identity: 42.222
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                                                                                                                                                                                                        Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 T; 0 other;
   alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSSSSSSS
 Claim 1; SEQ ID NO 2160; 327pp + sequence listing; English
                          New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes .
                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA43465;
                                                                                 WPI; 2001-496933/54.
                                                                                                          Penn SG,
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seq_documentation_block:
ID ABA43465 c+----
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US-08-973-363-14 x AAI04921
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                                                                                                                     04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-0508448; 30-JUN-2000; 2000US-05084488; 03-AUG-2000; 2000US-053366; 21-SEP-2000; 2000US-0234687; 27-SEP-2000; 2000US-0234589; 04-OCT-2000; 2000GB-0024263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human breast cell single exon nucleic acid probe #2160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319 AGGAGAAGGAGGAGGAAAATGAGAAGGAGAAGAAG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 ATAAACTTACGTGATCCTCATTTCAAGGAGAAGAAGGAGAAGTTGAAGAA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 420 BP; 157 A; 42 C; 122 G; 99 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA43465 standard; DNA; 452 BP
                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 lyGluLysArgGluThrLysGluLysGluAsnLys
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Hanzel DK, Chen W, Rank DR;
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alignment_block: alignment_scores: The invention relates to a spatially-addressable set of single exon CC nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids CC derived from mRNA of human breast, and then measuring the label CC bound to each probe of the microarray. The probes are useful for cc verifying the expression of regions of genomic DNA predicted to cc encode proteins. They are useful for gene discovery, and for cdetermining predisposition and/or prognosing breast disease. Gene cexpression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater cdiversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The Sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequencees. Align seg 1/1 to: ABA43465 from: 1 US-08-973-363-14 x ABA43465 Percent Similarity: 34 lyGluLysArgGluThrLysGluLysGluAsnLys 45 ||||||:::||| :::||||||:::||| 328 AGGAGAAGGAGGAGGAAGAAGGAGAAGAAG 362 237 ATAAACTTACGTGATCCTCATTTCAAGGAGAAGAAGGAGAAGTTGAAGAA 286 Sequence 452 BP; 168 A; 47 C; 130 G; 107 T; 0 other; 17 sGluAsnGluCluLysAspGluProGluIleGlyIleLysLysGluAlaG 34 Quality: Ratio: 79.00 2.469 71.111 Length: 45
Gaps: 2
Percent Identity: 42.222 to: 452

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gb_est2:B6028923
gb_est2:B6034011
gb_est2:B6034011
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gb_gss:A2176468
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Database: EST:*
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Query: US-08-973-363-14
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gb_gss:BH055497
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gb_est2:BF239967
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gb_est2:BM015597
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gb_est1:AI242163
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Database length: -1841457050
Search time (sec): 4390.400000
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-GGAPEXT-7.000 -YGAPCD-10.000 -YGAPEXT-0.500 -FGAPCD-6.000
-DELEXT-7.000 -YGAPCD-10.000 -YGAPEXT-0.500 -FGAPCD-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi
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-ALIGN-15 -MODE-LOCAL -OUTEMT-PIS -NORM-ext -HEAPSIZE-500
-MINLEN-0 -MAXLEN-200000000 -USER-US0897365_CGN1.1_2938
-NCPUG-5 -LOPU-3 -LOUGLOG -DEV_TIMEOUT-120 -WARRN_TIMEOUT-30
-NO_XLPXY -WAIT -THREADS-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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gb_est2:BF974760
gb_gss:AG061263
gb_est2:BG847842
gb_gss:CNS02VZT
gb_est2:BG026974
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
                         alignment_block:
US-08-973-363-14 x AA748563/rev
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ORIGIN
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LOCUS AA748563
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Ratio:
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AA748563.1 GI:2788521
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Eukaryota; M
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263.36
288.67
364.20
412.75
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AL Unpublished (1997)

L'Ontact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.

Ph.D., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lihi.gov/bbrp/image/image.html
Insert Length: 1312 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 282.

Button Amersham

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA748563 343 bp mRNA linear EST 27-JAN-1998 oa57c09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309072 3' similar to SW:CHD1_MOUSE P40201 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN CHD-1. [1] ;contains element L1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 343)

    Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the N
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
    a 59 c

Percent Identity: 68.889
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764 ! AG061263 Pan troglodytes DNA
852 ! B6847842 1024019C11.x2 C. re
1123 ! AL216434 Tetraodon nigrovir
1303 ! BG026974 602294001F1 NIH_MG
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
                                                         alignment_block:
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                                       US-08-973-363-14 x AI242163/rev
                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 lyGluLysArgGluThrLysGluLysGluAsnLys 45
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                                                                                                            Quality:
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430 bp mRNA linear EST 01-DEC-1990
qh81f02.x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA
clone IMAGE:1851099 3' similar to contains element LTR5 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 429.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 430)
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AI242163
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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   reverse of: AI242163
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                                                                                                                                                                                                                    constructed by Bento Soares and M.Fatima Bonaldo."
89 c 50 g 180 t
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/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
/note="Organ: Liver and Spleen; Vector: Pac I; Site_2: Eco RI;
/nis is a subtracted version of the original Soares fetal
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library lst strand cNNA was primed
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/clone="IMAGE:1851099"
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                                                                               Length: 45
Gaps: 0
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                                                                                                                           BASE COUNT
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AUTHORS
                                                     alignment_scores:
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seq_documentation_block:
LOCUS AA699918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 456)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptce,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            119
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/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
with a modified polylinker; Site_11 Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. 1st strand cDNA was primed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
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Ratio:

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86.667

Length: 45 Gaps: 0 Percent Identity: 68.889

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US-08-973-363-14 x AA699918/rev
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LOCUS BM015597
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                                                                                      Align seg 1/1 to: BM015597 from: 1 to: 677
                                                                                                                                                                                 US-08-973-363-14 x BM015597
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1 AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGluLy 17
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Ratio:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BM015597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:8006"
/clone="Ibb="NIH_MGC:8417887"
/clone="IbMAGE:5417887"
/clone="IbHAGE:5417887"
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/lab_host="BHHJB (phage-resistant)" SPORT6; Site_1: NotI;
/note="Organ: breast; Vector: pCMV-SPORT6; Site
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Percent Identity: 68.889
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US-08-973-363-14 x AI890775/rev
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LOCUS AI890775
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                                                                                             Align seg 1/1 to reverse of: AI890775 from: 1 to: 547
                                                                                                                                                                                                                 Percent Similarity:
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132 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 AAGAAAAGAGGGAAGCAAAAGAAAAGGAGAATAAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AGACAGTGAAGAAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCAG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 lyGluLysArgGluThrLysGluLysGluAsnLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG 34
                            1 AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGluLy 17
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                                                                                                                                                                                                                                                                 Quality:
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.B. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 1924 Std Error: 0.00

Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Emmail: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.85 kb. Life Technologies catalog #: 11539-012"
                                                                                                                                                                                                                 154.00
4.053
86.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2443725"
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adenocarcinoma, 3 pooled tumors"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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Percent Identity: 68.182
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US-08-973-363-14 x BF239967
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Quality:
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LOCUS BF239967
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                                                                                                Align seg 1/1
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Percent Similarity:
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TITLE
  234
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                 1 AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGluLy 17
GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est2:BF239967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF239967.1 GI:11153890 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: LLCM1033 row: k column: 18 High quality sequence stop: 562.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BF239967
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                                                                                                to:
                                                                                                                                                                                                                                                                                                                                                                                            345
                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:4133129"
/clone_lib="NIH_MGC_54"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DHIOB (Tl phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggcgcctgggc); Site_2: Sfil (ggcattatggcc); Double-stranded cDNA was prepared from cell line RNA.
5; and 3; adaptors were used in cloning as follows: 5;
adaptor sequence: 5; CACGGCATTATGGCC-3; and 3; adaptor sequence: 5; CACGGGCACATG-GT(30)BN-3; (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
45 a 149 c 190 g 137 t
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                                                                                                BF239967
                                                                                                                                                                                                                  146.00
3.744
84.783
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/db_xref="taxon:9606"
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                                                                                                from:
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Gaps: 1
Percent Identity: 67.391
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alignment_block:
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LOCUS AW387264
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                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                 159 GATGAGATCAGTTCTGTGAAACATCCAAATAAAAAAATTAAAACAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 AGACCAGTGAAGAAAAACCTGAGCCAGATGTTTATATAAAGAAGGAACCA 333
                    17 sGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAlaG
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gb_est1:AW387264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=wRl&t2=MRl-ST0088-
101199-003-b09&t3=1999-11-10&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                            Quality:
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AW387264
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The FAPESP/LICR Human Cancer Genome Pa
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                      reverse of: AW387264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                tissue mRNA and cDNA amplification were performed under low stringency conditions." 52\ c \qquad 41\ g \qquad 104\ t
                                                                                                                                                                                                                                                              128.00
3.459
82.222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="ST0088"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
                                                                                                                              alignment_block:
US-08-973-363-14 x BH055497
                                                                                                                                                                                                                     alignment_scores:
Quality:
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LOCUS BH055497
                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
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ORGANISM
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                                                                                       Align seg 1/1
                                                                                                                                                                                              Percent Similarity:
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JOURNAL
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  140 AAGAAGAAGAAGAAGAAGAAGAAGAAGATTGAATGAAAGAAAGAA 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
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                       7 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC (page: http://www.tigr.org/tab/bac_ends/mouse/bac_end_intro.html Plate: 278 row: I column: 16
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhao S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C. M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-278I16.TV
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 653)
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                                                                                    to: BH055497
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301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/Strain="C57BL/6J"
/db_xref="taxon:1090"
/clone="RPCI-24-278116"
/clone_lib="RPCI-24"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; blamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; produced by Pieter de Jong. The
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
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genomic clone RPCI-24-278I16
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LOCUS BF068827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 213
South Memorial Parkway Huntsville, AL 35601 For further infor
call: (800)-533-453 or contact via email: ccu@resgen.com
Insert Length: 822 Std Error: 0.00
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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Public Soybean EST Project
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Location/Qualifiers
                             Another Vector: Bluescript II SK+; Site_1: EcoRI; Site_2: Another Vector: Bluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The CDNA library was constructed from mRNA isolated germinating shoots of the cultivar Williams. The seeds were allowed to germinate for 24 hours prior to being cold stressed for 2 days at 4C. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DHIOB host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Sheemaker.*
                                                    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Glycine max"
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1065-237"
/clone_1ib="Gm-c1065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="germinating shoots"
/lab_host="DH10B"
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Beck,C.,
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Quality:

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Length:

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SOURCE
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LOCUS BG790466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wylie,T., Underwood,K., Steptoe,M., Theising,B., Martin,J., Beck.C.
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: chartery 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, 17el: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG790466 537 bp mRNA linear EST 29-NOV-2001 sae69h05.yl Gm-c1064 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1064-3801 5' similar to TR:003982 003982 HYPOTHETICAL 19.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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Glycine max
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BG790466.1 GI:14126028
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/note="Tector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhOI; The cDNA library was constructed from mRNA isolated from the epicotyls of 2 week old seedling for the cultivar Williams. The seedlings were germinated in a growth chamber, excised above the soil level, and the plants were placed in a 100 ppm solution of auxin for 24 hours prior to harvesting. Complementary DNA was synthesized
                                                                                                                                                                                                                                                                                                                                                                                                /clone="GENOME SYSTEMS CLONE ID: Gm-c1064-3801"
/clone_lib="Gm-c1064"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cultivar="Williams"
/db_xref="taxon:3847"
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71.111
                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                      /tissue_type="seedling epicotyls"
/dev_stage="2 week old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Glycine max"
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Percent Identity: 46.667
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US-08-973-363-14 x BG790466
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                                                   FEATURES
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Align seg 1/1 to: BG790466
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Email: 1-vodkin@uiuc.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134. Foor further information
call: (800) 430-0030 or (314) 427-322 FAX:(888) 919-3324 or (314)
427-3324 or contact:clones@genomesystems.com or info@genome
ystems.com web site:www.genomesystems.com
Seq primer: 5'.TTTTTTTTTTTTTTTTTT(A/C/G)-3'.
                                                                                                                                                                  Tel: (217) 244-6147
Fax: (217) 333-4582
Email: 1-vodkin@uiuc
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Other_ESTs: AW277969 corresponding to Gm-c1019-3195 (5')
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Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Erpelding, J., Raph, C., Shoop, E., Pardinas, J., Liu, L. and A Functional Genemics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                      Contact: Vodkin, L.O., PI, A Functional Genomics Soybean (NSF 9872565)
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Papilionoideae; Phas
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Gm-r1070-6747 3',
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seq_documentation_block:
LOCUS BE211196
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US-08-973-363-14 x BE822468/rev
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                                                                    Glýcine max
Glýcine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Fabaceae; Papilionoldeae; Phaseoleae
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Phaseoleae
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Ratio:
       1 (bases 1 to 294)
Shoemaker,R., Keim,
                                                                                                                                                                                                                                                                                                                                                                                      BE211196 294 bp mRNA linear EST 04-DEC-2001
so58b05_yl Gm-c1039 Glycine max CDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1039-2194_5' similar to TR:003982 003982 HYPOTHETICAL 19.8 KD
                                                                                                                                                                                                                                                                                                                         PROTEIN. ;, mRNA sequence.
BE211196
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//db_xref="taxon:3847"
//clone="dm:rt070-6741"
//clone_lib="cm:rt070"
//note="The library Gm:r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,700 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm:r1070. The cDNA clones of the reracked to form library serve then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.unm.edu/ResearchFrojects/Soybean/index.html. Reracking was performed by Genome Systems, 5t. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics, University of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm:r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of 'OTHER EST'. The CONA library that is also listed under 'OTHER EST'. The cona also cons and the original cONA library that is also listed under 'OTHER EST'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.00
2.897
74.359
   Keim, P., Vodkin, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 39
Gaps: 1
Percent Identity: 48.718
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Erpelding, J., Coryell, V., Khanna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 others
                                                                                                   Phaseoleae
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BASE COUNT ORIGIN

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

DEFINITION

539

SOURCE

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TITLE
JOURNAL
COMMENT
DEFINITION sh95g08.yl Gm-c1016 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1016-7959 5' similar to TR:003982 003982 HYPOTHETICAL 19.8 KD PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-973-363-14 x BE211196
                                                                                                                                                                                                             seq_name: gb_est1:AW459832
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ORIGIN
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                                                                                                                                                                                                                                                                                128
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                                                                                                                                                                                                                                                                                                                                            40
                                                                                                                                                                                                                                                                                                                                                                                                       90 AGAGCCT.....AAGAAAGAAGAAGAAGAAGAAGAAGAAGACAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                23 pGluProGluIleGlyIleLysLysGluAlaGlyGluLysArgGluThrL 40
    :!|||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 GAGGAGCCAAAGAAGGAGGGTGAAGCCAAAAAGGAAGAGGAGAAAAAGGA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23 ::::::||| ||||::: :::|||:::||||:::|||:::
                                                                                                                                                                                                                                                                                AGAAAGAAGAAGAAG 144
                                                                                                                                                                                                                                                                                                                                        ysGluLysGluAsnLys 45
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkay Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1211 Std Error: 0.00
High quality sequence stop: 245.
Location/Qualifiers
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Fax: 314 286 1810
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="whole seedling without cotyledons"
/lab_host="phildb"
/lab_host="perfector: pbluescriptII SK+; Site_1: EcoRI; Site_2:
/note="Perfector: pbluescriptII SK+; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from 2 week old seedlings with the cotyledons removed at
the time of harvest. The seedlings for the cultivar ogden
were grown in a growth chamber using germination paper:
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI-XhoI restriction
site of the pbluescript vector. The ligated cDNA fragments
were transformed into DHIOB host cells (Gibco BRI). This
library was constructed by Dr. Randy Shoemaker."
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/db_xref="taxon:3847"
/clone="GeNOME SYSTEMS CLONE ID: Gm-c1039-2194"
/clone_lib="Gm-c1039"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.00
2.677
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Gaps: 1
Percent Identity: 46.154
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KEYWORDS
SOURCE
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AUTHORS
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US-08-973-363-14 x AW459832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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     103
                                  23 pGluProGluIleGlyIleLysLysGluAlaGlyGluLysArgGluThrL 40
    :!!!!!
                                                                                                             53
                                                                                                          GAGGAGCCAAAGAAGGAGGGTGAAGCCCAAAAAGGAAGAGGAGAAAAAAGGA 102
                                                                                                                                                                 LysHisProHisLysLysIleLysAlaGluLysGluAsnGluGluLysAs 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information (800)-533-4353 or contact via email: ccu@resgen.com Seq primer: -40RP from Gibco High quality sequence stop: 399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nhoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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, A., Bolla, B., Marra, M.,
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shoemaker R/Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="immature flowers of field grown plants"
/lab_host="Xtl0-Gold"
/lab_host="Xtl0-Gold"
/note="vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into XL10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Erpelding."
109 82 t
                                                                                                                                                                                                                              AW459832
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2.677
79.487
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AAGAAAGAAGAAGAAGAAGAAGAAGAAA 140
                                                                                                                                                                                                                           from:
                                                                                                                                                                                                                                                                                                                                                               Gaps: 1
Percent Identity: 46.154
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6
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BASE COUNT
ORIGIN
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US-08-973-363-14 x AL628267
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SOURCE
seq_name: gb_gss:AG173980
                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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LOCUS AL628267
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                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
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                                                                                                                                                                                                             280 AATAATAAAAGGAGAGCAGAGAAAGAAAATGAGGACCGAACAGAGTTAGA 329
                                          380 AAAAGGACCCTAAGAAAGAAAAGAAG 405
                                                                                                                                                    26 uIleGlyIleLysLysGluAlaGlyGluLysArgGluThrLysGlu....
                                                                                                                                                                                                                                                  10 HisLysLysIleLysAlaGluLysGluAsnGluGluLysAspGluProGl 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 ysGluLysGluAsnLys
                                                                                                                            TGTCAGTGTTAACAAAGAGCCAGAAGAAAAGAAAAGAGATAAAAGAAAATA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
AL628267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST
TROPICALIS_SEQUENCE_ID: TGASOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Huckle E
Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 western clawed frog. silurana tropicalis
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                                                                               ...LysGluAsnLys 45
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2.767
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/lab_host="Escherichia coli XLI-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
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/db_xref="taxon:8364"
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Ratio: 3.154 Gaps: 0
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                                                44 snLys 45
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Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical Submitted (102-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

Tel:81-45-503-9111, Pax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the RSD process and may have higher chance of clone tracking errors.
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-044B16.TJ.
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Pan troglodytes
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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LIBRARY
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
1 380 c 93 g 407 t 15 others
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                           Patent: WO 9639505-A 2 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
L. .153
                                                                                                                                                                                    unclassified.

1 (bases 1 to 153)
Griffiths, R. and Tiwari, B. AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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Sequence 2 from Patent W09639505.
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AC012624 Homo sapi
AC012449 Homo sapi
AC0018531 Homo sapi
AC091946 Homo sapi
AC0921821 Homo sapi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced gi:293322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse DNA-binding protein L10410 X66028 L10410.1 GI:455014
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Delmas, V., Stokes, D.G. and Perry, R.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                      MMIRTHEWMHPQTKRLKFNILLTTYEILLKDKAFLGGLNWAFIGVDEAHRLKNDDSLL
YKTLIDFKSNHRLLITGTPLQNSLKELMSLLHFLMPEKTSSWEDEEHGKGRENGYK
SLHKELEPFLLRRVKKDVEKSLPAKVEÖLLREMENSALOKOYYKWILTRUYKALSKSK
GSTSGFLNIMMELKKCCNHCYLIKPPDNNEFYNKQEALQHLIRSSGKLILLDKLLIRL
                                                                                                                        IAHSNQKSAAGLPDYYCKWQGLPYSECSWEDGALISKKFQTCIDEYFSRNQSKTTPFK
DCKVLKQRPRFVALKKQPSYIGGHEGLELRDYQLNGLNWLAHSWCKGNSCILADEMGL
GKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDINSR
RERGNRVL1FSQMVRMLD1LAEYLKYRQFPFQRLDGS1KGELRKQALDHFNAEGSEDF
CFLLSTRAGGLG1NLASADTVV1FDSDWNPQNDLQAQARAHR1GQKKQVN1YRLVTKG
                                                                                                                                                                                    SDSESEEERDKSSCOGTESDYEPKNKVRSRKPQNRSKSKNGKKILGQKKRQIDSSEDE
DDEDYDNDKRSSRQATVNVSYKEDEEKKTDSDDLEEVGEDVPGQEDEEETIERVM
DCRVGRKGAGATTIYAVAVEADGDPNAGFERNKEPGDIQYLIKWRGWSHIHNTWETEE
TLKQQNVRGMKKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERI
                                                                                                                                                                                                                                                                        SQSGSSDSDSGSDSGSQSESESDTSRENKVQAKPPKVDGAEFWKSSPS1LAVQRSAMLRKQPQQAQQQRPASSNSGSEEDSSSSSEDSDSSSGAKRKKHNDEDWQMSGSGSPSQLG
                                                                                                                                                                                                                                                                                                                                    /product="DNA-binding protein"
/protein_id="AAB08486.1"
/db_xref="GI:455015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell
                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="CHD-1"
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171. .5306
                                                                                                                                                                                                                                                                                                                   translation="MNGHSDEESVRNGSGESSQSGDDCGSASGSGSGSSSSGSSSDGSS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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.5349
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AR029026
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54; Conserv
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de Lange, T., Steensel, Bvan. and Bianchi, A.
Altered telomere repeat binding factor
Patent: US 5859183-A 3 12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown.
Unclassified.
Woodage, T., Basrai, M.A., Baxevanis, A.D., Hiete Characterization of the CHD family of proteins
                                                                                                                                                   AF006513.1
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                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5947)
                                                                                             Homo sapiens
                                                                                                                                                                      Homo sapiens CHD1 mRNA, AF006513
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ilarity 100.0%;
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RSRRYSGSDSDSISERKPKKRORPRILERENIKGFSDAEIRRIKSYKKGGPFRIEG
DAIARDAELUDKSETDLARLGELVHNGCVKALKDSSSGTERAGGRLGKVKGPFRIEG
VOVNAKLVIAHEDELIPLHKSIPSDPEERKOYTIPCHTKAAHEDIDWGKEDDSNLLIG
IYEYGYGSWEMIKMDPDLSLTIHKILPDPDFKKPOAKOLOTRADYLIKLLSRDLAKREA
QRLCGAGGSKRRKTRAKKSHAWSITYVEEIKSDSSPLPSEKSDEDDUKLNDSKPESK
QRLCGAGGSKRRKTRAKKSHAWSITYVEEIKSDSSPLPSEKSDEDDUKLNDSKPEK
RSKKSVYSDAPVHITASGEPVPIAEESEELDOKTFSICKEEMPVKAALKOLDRPEK
GLSERGULEHTROLLIKGDHITELLKEIVNEDELSKESTSDRLLS
GRSKKSVYSDAPVHITASGEPVPIAEESEELDOKTFSICKEEMPVKAALKOLDRPEK
GLSERGULEHTROLLIKGDHITELLKEIVNEDGSSTSSDRLLS
GYHDHIKDRHOGDSYKKSDSRRPYSSFSNGKDHRWDDYSRDSYSSDRHLS
GYHDHIKDRHOGDSYKKSDSRRPYSSFSNGKDHRWDDYRDDSSRDSYSSDRHLS
GYHDHIKDRHOGDSYKKSDSRRRPYSSFSNGKDHRWDDYNDDSSRDSYSDDREKKENDD
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257 c 316 g
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s; Pred. No.
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Pred. No. 2.1e-48;
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                       and Collins, F.S
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97470991
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Location/Qualifiers
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//PICTURE 1de*AB87381.1*
//PICTURE 1de*AB873865EEDSSSSEDSSSEWKENERSKRIGKKILGOKKSGSSESOSS
SOSGSSDSDESEEREKKSCEDETSSDY EFRIKTVESKROGTENED LEVGEDVPOPEEEEFETTER
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Direct Submission

3 (bases 1 to 134365)

DOE Joint Genome Institute.

Submitted (31-OCT-1999) Production Sequencing Facility,
Submitted (31-OCT-1999) Production Sequencing Facility,
Senome Institute, 2800 Mitchell Drive, Walnut Creek, CA

3 (bases 1 to 134365)

DOE Joint Genome Institute and Stanford Human Genome Cen
Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800
Drive, Walnut Creek, CA 94598, USA

4 (bases 1 to 134365)

DOE Joint Genome Institute and Stanford Human Genome Cen
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20 (bases 1 to 101220)
DOE Joint Genome Institute.
DIRECT SUBMISSION
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
Draft Sequence Produced by DOE Joint Genome Institute
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Homo Sapiens
Homo Sapiens
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Chordata; Craniata; Vertebrata; Euteleos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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DOE Joint Genome Institute and Stanford Human Genome Center.

DIrectt Submission
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NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624. The number of bases overlapped is 90404.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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HOMO Sapiens chromosome 5 clone CTD-2082I17, complete sequence.
AC012624 AC012624.6 GI:14993679
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Plerre, M., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Don'the Control of the Connor of 
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-58M12
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                                                                                                                                                                                                                                                                                                         All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 143079)
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5154
Center clone name: 58_M_12
                                                                                                                                                    Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center
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Conservative 0;
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/db_xref="taxon:9606"
/chromosome="5"
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24497 c 25503 g 43951 t
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                                                                                                                                                                                                                                                                         ·-- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                     Genome Research
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                                                                                                               misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will be preserved.
                       43971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
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38921 40411: contig of 1491
40412 40511: gap of 100 bg
40512 43279: contig of 2768
43280 43379: gap of 100 bg
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43380 46905: contig of 3526 bp in length
46906 47005: gap of 100 bp
47006 51830: contig of 4825 bp in length
51831 51930: gap of 100 bp
51931 62619: contig of 10689 bp in length
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                                              clone_end:T7
vector_side:
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38921. .40411
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106510. .143079
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/db_xref="taxon:9606"
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                       26246 c
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20: gap of 100 bp
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                    906 others
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Query Match

17.6%;

Score 27;

DB

2;

Length 143079;

Best Local Matches :

Similarity

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Db 116192 CAGACCCGTGCAGACTACCTCATCAAA 116218
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                                                                                                           Summary Statistics
Consensus quality: 14256 bases at least Q40
Consensus quality: 14256 bases at least Q40
Consensus quality: 143744 bases at least Q30
Consensus quality: 143744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Batimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation.
** NOTE: This is a 'working draft' sequence. It currently
** consists of 7 contigs. Gaps between the contigs
** are represented as runs of N. The order of the pieces
** is believed to be correct as given, however the sizes
** of the gaps between them are based on estimates that have
** provided by the submittor.
** This sequence will be replaced
** by the finished sequence as soon as it is available and
** the accession number will be preserved.
** 10875 100874: contig of 56174 bp in length
** 10875 100874: gap of unknown length
** 10875 100874: gap of unknown length
** 11328 11327: contig of 44600 bp in length
** 11328 11327: contig of 44600 bp in length
** 11328 11327: contig of 12153 bp in length
** 118291 118290: gap of unknown length
** 118191 118290: gap of unknown length
** 118191 118290: contig of 3503 bp in length
** 118191 118290: gap of unknown length
** 113298 123297: contig of 3503 bp in length
** 113298 123297: contig of 3503 bp in length
** 113298 123297: contig of 3503 bp in length
** 123398 123597: contig of 22262 bp in length.
** 123598 123597: contig of 3503 bp in length
** 123598 123597: contig of 3503 bp in length
** 123598 123597: contig of 3503 bp in length
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** 123598 123597: contig of 22262 bp in length
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Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
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DOE Joint Genome Institute.
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Center: Joint Genome Institute
Center Code: JGI
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Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.jgi.doe.gov
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DOE Joint Genome Institute.
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              /organism="Homo sapiens"
/db_xref="taxon:9606"
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REFERENCE
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TITLE
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q20
Consensus quality: 180775 bases at least Q20
Consensus quality: 180775 bases at least Q20
Consensus quality: 184775 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are trepresented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193446)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     * as soon as it
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center Project Name: 544799
Center clone name: RPCI-11_36012
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Center Code: JGI
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Direct Submission

Submitted (09-UN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC091946 193446 bp DNA linear HTG 09-JUN-2001 HOMO Sapiens chromosome 5 clone RP11-360I2, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces AC091946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summary Statistics
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DOE Joint Genome Institute.
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1358: contig of 1358 bp in length
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2667: contig of 1209 bp in length
2767: gap of unknown length
3823: contig of 1056 bp in length
3923: gap of unknown length
5920: contig of 1097 bp in length
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7494: contig of 1474 bp in length
7594: gap of unknown length
7594: contig of 1502 bp in length
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100.0%; Pred. No.
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REFERENCE

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AUTHORS TITLE

JOURNAL

COMMENT

KEYWORDS SOURCE ORGANISM

Homo sapiens

VERSION DEFINITION ACCESSION

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CAGACCCGTGCAGACTACCTCATCAAA 87729
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/clone_lib="RPCI human BAC library
/s3252 c 37081 g 60360 t 3202
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/db_xref="taxon:9606"
/chromosome="5"
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1. .193446
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10360: contig of 1064 bp in len
10360: gap of unknown length
10360: gap of unknown length
1640: contig of 2100 bp in len
12560: gap of unknown length
16511: gap of unknown length
16381: contig of 1670 bp in len
16481: gap of unknown length
17968: contig of 1487 bp in len
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27763: contig of 3948 bp in len
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30987: contig of 3934 bp in len
27663: gap of unknown length
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36165: gap of unknown length
45763: gap of unknown length
47745: contig of 5982 bp in ler
57459: gap of unknown length
57745: contig of 5563 bp in ler
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67995: contig of 6065 bp in ler
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                                                                                                                                                                                                                  89405 CAGACCCGTGCAGACTACCTCATCAAA 89379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                 76 CAGACCCGTGCAGACTACCTCATCAAA 102
                                            AC092382

Homo sapiens chromosome 5 clone Rt
47 unordered pieces.
AC092382.1 GI:14589571

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
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Homo sapiens chromosome 5 clone
AC022121
AC022121.6 GI:15375145
                                                                                                                                                                                                                                                                                 l Similarity
27; Conserv
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Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 219258)
DOE Joint Genome Institute.
                 Homo sapiens
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SHGC-103595 G57841
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WI-13675 G23101
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DOE Joint Genome Institute and Stanford Human Genome Center
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Drive, Walnut Creek, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2007H13"
a 42062 c 40933 g 64309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                               17.6%;
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b; Pred. No. 0.0
0; Mismatches
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94598, USA
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RP11-75H1,
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ches 0;
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CTD-2007H13, complete sequence.
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Consensus quality: 256163 bases at least Q20
Consensus quality: 256163 bases at least Q20
Consensus quality: 26799 bases at least Q20
Consensus quality: 26799 bases at least Q20
Estimated insert size: 174820; agarose-fp estimation
Estimated insert size: 271581; sum-of-contigs estimation
Quality coverage: 8.62 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 276181)
DOE Joint Genome Institute.
Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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1 (bases 1 to 276181)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Project Name: 435334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing
Unpublished
   as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1061: contig of 1061 bp in length
1161: gap of unknown length
2827: contig of 1666 bp in length
2927: gap of unknown length
4227: contig of 1300 bp in length
4327: gap of unknown length
5618: contig of 1291 bp in length
5718: gap of unknown length
6983: contig of 1265 bp in length
6983: contig of 1265 bp in length
   f unknown

of 1327

f unknown

of 1116

of 1182

of 11454

f unknown

f unknown

of 1623

of 1623

of 1160

of 1755

of unknown

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of 1751

of unknown

of unknown
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of 1339
unknown
of 1249
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                                                                 ch 17.6%; So 18 Similarity 100.0%; F 27; Conservative 0;
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135115
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46737
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                                                                                                                                                                                                                                                                                      146813: gap of unknown length
157894: contig of 11081 bp in length
157994: gap of unknown length
171752: contig of 13758 bp in length
171852: gap of unknown length
201687: contig of 29835 bp in length
201687: contig of 29835 bp in length
201787: gap of unknown length
231368: gap of unknown length
231368: gap of unknown length
276181: contig of 44813 bp in length
276181: contig of 44813 bp in length
                                                               Score 27; DB 2; Le
Pred. No. 0.00014;
0; Mismatches 0;
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f unknown
f unknown
f unknown
g unf 4660
f unknown
g unf 2802
f unknown
g unf 5468
f unknown
g unf 5466
f unknown
g unf 606
f unknown
g unf 5874
f unknown
f unknown
g unf 7887
f unknown
g unknown
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g uf 1994
g uf 1994
g uf 2009
g uf 2861
g unknown
g uf 259
g uf 259
g unknown
f unknown
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g uf 3472
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KEYWORDS
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Matches 25
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Sequence
A58684
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D14316.1 GI:391639
ORF2.
                                                                                                                                                                                                     Funahashi, J., Sekido, R., Murai, K., Kamachi, Y. and Kondoh, H. Delta-crystallin enhancer binding protein delta EF1 is a zinc finger-homeodomain protein implicated in postgastrulation
                                                                                                                                                                                                                                                            Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Devel., Aging Cancer, Tohoku Univ.; 4-1 Seiryo-machi, Aoba-ku, Sendai 980-77, Japan (Te:022-272-9499, Fax:022-272-3982)
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 2292)
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Other publication AU 5906996 961224
Location/Qualifiers
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                                   Unpublished (1994)
                                                                                                                                                                                            embryogenesis
                                                                                                                                                                                                                                                                                                                      Funahashi,J
                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus (library: lambda gt11) 13 day embryo mRNA, clone JF11.
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                                                                                                                                                                           Development 119 (2), 433-446 (1993)
                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                              (bases 1 to 2292)
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/clone_lib="lambda gt11"
/dev_stage="13 day embryo"
257...1939
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3 from Patent WO9639505.
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Pred. No.
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Griffiths,R. and Tiwari,B.

Griffiths,R. and THEIR USE IN METHODS
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/product="ORF2"
/product="BAA03262.1"
/protein_id="BAA03262.1"
/db_xref="G1:391540"
/translation="MELKKCCNHCYLIKPPDDNEFYNKQBALGHLIRSSGKLILLDKL
/translation="MELKKCCNHCYLIKPPDDNEFYNKQBALGHLIRSSGKLILLDKL
/translation="MELKKCCNHCYLIKPPDDNEFYNKQBALGHLIRSSGKLILLDKL
/translation="MELKKCCNHCYLIKPPDDNEFYNKQBALGHLIRSSGKKQNLIYLL
SEDCFFLSTRAGGLGILLASADTVUIFDSQMMPQNDLQAQARAHRIGOKKQNIYLL
VTKGSVEEDILERAKKMVLDHLVIQRMDTTGKTVLHTGSTPSSTPFNKEELSAILK
FGAEBLFKEPEGEPQEMDIDEILKARAFTRNEPEGPLTVGGETLSGFKVANFSNMD
EDDDIELPERNSRNWABEIIPESQRRATEEEEROKELEEIYMLPRMRVCAKQISFKGS
ERRSRSRSRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGF
GRRSRSRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGF
                                                              6872 bp mRNA allus chromo-helicase-DNA-binding variant with hydrophilic domain,
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385 c 546 g 534 t
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RISGVQVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSN
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HN fragment of delta-crystallin enhancer."
/codon_start=1
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1207 c 1459 g 10
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                                                              Ouery Match 16.3%; score 25; DB 5; Length 6872; Best Local Similarity 100.0%; Pred No. 0, 0017; Matches 25; Conservative 0; Mismatches 0; Indels
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Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked in the chicken Gallus domesticus
Gene 197 (1-2), 225-229 (1997)
97473516
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Griffiths,R. and Korn,R.M.
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MIRTHEWMHOQTKELKFNILLTTYEILLKDKSSFLGGLNWAFIGDITSRN
MIRTHEWMHOQTKELKFNILLTTYEILLKDKSSFLGGLNWAFIGDEDHGKGREGYGYAS
LHKELEPFLLRVKKDYEKSLPAKYBQILRMEMSALQKQYYKWILTRNYKALSKGSKG
STSGFLNIHMELKKCCHRCYLLKPDDNEFYNKQEALQHLIRSKGSKG
STSGFLNIHMELKKCCHRCYLLKPDDNEFYNKQEALQHLIRSKGSKG
STSGFLNIHMELKKCCHRCYLLKPDDNEFYNKQEALQHLIRSKGSLDFC
FLLSTRAGGLGTNLASADTVVIFDSDWNPONDLQAQARAHRIGQKKQVNIYRLVTKGS
VEEDILERAKKKWYLDHLYIQMADTTGKTVLHTGSTPSSSTPKKEELSALLKFGAEE
LFKEPGGEEGDEPQENJIDEILKRAETERENEFQFLYWGDELLSQFKVANFESNMEDDIE
LEPERNSRNWEEIIPSGARRIEEEERQKELEEIYWLPRARKKGYKAGGPLGRKG
SRRYGSGDSDSITERKRKGRPRTIERENIKGFSDAEIRRCKKGYKAGGPLGRKG
SRRYGSGDSDSITERKRKGRPRTIERENIKGFSDAEIRRCKKKWKFGFLERL
AVARDAELVUKSSTDLERLGELVHGGTKALKDNSSGQERAGGRLGKVKGPTRISGV
QVNAKLVIGHEEELAPLHKSIPSDPEERKRKVIDGHTKAAHDDINGKEDDSKLUVGI
VARKLELVUKSTCHLATGGLYKHGGTKALKDNSSGQERAGGRLGKVKGPTRAISGV
QVNAKLVIGHEEELAPLHKSIPSDPEERKRKVIDGHTKAAHDDINGKEDDSKLUVGI
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HRSPFEHSSDHKSTPEHTWSSRKT"
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1223 c 1520 g 1683 t
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SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
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NKEKRENK/KESTOKEKEPKEEKVNEMKSENKEKKKIPLLDPYHITATSEPVHISE
ESEELHOKTFSVCKERMRVKAALKOLDPEKGLSEREOLEHTROCLIKIGHITECL
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RLAGAGNSKRRKTRNKKNKMKASKIKEEIKSDSSPQPSEKSDEDDEEEDNKDEIVSYK
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CKVLKORPRFVALKKOPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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DDDEDVDKRGSRAQATVAVSYKBAEBTYTDSDDLLEVGGEDVPGTEEDEFETI EKEMD
SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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/translation="MNGHSDEESVRNSSGESSRSDDDSGSASGSGSGSSSGSSSDGSS/
SQSGSSDSESGSESGSGSEESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
LKKQQQQQKAASSDSGSEEDSSSSEDSADDSSSETKKKKHKDEDWQMSGSGSVSGTGS
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/db_xref="taxon:9031"
1. .6872
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/function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_032802:*
1: /SIDS1/gcgdata/
2: /SIDS1/gcgdata/
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153
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Copyright (c) 1993 - 2000 Compugen Ltd
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AAT42756
AAV59280
AAT42757
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                                                                                                                                                                                                                         SUMMARIES
            Mouse CHD-1 gene (
Altered telomerer r
Chick CHD-1A gene
Chicken CHD-1A gene
Enterococcus faeca
Chick CHD-W gene f
DNA encoding novel
Trichoderma reesei
                                                                                                                                                                    Description
  encoding novel
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                                                  06-JUN-1995;
                                                                                                                   12-DEC-1996.
                                                                                                                                                      WO9639505-A1.
                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                         Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1997
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                                                  95GB-0011439
                                                                                 96WO-GB01341
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excret	AAI99227	22	56	10.5	16	
dopsis t	AAC50871	21	N	•	16	
Human type-I amino	AAH44685	22	25		16	
	AAX85048	20	1064		16	
	AAC57473	21	00		16	
Arachidonic acid r	AAC57472	21	00		16	
Drosophila melano	ABL18639	23	992	•	16	
Proliferative glor	ABA77010	22	927	•	16	
۳	AAF11160	21	653	•	16	
#9622	AAI40936	22	517		16	
bone m	AAK35220	22	\vdash	10.5	16	
brain e	AAK09331	22	517	•	16	
foetal 1	ABA61038	22	\vdash		16	
nervous	ABA17398	22	ω		16	
	ABA17397	22	w		16	
Human nervous syst	ABA17396	22	ω		16	
	AA153991	22	ω		16	
bone n	AAK48161	22	w	٠	16	
	AAK21998	22	133	•	16	
Human foetal lives	ABA73552	22	133		16	
Genomic sequence	AAS28165	22	199		17	
DNA encoding novel	AAS30619	22	99	•	17	
Human immune/haema	AAK69459	22	17	11.1	17	
Genomic sequence	AAS41719	22	172	11.1	17	
Human genomic DNA	ABA06775	22	172	11.1	17	
Drosophila melanoo	ABL10922	23	69	11.1	17	
Mouse ischaemic co	ABI99584	24	81	٠	17	
use Tcp-1 cI	AAQ97803	16	1	11.1	17	
	AAX81997	20	51	11.1	17	
ľΩ	AAX82003	20	\mathbf{L}	11.1	17	
secreted	AAC79872	21	S	11.1	17	
secreted p	AAC05229	21	\vdash	11.1	17	
digestive	AAK90736	22	Ν	11.1	17	
digesti	AAK90734	22	N	11.1	17	
immune/	30	22	225	11.1	17	
Human immune/haema	AAK83089	22	\sim	11.1	17	

ALIGNMENTS

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Key Location/Qualifiers misc_difference 52..81 /*tag= a
                                                                                                                                                                                                                                         Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1; CHD-W; W chromosome; ss.
/note= "bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
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RESULT
AAV59280
ID AAV5
XX AAV5
XX AAV5
XX AAV5
XX AAV5
XX AAV6
XX AAV6
XX AAV6
XX CA
COS SYNT
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Matches 153
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                                                                                            04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                  13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                ROCKEFELLER
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Lange
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97US-0800264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              re repeat binding facto ataxia telangeictasia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor;
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RESULT
AAT42757
ID AAT4
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-diners and antibodies, use to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                       P-PSDB; AAW08147
                                                                                                                                                                                                                                                                                                           Gallus
                                                                                                                                                                                                                                                                                                                                   Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                       Chick CHD-1A gene fragment.
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                                                                                                               06-JUN-1995;
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                                     WPI; 1997-043127/04
                                                             Griffiths R,
                                                                                                                                       05-JUN-1996;
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                                                                                      INNOVATION
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                                                             Tiwari
                                                                                                               95GB-0011439
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                                                                                                                                                                                                                                                                     Location/Qualifiers 52..81
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                                                                                                                                                                                                              "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
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0; Mismatches
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1.4e-17;
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Fig 3"
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amino
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Avian chromodomain-helicase-DNA binding genes

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AAT42751
The chicken CHD-W gene (AAR42754) acting alone or in conjunction with the closely related CHD-1A gene (AAR42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo CDNA library using a great tit CHD-W sequence (see also AAR42755) as probe. The CHD-1A (A = AVIAA) gene shows close identity to the mouse CHD-1 gene (see also AAR42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic
                                                                                                                                                                                                                                                                                                                                                      06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken CHD-1A gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42751) and the great tit CHD-W gene (see also AAT42759). Translated amin acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                             Claim 1; Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                       Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9639505-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   birds - used
                                                                                                                                                                                                          Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                        Tiwari B;
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228..5390
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Pred. No.
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                  Query Match
Best Local :
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06-MAY-1997;
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                                                                                                             intection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barash SC, Dillon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX13278 standard; DNA; 13884
                Local
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 l Similarity
22; Conserv
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97US-0044031.
97US-0046655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US08985
             14.48;
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                Score 22;
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DB 20; 0.14;

Length 13884;

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A computer readable medium has been developed which has recorded on it 982 nucleotide sequences isolated from the Enterococcus faecalis genome. AXX1938 to AXX1919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcual infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
Sequence 13884 BP; 4353 A; 2723 C; 2370 G; 4422 T; 16 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1453-1460; 2084pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; attenuation; computer readable medium; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       faecalis; contig; detection; Enterococcal infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25;
Pred. No.
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                                                                                                                                                                     Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAM08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
          AAS81107 standard; cDNA; 803 BP
                                                                                                                                                    Sequence 153
                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chick CHD-W gene fragment
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                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS
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                                                          1997-043127/04
DB; AAW08148.
                                                                                                                                                                                                                                                                 8; Fig 3; 76pp; English
                                                                                                                                                                                                                                                                                                chromodomain-helicase-DNA binding genes determine sex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex determination; chromodomain-Helicase-DNA binding
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                                                                                                           Similarity
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                                                                                                   Conservative
                                                                                                                                                     B₽;
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                                                                                                                                                                                                                                                                                     for sex determn. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                          95GB-0011439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                     56 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                          100.0%;
                                                                                                                                                     36 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "bases 52-81 are a repeat of bases and are ignored in the translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid sequence given in Fig 3"
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                                                                                                            Score 20;
Pred. No.
                                                                                                                                                     31 G;
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                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                     to control sex of progeny
                                                                                                                                                     30 T; 0 other;
                                                                                                                      DB 18;
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Best Local Similarity
Matches 19; Conserva
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AC X
                                                                                                                                                                                                                                                                                             imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                              AAF15189 standard;
                                                                                                                                                                                                                                                   Sequence 803 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding novel human diagnostic protein #16911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            food supplement;
                                                                                                                          26 AACCACAAGCAAAACAGTT
                                                                                                          aaccacaagcaaaacagtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome mapping; gene mapping; gene
upplement; medical imaging; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG16920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID No 16911; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c,
                                                                                                                                                                                                                                                   221 A;
                             CDNA; 905
                                                                                                                                                                                     12.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang
                                                                                                                                                                                                                                                   195 C;
                                                                                                                                         44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TY
                                                                                                                                                                        0;
                                                                                                                                                                                        Score 19;
Pred. No.
                                                                                                                                                                                                                                                   240 G;
                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                   147
                                                                                                                                                                                      4.8;
                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                   H.
                                                                                                                                                                                                     23;
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                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; forensic genetic disorder;
                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                   Length 803;
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forensic;
                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        techniques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SS
                                                                                                                                                                        Gaps
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ВP

0,

SS

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The present invention describes a method for monitoring differential CC expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal (CC et ls. The method uses fluorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the genes can be used to production of the global expression of genes from FF cells allows the production of the global expression of genes from FF cells allows the production be undertified and gene copy number variation and stability can be constituted and gene copy number variation and stability can be consisted in culture conditions, environmental stress, spore captured to changes in culture conditions, environmental stress, spore complined in the expression of genes can be used to study how FF cells captured to changes including elimination or catabolic pathway compliance or or open reading frame, and organisation of the conditions environmental stress, spore complined to the gene products to facilitate and conditions of the gene products to facilitate can super; and the results. AAFO1478 to AAF11247 represents ESTs from Aspergillus of the results. AAFO1478 to AAF11257 from Aspergillus oryzae; and can superifically claimed in the present ESTs from Aspergillus oryzae; and can specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reeses; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 89; Page 3111; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200056762-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trichoderma reesei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trichoderma reesei EST SEQ ID NO:7712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                            Sequence 905 BP; 226 A; 265 C; 185 G; 218 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 substrate of expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-594572/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVO NORDISK BIOTECH INC. (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAR-2000; 2000WO-US07781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multiple gene expression; filamentous fungal cell; EST;
                                                                  291 acagaccaaaaaaccaca 308
                                                                                                                             45 ACAGACCAAAAAACCACA 62
                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rey MW,
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shuster JR, Kauppinen S, Clausen IG,
                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                        0;
                                                                                                                                                                                                                      Score 18;
Pred. No.
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                DB 21; Length 905;
                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olsen PB;
                                                                                                                                                                                     0;
                                                                                                                                                                                        Gaps
                                                                                                                                                                                        0,
                                                                                                                                                   QΥ
                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                            뭥
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and CD polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques (II), (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating climaging of sites expressing (II), (I) and (II) are useful for treating climaging of sites expressing (II), (I) and (II) are useful for treating climaging of sites expressing (II), (I) and (II) are useful for treating climaging of sites expressing (II), (I) and (II) are useful for treating climaging of sites expressing (II), (I) and (II) are useful for treating climaging of sites expressing (II), (I) and (II) are useful for treating climaging of sites expressing (II), (I) and (II) are useful for treating climaging of sites expressing (II), (I) and (II) are useful for treating climaging of sites expressing (II), (II), (II) and (III) are useful for treating climaging of sites expressing (II), (II), (II), (II), (II), (II), (II), (III), (III)
                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 17354; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Liu C,
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23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #17354.
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 5168 BP; 1428 A; 1397 C; 1194 G; 1149 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABG17363
                                                                                        725 ttccagatgatcctgata 742
10
                                                                                                                          5 TTCCAGATGATCCTGATA 22
                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-639362/73
                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                11.8%; Score 18; DB 23; Length 5168; 100.0%; Pred. No. 15;
                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                              0 other
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밁

AAK83089

AAK83089 standard; DNA;

Gaps

0;

	X
7-JUL-2000 1-JUL-2000 1-JUL-2000 4-JUL-2000 4-JUL-2000 4-AUG-2000 4-AUG-2000 4-AUG-2000 4-AUG-2000 4-AUG-2000 4-AUG-2000 4-AUG-2000 4-AUG-2000 4-AUG-2000 4-AUG-2000 1-SEP-2000	AAK83089; 07-NOV-2001 Human immune/ Human; immune cytostatic; g Homo sapiens. W0200157182-A 09-AUG-2001. 17-JAN-2000; 04-FEB-2000; 04-FEB-2000; 04-FEB-2000; 16-MAR-2000; 17-MAR-2000; 17-MAR-2000; 19-MAR-2000;
2000US-0216647. 2000US-0216880. 2000US-0217496. 2000US-021964. 2000US-022963. 2000US-02295213. 2000US-0225214. 2000US-0225214. 2000US-0225270. 2000US-0225770. 2000US-0225770. 2000US-0225778. 2000US-0225788.	(first entry) //haematopoietic antigen genomic sequence SEQ ID NO:37901. se; haematopoietic; immune/haematopoietic antigen; cancer; gene therapy; vaccine; metastasis; ds. 2001WO-US01354. 2000US-018658. 2000US-018654. 2000US-0186350. 2000US-0186350. 2000US-0198123. 2000US-0198123. 2000US-0205515. 2000US-020467. 2000US-0214886. 2000US-02141886.
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20-OCT 2000 20-OCT 2000 20-OCT 2000 01-NOV 2000 08-NOV 2000 17-NOV	14 - SEP - 2000; 21 - SEP - 2000; 21 - SEP - 2000; 25 - SEP - 2000; 26 - SEP - 2000; 27 - SEP - 2000; 27 - SEP - 2000; 29 - SEP - 2000; 20 - OCT - 2000; 02 - OCT - 2000; 03 - OCT - 2000; 04 - OCT - 2000; 05 - OCT - 2000; 07 - OCT - 2000; 08 - OCT - 2000; 09 - OCT - 2000; 01 - OCT - 2000; 02 - OCT - 2000; 03 - OCT - 2000; 04 - OCT - 2000; 05 - OCT - 2000; 06 - OCT - 2000; 07 - OCT - 2000; 08 - OCT - 2000; 09 - OCT - 2000; 01 - OCT - 2000; 02 - OCT - 2000; 03 - OCT - 2000; 04 - OCT - 2000; 05 - OCT - 2000; 06 - OCT - 2000; 07 - OCT - 2000;
2000US-0241808 2000US-0241809 2000US-0241809 2000US-0246474 2000US-0246475 2000US-0246476 2000US-0246525 2000US-0246525 2000US-0246525 2000US-0246525 2000US-0246528 2000US-0246610 2000US-0246610 2000US-0246611 2000US-0249207 2000US-0249207 2000US-0249211	0.023 0.023

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RESULT 11
AAK830
ID AAK830
XX AAK830
XX O7-NOV
XX UMMAN
DE HUMAN
XX Cytost
XX Cytost
XX Cytost
XX O9-AU
PR 17-JAI
AAK830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) corporations and polynucleotides may be used in the prevention, diagnosis and creatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased corporated, they may be used to treat sociated with the creased corporated of the activity of (I) by expressions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting corporated (I) proteins of a host cell and culturing the cell to express the corporate and treat immune/haematopoietic related diseases, especially concers and cancer metastases of haematopoietic antigen genomic concers and the present human immune/haematopoietic antigen genomic concers and the protection of the present invention. AAK64902 to AAK64903 and AAM82169 concers and cancer metastases of haematopoietic antigen genomic conconcers and cancer metastases of haematopoietic antigen genometas 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 17
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08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254997.
05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 37901; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
      31-JAN-2000; 2000US-0179065.
                                                       17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37902
                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK83090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK83090 standard; DNA; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 225 BP; 52 A; 55 C;
                                                                                                            09-AUG-2001.
                                                                                                                                                                WO200157182-A2
                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.18; Solution 11.18; Solution 100.08; 17; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 G; 63 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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   22 - AUG-
22 - AUG-
23 - AUG-
30 - AUG-
30 - AUG-
91 - SEP-
91 - SEP-
90 - S
14 - SEP
14 - SEP
14 - SEP
21 - SEP
25 - SEP
25 - SEP
26 - SEP
27 - SEP
27 - SEP
29 - SEP
20 
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24-FEB-2000;
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2000US-0227182
2000US-0229344
2000US-0229343
2000US-0229343
2000US-0229343
2000US-0229343
2000US-0229312
2000US-022911242
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2000US-0184664
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20-OCT-2000

01-NOV-2000

08-NOV-2000

09-DEC-2000

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08-DEC-2000

08-DEC-2000
Nucleic acids encoding useful for preventing, metastasis -
                                                                                    2001-483426/52.
                                                                                                                                                                      HUMAN GENOME
                                                                                                                               Barash
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2000US-0246477.
2000US-0246476.
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2000US-0241786.
2000US-0241787.
2000US-0241808.
2000US-0241809.
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                                                                                                                                                                         SCI INC
                     human immune/hematopoietic antigen diagnosing and/or treating cancers
                                                                                                                             MS
                       polypeptides, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC ankno acid sequences given in AAM82170 to AAM91921. (I) have cytostatic antino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and ctreatment of diseases associated with happropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome cthat affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting cthe nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cto AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54920 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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07-JUL-2000

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11-JUL-2000

11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease; digestive system disorder; Meckel's diverticulum; ds.
                                                                                                                                                                                                                                                                                                                                   17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human digestive system antigen genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK90734 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 AAAGAGAGGCTCAGAGA 141
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 2000US-0179065
2000US-0186628
2000US-0188664
2000US-01886350
2000US-019974
2000US-0199076
2000US-0199123
2000US-0209467
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 A;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chronic colitis;
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                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -  \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{2}
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                                                                                                                                                                                 Sequence 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 4310; 986pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-502630/55.
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11.1%;
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17; Conservative
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    Score 17; DB Pred. No. 49; 0; Mismatches
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2000US-022526 2000US-022526 2000US-022526 2000US-0225275 2000US-0225757 2000US-0225757 2000US-0225758 2000US-022578 2000US-0225681 2000US-0225681 2000US-022984 2000US-022984 2000US-022984 2000US-022984 2000US-022984 2000US-022984 2000US-022984 2000US-022984 2000US-022984 2000US-023124 2000US-023124 2000US-023124 2000US-023124 2000US-023141 2000US-023140 2000US-02314180 2000US-0241180 2000US-0244478 2000US-0244477 2000US-0244477

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RESULT 13
AAK90736
ID AAK907
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XX Human
XX Human
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  2000US-0179065.
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lum; ds.
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chronic colitis;
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                                                                                                                                                           gene therapy;
                                                                                                                                                                                                                                                                                 AAC05229 standard; cDNA; 311 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 225 BP; 52 A; 55 C; 55 G; 63 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of human digestive system antiques. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antiqen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
 (GEST ) GENSET
                                                                                                                                  Homo sapiens
                                                                                                                                                                           Human;
                                                                                                                                                                                                  Human secreted protein 5' EST, SEQ ID NO: 9304.
                                                                                                                                                                                                                           06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 4312; 986pp; English.
                            26-FEB-1999;
                                                                                06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-502630/55.
                                                     21-FEB-2000; 2000EP-0200610
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                                                                                                                                                                                                                                                                                                                                                               125 AAAGAGAGGCTCAGAGA 141
                                                                                                                                                                                                                                                                                                            14
                                                                                                                                                                                                                                                                                                                                                19 aaagagaggctcagaga 35
                                                                                                                                                                                                                                                                                                                                                                                                     . Match 11.1%; Score 17; DB 22; Length 225; Local Similarity 100.0%; Pred. No. 49; Local Similarity 0; Mismatches 0; Indels
                                                                                                                                                        5' EST; expressed sequence tag; secreted protein; cDNA isolation;
herapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
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2001US-0259678
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2000US-0249300
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                          990S-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM;
                                                                                                                                                                                                                                                                                                                                                                                                    0;
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망
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
AAC79872/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
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WPI; 2000-638176/61
P-PSDB; AAB44853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 311 BP; 90 A; 74 C; 63 G; 84 T; 0 other;
                                                                                                                                                                        21-SEP-2000
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORR has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT prined cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs with intact 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 9304; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-500381/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano
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\$\text{97} \text{77} \text

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12-MAR-1999;
11-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                            Human; secreted protein; cytostatic; antiarthritic; antiasthmatic; immunosuppressive; antiarteriosclerotic; antiinflammatory; noctropic; neuroprotective; antidiabetic; tranquiliser; vulnerary; antibacterial; antipsoriatic; antiarhythmic; antirheumatic; cardiant; anti-HIV; autoimmune disorder; allergic condition; cardiovascular disorder; cancer; neurological disease; tissue repair; ss.
                                                                                                                                                                                                                                                WO200055176-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC79872 standard; cDNA; 657
                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                 09-MAR-2000; 2000WO-US06057
                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein encoding cDNA for gene 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 GAGGCTCAGAGACTTTG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 gaggctcagagactttg 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
17; Conserv
Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                           99US-0124142.
99US-0138597.
99US-0168666.
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100.08; Prr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 311;
48;
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This invention describes a novel isolated polypeptide (I) comprising an camino acid sequence at least 95 % identical to a polypeptide sequence selected from 49 polypeptides encoded by polynucleotide sequences concluded in American Type Culture Collection (ATCC) deposit number collection antiarthritic, antiarthatic, immunosuppressive, nootropic; contiarteriosclerotic, antiartlammatory, neuroprotective, antiathetic, containthritic, antiarthatic, immunosuppressive, nootropic; containthritic, cardiant and anti-HIV activity. (I) or a nucleic acid (II) encoding (I) is useful for preventing, treating or ameliorating amedical condition and for diagnosing a pathological condition or susceptibility to the condition. (I) is useful for identifying a binding partner which affects the activity of the polypeptide and for identifying an activity in a biological sample. (I), (II) or an antibody (IV) specific to (I) is calso useful for treating or preventing a disease, disorder or condition associated with aberrant expression of (I). Diseases treated or diagnosed condition rejection or graft-versus-host disease, inflammation, hyper consider an arrhythmias, arterioscations and conditions such as astima, corpan rejection or graft-versus-host disease, inflammation, hyper creditions are particular and adiabetic retinopathy, concern hose as parkinson's disease, viral, bacterial, bacterial, absorbers such as parkinson's disease, viral, bacterial,
                          Query Match
Best Local
Matches
                                                                                                                                                               neurological diseases such as Parkinson's disease, viral, bacterial, fungal or parasitic diseases. They are also used to repair, replace or protect tissue damage by congenital defects, to treat trauma, in surgery, including cosmetic plastic surgery, to treat fibrosis, reperfusion injury or systemic cytokine damage, to stimulate chondrocyte growth, to prevent skin aging due to sunburn, to change a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression, memory, stress and for accelerating wound healing. (I), (II) and/or their agonist or antagonist are useful as food additives or preservatives to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamin, mineral or other nutritional components. (I) is useful for screening therapeutic compounds. (II) is useful in forensic biology for detecting DNA sequences and as diagnostic probes for detecting the presence of specific mRNA in a particular cell type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel 49 human secreted proteins useful for diagnosis, prevention and treatment of disorders including neurological, cell proliferative, cardiovascular, and autoimmune/inflammatory disorders and microbial
                                                                                                                        Sequence 657 BP; 186 A; 125 C; 203 G; 143 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1a; Page 349; 405pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infections
Local Similarity
nes 17; Conserv
Conservative
                    11.1%;
0,
                       Score 17;
Pred. No.
Mismatches
                          48;
                                                 DB
                                            21;
                                                                                                                        0
0;
                                                                                                                        other;
                                         Length 657;
Indels
0;
Gaps
0;
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Search completed: August Job time: 32187 sec

3, 2002, 01:50:02

B 8

72

GCTCAGAGACTTTGTGG

56

133 GCTCAGAGACTTTGTGG 149

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OLIGO_NUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-973-363-2
153
                                                                                                                                                                                                                                                                                                                                                                                                                         EST:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                               gb_est1:*
gb_est2:*
gb_htc:*
gb_gss:*
                                                                                                                                                                                                                                                                                                         em_estpl:*
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em_gss_inv:*
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SUMMARIES
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Result No.	Score	Query Match		B B	ID ID
21	102 102	66.7 66.7	619 660	9 9	BB155356 BB461065
ω 4	351	33.3	438	9	BB830730
4 0	35 27	22.9 17.6	446 430	99	BB834922 AL601246
6	27	17.6	547	9	AI890775
c 7	27		686	9	AW997058
8	27	17.6	821	10	BF239967
9	27		866	9	AU125712
10	27		1028	10	BE895133
c 11	26		337	9	AW996787
12	23	15.0	1200	12	AG131555
13	22	14.4	1312	10	BG858209
c 14	19	12.4	217	10	BF147109
15	19	12.4	404	12	CNS02EDQ
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18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	19	19
11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8	11.8			11.8			12.4	12.4
1176	969	901	810	709	703	700	869	663	655	607	587	545	530	517	507	495	491	481	456	451	448	440	380	329	932	654
10	12	10	10	12	12	10	9	9	10	10	12	10	9	12	10	12	10	9	10	9	12	12	9	9	10	9
BG036467	AG134136	BE259673	BG666296	AQ545887	AG144450	BG176934	AW639551	AL638257	BJ043477	вJ060189	AZ096348	вJ068556	BB752282	AQ168710	BG370667	вн570623	вJ029393	AW634969	R40931	AI465697	AQ024759	AQ997521	AA148843	AA856136	BG169355	AI623066
BG036467 602326413		BE259673 601145816	BG666296 DRABSA07		AG144450 Pan trogl	BG176934 602313611		ъ				9	BB752282 BB752282	AQ168710 HS_3166_A		BH570623 BOGRX18TR		AW634969 bl27cl1.w	R40931 yf76a12.s1	AI465697 vw83d08.y		\mathbf{L}	AA148843 zo09e04.r	AA856136 vw83d08.r	BG169355 602320903	AI623066 AEMTAD31

ALIGNMENTS

RESULT 1

BB153356

DNA-binding protein (CHD-1) mRNA, mRNA sequence.

DNA-binding protein (CHD-1) mRNA, mRNA sequence.

BB153356

BB15336

BB1536

BB

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 619)

RS Arakawa,T., Carninci,P., Fikuda,S., Firuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishi,Y., Ito,M., Kawai,J., Komo,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

MIKEN Mouse ESTS (Arakawa,T., et al. 2001)

On Jun 29, 2000 this sequence version replaced gi:8811286.

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehliro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9216

Femail: Genome-research viken of the

COMMENT

Tel: 81-45-503-922

Fax: 81-45-503-9216

Fax: 81-45

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RESULT
BB461065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
ACCESSION
                                                                     DEFINITION
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                                                                                                                                                                                                                                                                                                510 AAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGC
                                                                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                               AGAGATCTTGCAAAAAAGAGAGGCTCAGAGACTTTGTGGTGCG
                                                                                                                                                                                                                                                                                                                          AAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAAACTACTTAGC
                                                                                                                                                                                                         AGAGATCTTGCAAAAAGAGAGGCTCAGAGACTTTGTGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                             102;
       BB461065 RIKEN full-length enriched, 12 days embryo spinal gar Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
  BB461065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
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Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            do,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I. Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GRAGAGAGAGAGAGCTCTTTTTTTTTTTTTTTTYN 3'], cDNA was GRAGAGAGAGCATCCAAGAGCTCTTTTTTTTTTTTTTTTYN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified pBluescript KS(+) after bulk excision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="A130024L16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="16 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                66.7%;
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Pred. No. 3.1e-42;
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                                                                                                                                                                                                         611
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                                                            spinal ganglion
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                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                      Division
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
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Arakawa, T., Carninci, P.,
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                                                                                                                                                                                                                                                spinal ganglion"
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/clone="D130070B13"
                                                                                                                                                         /note="Site_1:
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sug,Y. and Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KOndo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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                                                                                                               prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory RIKEN, Division of Experimental Animal Research in Ril
/tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RIKEN full-length enriched, 12 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                                                                                                                                                                               Sall; Site_2: BamHI; cDNA library was
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562 AGAGATCTTGCAAAAAGAGAGGCTCAGAGACTTTGTGTGCG
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Saito, R., Shiraki, T., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watchiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)
                                                                                                                                                                                                             Email: genome-resegs.riken.go.jp,
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    M., Konno,H., Okazaki,Y. Muramatsu,M. and Hayashizaki,Y.
    Normalization and subtraction of cap-trapper-selected cDNAs to
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    wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
    wathiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
    "S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
    Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9216
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JYg.MC(B) CDNA Mus muscullus CDNA clone G930013K04 3', mRNA
                                                                    RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
            Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kanagawa 230-0045, Japan
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P. Shibata/K., Hayatsu/N., Sugahara/Y., Shibata/K., Itoh
// M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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Hayashizaki, Y.
RIKEN Integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Ress. .
10 (11), 1757-1771 (2000)
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Mus musculus
Eukaryota; Me
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BB834922 RIKEN f
Jyg-MC(B) cDNA N
sequence.
BB834922
BB834922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(SC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthería; Rodentia; Sciurognathí; Muridae; Murinae; Mus 1 (bases 1 to 446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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//db.xref="taxon:1090"
//clone='G930013K04"
/clone_lib="RIKEN full-length enriched, mammary
RCB-0527 Jyg-MC[B] cDNA"
/ctssue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC[B]"
/cell_line="RCB-0527 Jyg-MC[B]"
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Pred. No.
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7.le-16;
hes 0; Indels
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ACCESSION VERSION KEYWORDS

sequence.
BB830730
BB830730.1 GI:17008973

SOURCE ORGANISM

Mus musculus

REFERENCE AUTHORS

COMMENT

JOURNAL

Unpublished (2001) Contact: Yoshihide Hayashizaki

TITLE

RESULT BB830730

DEFINITION

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0;

BASE COUNT ORIGIN

211

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Query Match Best Local Similarity

66.7%; 0;

Matches

102;

Conservative

Mismatches

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KEYWORDS
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Best Local (
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                                                                                                                                                                                                                                                                                                                          Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dKfz- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 bp mRNA linear EST 14-AUG-2001
DKFZp313J1040_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp313J1040 5', mRNA sequence.
                                                                                                                                                                                                                               This clone (DKFZp313J1040) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encyclopedia: real-time sequence clustering for construction o
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                             No s1 sequence available
                                                                                                                                                                                                                                                                                                                German Genome Project
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiemann, S
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e mouse tissues
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                    163
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      cDNA-collection" 81 c 86 ~
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/r____
                                                                                             /clone="DKFZp313J1040"
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/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
108 g 100 t
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/db_xref="taxon:9606"
                                                                                                                                                                                                              Location/Qualifiers
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Pred. No.
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                                                        SfiIA; Site_2:
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                                                                                                                                         76 CAGACCCGTGCAGACTACCTCATCAAA 102
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                                                                                                                       CAGACCCGTGCAGACTACCTCATCAAA 307
AW997058 686 bp mrNA lir
QV3-BN0047-150400-152-c03 BN0047 Homo sapiens
AW997058
                                                                                                                                                                                         ch 17.6%;
l Similarity 100.0%;
27; Conservative (
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27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40UP from Gibco
High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lini.gov/bbrp/image/image.html
Insert Length: 1924 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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AI890775.1
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                                                                                                                                                                                                                                                                                                            /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.85 kb. Life Technologies catalog #:
11539-012"
                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:2443725"
/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated
/denocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
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Pred. No.
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Pred. No.
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                                   linear
                 cDNA,
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                mRNA sequence.
                                   EST 05-JUN-2000
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ACCESSION

AW997058.1 GI:8257292

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 821)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordín, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                 BFZ39967 821 bp mRNA linear EST 14-NG 601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 19
High quality sequence stop: 678.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150
400-152-c03&t3=2000-04-15&t4=1)
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 686)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

154 c 126 g 241 t
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/dev_stage="Adult"
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76 CAGACCCGTGCAGACTACCTCATCAAA 102
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                                                                                                                                      Contact: Takao Isógai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM1033 row: K. Column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai.T.
HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S. Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzu,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU125712 NTZRM4 Homo sapiens cDNA clone NTZRM40020615', mRNA
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Contact: Robert Strausberg, Ph.D.
Email: genomics@lri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 866)
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/Clone=lib="NIFLMGC_54"
/Clone_lib="NIFLMGC_54"
/Lissue_type="from chronic myelogenous leukemia"
/lab_host=Dh10B (T1 phage-resistant)"
/note="Organ: bone marrow; vector: pDNR-LIB (Clontech);
/note="Organ: bone marrow; vector: pDNR-L
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/db_xref="taxon:9606"
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CAGACCCGTGCAGACTACCTCATCAAA 102
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                                27;
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Location/Qualifiers
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BE895133
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                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                               /lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo (
Average insert size 2 kb. Library constructed by Lif-
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"
                                                                                                                                                                                                          /clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db xref="taxon:9606"
                                                                                                                                                                                                                                  /clone="IMAGE:3921087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4002061"
/clone_lib="NT2RM4"
                                                                                                                                                                                                                                                   /db_xref="taxon:
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100.0%; Pr
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Pred. No.
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AUTHORS
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Best Local
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VERSION
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AG131555 1200
Pan troglodytes DNA, clone:
AG131555
AG131555.1 GI:16661233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-23&t4=1)
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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QV3-BN0047-230200-102-d03 BN0047
AW996787
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High quality sequence stop: 337,
Location/Qualifiers
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           note-"Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0047"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                17.0%;
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Pred. No.
                                                                       1200
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PTB-143K14.F,
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0.0059;
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                                            linear
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                                               survey
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Eukaryota; Viridiplantee; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.

El (bases 1 to 1312)

S Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtil Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2

Unpublished (2000)

Contact: Charles Hauser
DCMB Box 91000

Duke University
Durham, NC 27708-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (SSC); and Chemical Research (RIKEN), Genomic Sciences Center (SSC); 1-7-22 Suehito-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                      Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                            BG858209
BG858209.1 GI:14239393
EST
                                                                                                                                                                                                                                                                                                                                                                   BG858209 1312 bp mRNA linear EST 29-MAY-: 1024056D08.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H., and Sakaki, Y.
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Eukaryota; Meta:
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Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
BAC Library_clone:PTB-143K14.F.
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23; Conservative
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R.Site 2
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/db_xref="taxon:9598"
/clone="PTB-143K14.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
371 c 199 g 39 t 65 others
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100.0%; Pre
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: SacI.
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BF147109/c
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 CAAAAAACCACAAGCAAAACAG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@du
                                                                                                        High quality
                                                                                                                         Seq primer: Primer name ambiguous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF147109.1 GI:11028504
                                                                                                                                               MGI:1419614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .1312
                          /strain="CD-
                                                                                   Location/Qualifiers
    /db_xref="taxon:10090"
                                          /organism="Mus musculus"
```

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Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Alie, Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Waterston, R. and Wilson, R. and Wi
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 217)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mid-log phase in TAP (acetate containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CO2 and HS medium bubbled with 5% CO2. POLYA MRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the BCORI (5') and XhOI (3') sites. Paluescript II SK plasmids were excised from the lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript II SK.; Site_1: EcoRT; Site_2: XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 TAGCAGAGATCTTGCAAAA 175
Submitted (12-APR 2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovi genome. For more information, please take a look at http://www.genoscope.ons.fr/Tetraodon.
                                                                                                                                                                                                                                                                                               2 (bases 1 to 404)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 404)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 262M09 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS02EDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodontidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Health Sciences). Original lambda-based library is available through ATCC, catalog #63422."

a 38 c 60 g 73 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="60 day"
/lab host="bH10B (phage-resistant)"
/lab host="bH10B (phage-resistant)"
/note="Organ: testis; Vector: pBluescript SK+ (Stratagene / Site_1: XhoI; Site_2: EcoRI; cDNA oligo dT-primed (5'-(GA)10-ACTAGTCTCGAGTTTTTTTTTTTTTTTTTT-3'] and directionally cloned using 5' linkers 5'-AATTCGCACAGAG's and 5'-CTCGTGCG-3'. Size selection of >400bp material gives average insert size ranging from 1-2 kb. Library was mass excised (from lambda-UnizAP-XR) and resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
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/clone_lib="McCarrey Eddy spermatocytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tetraodon.
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RESULT 1 CNS02EDQ LOCUS

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Matches

ACCESSION VERSION

SOURCE KEYWORDS

ORGANISM

JOURNAL COMMENT

FEATURES

JOURNAL REFERENCE

TITLE

AUTHORS TITLE

REFERENCE AUTHORS

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Search completed: August 2, Job time: 30148 sec
                                                                                                                 Query Match
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                                                                  352 AAAAACCACAAGCAAAACA 370
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                                                                                                                                                                                               103 a
                                                                                                                   Conservative
                                                                                                                                                                                                        /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="262M09"
/clone_11b="G"
/clone_11b="G"
/note="Genoscope sequence ID : COAG2
PUC-Ori"
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                                                                                                                  Score 19; DB; Pred. No. 25; 0; Mismatches
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                                                                                                                                            12;
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Minimum DB seq length: 0
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                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                Score
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                                                                                                                                            Patent: WO 9639505-A 3 12-DEC-1996;
ISIS INVOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   unclassified.

1 (bases 1 to 153)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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AF004397 Gallus ga
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AF006513 Homo sapi
AC01224 Homo sapi
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AC040158 Homo
AB053170 Homo
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AC092137 Homo
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Other publication AU 5906996
Location/Qualifiers
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                           Gallus gallus
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                                                                                             AF004397.1
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                                                                                                                              protein,
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111 TAAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGGTGCA 153

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Query Match
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Submitted (16-MAY-1997) Zoology,
Glasgow G12 8QQ, UK
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Gene 197 (1-2), 225-229 (1997)
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CKVIKQRPREVALKQDSY IGGHESLELEDYQLIKGLWILAHSWCKGNSCILADEMGLG
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RHAGAGNSKRRKTRNKKNKMKASKIKEEIKSDSSPQFEKSEDEDEEEDNKDEITVSVK
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1223 c 1520 g
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SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
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NKEKRENKVKESTOKEKEVKEEKVNEMKSENKEKSKK IPLLDTPVH ITATSEPVP ISE
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SQSGSSDSESGSESGSQSESESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
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228. .5654
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                                                                                                                                                                                                                                                                                            KEYTNPEQIKQWRKNLWIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="role in chromatin architecture"
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                                                                       1960 GAAG 1963
                                                                                                                130 GAAG 133
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al Similarity 100.0%; Pred. No. 3.1e-26;
64; Conservative 0; Mismatches 0;
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosaurita; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 2292)
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ORF2.
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Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Devel., Aging and Cancer, Tohoku Univ.; 4-1 Seiryo-machi, Aoba-ku, Sendai 980-77, Japan (Tel:022-272-9499, Fax:022-272-3982)
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LUVGIYEFXAGSWGCKVNGSRGLNTEILPDDPDRTPRONSYREYQTTSLNY"
27 a 385 c 546 g 534 t
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/clone_lib="lambda gtl1"
/dev_stage="13 day embryo"
257. .1939
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/db_xref="taxon:9031"
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153 bp
Sequence 5 from Patent W09639505.
A58686.1 GI:3714249
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Sequence 15 from Patent WO9639505.
A58696
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Location/Qualifiers
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Griffiths, R. and Ti
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Sequence 4 from Patent WO9639505.
A58685
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AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                  unclassified
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205 c 308 g 30
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100.0%; Pred. No. 2.6e-16;
tive 0; Mismatches 0;
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Sequence 3 from patent US
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Griffiths,R. and Ti
AVIAN GHD GENES AND
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE, IN METHODS
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/db_xref="taxon:32644"
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AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced gi:293322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A mammalian DNA-binding protein that contains a chromodomain and SNF2/SWIZ-like helicase domain Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
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Delmas, V., Stokes, D.G. and Perry, R.P.
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TLKQQNVRGMKKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERI
IAHSNQKSAAGLPDYYCKWQGLPYSECSWEDGALISKKFGTCIDEYFSRNQSKTTPFK
DCKVLKQRPRFVALKKQPSYIGGHEGLELRDYGLNGLNWAHSWCKGNSCILADEMGL
GKTLQTISFLAYLFHEBQDYGFFLLVVPLSTLTSWQREIGTWASQMNAVYLGDINSR
GKTTGTTHEWMHPQTKRLKFNILLTTYEILLKDKAFLGGLNWAFTGVDEAHRLKNDDSLL
YKTLLDFKSNHRLLTTGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYA
SLHKELEPFLLRRVKDVEKSLDAKVEQILKDKAFLGYYKWILTRNYKALSKGSK
GSTSGFLNIMMELKCOHCYLIKPEDNNEFYNKQEALQHLTRSYKLILDKLIRL
REGGNRVLIFSQMVRMLDILAEYLKYRQFPGRLDGSIKGELRKQALDHFNAEGSEDF
CFLLSTRAGGLGINLASADTVIFDSSWNPQNDLDGARAHRIGQKKQVNIYELVTKG
CFLLSTRAGGLGINLASADTVIFDSSWNPQNDLDGARAHRIGGKKQVNIYELVTKG
CFLLSTRAGGLGINLASADTVIFDSSWNPQNDLDGARAHRIGGKKQVNIYELVTKG
                                                                                                                                                                                                                               RRQPQQAQQQRPASSNSGSEEDSSSSEDSDDSSSGAKRKKHNDEDWQMSGSGSPSQLG
SDSESEERDKSSCDGTESDYEPKNKVRSKERDKSKSNGKKLLIGQKRQLIDSSEDE
SDSESEERDKSSCRQATVNGSYKEDEEMKTDSDDLLEVGSBUPGQPEDEEFETTIERW
DDEDYDNDKRSSRRQATVNGSYKEDEEMKTDSDDLLEVGSBUPGQPEDEFETTIERW
DCRVGRKGATGATTTIYAVEADGDPNAGFERNKEPGDIQYLIKWKGWSHIHNTWETEE
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                                                                                                                                                                                                                                                                                                                                         /product="DNA-binding protein"
/protein_id="AAB08486.1"
/db_xref="G1:455015"
/translation="MNGHSDEESVRNGSGESSQSGDDCGSASGSGSGSSSGSSSDGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CHD-1"
171. .5306
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/db_xref⇔"taxon:10090"
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1 (bases 1 to 5947),

Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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//product="CHD1"
//produc
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RSRTYSGSDSDSISERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLERL
DAIARDAELYDKSSTDLERLGELYHNGCYWALKDSSSGTERAGGRLGKVKGFFFRISG
VQVNAKLVIAHEDELFPLHKSIFSDERKQYTIPCHTKAAHFDIDMGKEDDSNILIG
IYEKGYGSWEMIKUNDPDISTJHKILDPDDKKFQAKOLOTRADYLIKLLSRDLAKREA
QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK
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QYHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHEWDHYRQDSRYYSDREKHRKLDD
HRSREHRPSLEGGLKDRCHSDHRSHSDHRMHSDHRSSSEHTHHKSSRDYRYLSDWQLD
HRARASGGPRSPLDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKT*

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GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLH
                                               FKDCKYLKQRPRFVALKKQPSYIGGHEGLELRDYQLNGLNWLAHSWCKGNSCILADEM
GLGKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDIN
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1. .5947
SRNMIRTHEWTHHQTKRLKFNILLTTYEILLKDKAFLGGLNWAFIGVDEAHRLKNDDS
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/db_xref="taxon:9606"
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MEDLINE REFERENCE

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FEATURES

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gene CDS

LLYKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREY0

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REFERENCE AUTHORS TITLE

RESULT 11 AF006513

DEFINITION

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Matches

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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                                         Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 101220)
DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                              2: This insert is not the entire sequence of the clone (entire sence is 146.7kb). It is clipped at the overlap with ACO12624. number of bases overlapped is 90404.
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SKGSTSGFINISMELKCCHHCYLIKPDINNEFYNKQEALQHLIRSSCKLILLDKILI
RLERGMRVLIFSQMFVMIDILASLIKYROPEPORLDGSIKGELRKOALDHFNAEGSE
DFCFILSTRAGGLGTMLASADTVVIFDSDMNEDNIDAQARAHFIGOKKOVNIYRLVT
KGSVEEDILERAKKMVLDHLVIQRMDTTGKTVLHTGSAPSSSTFFNKEELSAILKFG
AEELFKBEEGEDOEPOEMDIDEILKRAETHEBUEGFFTVUSDELLSQFKVANTSNMDED
DIELEPENSKKWEELIPEDORRRILEEEEROKELEEIYMLFRHINCAKOISFNGSEGR
RSBRRYGGSDSDSISEGKREKKRAFNTIPERENIGGSDAEIRFIKSYKKFGGFLE
RLDAIARDAELVDKSFTDLERLGELVHNGCIKALKOSSSGTERFGGRLGKVKGPTFRI
SGYQVNAKLVISHEELIFLKGSIFSDEERKOYTIPCHTKAAHFDIDMGKEDDSNLL
IGIYEYGYGSWEMIKNDEDLSLTHKILFDDPDKKPQAKQLGTRADYLIKLSRDLAKK
EALSGAGSSKRRKARAKKNAMKSIKVKEEIKSDSSFLPSKSDEDDDKLSESKSDGR
ERSKKSYSDAPVHTTAGGEPVISESSELDQKTFSGKCKERHRFYKAALFDLDHKERSKSGFREK
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KLYKHAIKKQGESQONSONSNINHPHURNDPUERLKERTWHDDSSDSSSDRHLTO
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YHDHHKDRRQGBSYKKSDSRKFPYSSFSNGKDHRDHDYKODSRDSSVSSDRHLTD
RASSGFRASLOLDSSSLANDSHSDHRSHSDHRLHSDHRSSSEYTHKSSRDYRYHSDWQWDH
RASSGFRASLOLDSSSLANDSHSDHRSHSDHRLHSDHRSSSEYTHKSSRDYRYHSDWQWDH
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/clone="RP11-58M12"
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                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                         AC021449
Homo sap:
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Drive, Walnut Creek, CA
4 (bases 1 to 134365)
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US
   Homo sapiens
Eukaryota; M
                                                             AC021449
AC021449.3 GI:10047806
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DOE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute and
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AC012624.6 GI:14993679
                                               HTG; HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            /clone="CTD-2082I17"
24497 c 25503 g 43951 t
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                         .134365
                                                                                                      143079 bp DNA clone RP11-58M12, WORKING
                                                                                                                                                                                                                                                    100.08;
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100.0%;
                                               HTGS_DRAFT.
                                                                                                                                                                                                                                                                      Score 23; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01) DOE Joint Genome Institute, 2800 Mitchell CA 94598, USA
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Pred. No.
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. 0.021;
                                                                                                                                                                                                                                                                   DB 9; Length 134365; 0.021;
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                                                                                                         DRAFT
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10 unordered
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REFERENCE
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TITLE
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo, sapiens, clone RP11-58M12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 144000: agarose-fp
Insert size: 1442179; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
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Center code: WIBR
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46906 47005: gap of 100 bp
47006 51830: contig of 4825 bp in length
51831 51930: gap of 100 bp
51931 62619: contig of 10689 bp in length
62620 62719: gap of 100 bp
62720 75408: contig of 12689 bp in length
75409 75500: gap of 100 bp
75509 92516: contig of 17008 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40412 40511; gap of 100 bp
40512 43279; contig of 2768 bp in length
43280 43379; gap of 100 bp
43380 46905; contig of 3526 bp in length
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38921 404:
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920: gap of 100 bp
40411: contig of 1491 bp in length
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COMMENT

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JOURNAL
REFERENCE
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TITLE
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AUTHORS
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AC008531
                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
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                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 116192 CAGACCCGTGCAGACTACCTCAT 116214
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 CAGACCCGTGCAGACTACCTCAT 98
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.institute
                                                                    Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:7528342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC008531 145659 bp DNA linear HTG 14-FEB-2001
Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14559)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 15.0%; Score 23; DB 2; Le Similarity 100.0%; Pred. No. 0.021; 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     AC008531.3 GI:12830078
HTG; HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                 2 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                                                            sequencing of Human Chromosome 5
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92617 106409: contig of 13793 bp in length
106401 106509: gap of 100 bp
106510 143079: contig of 36570 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                ed pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector_side:right"
1 26246 c 26678 g 45278 t
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clone_end:T7
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62720. .75408
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51931. .62619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector_side:left"
38921. .40411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"assembly_fragment
clone_end:SP6
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92617. .106409
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47006. .51830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
43380. .46905
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40512. .43279
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/clone_lib="RPCI-11 Human Male BAC"
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/db_xref="taxon:9606"
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    http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 143079;
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Db 46815 CAGACCCGTGCAGACTACCTCAT 46837
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                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                  Query Match
Best Local Similarity
"~+~hes 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                             76 CAGACCCGTGCAGACTACCTCAT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 139128 bases at least 040
Consensus quality: 142556 bases at least 020
Consensus quality: 143744 bases at least 020
Consensus quality: 143744 bases at least 020
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in 020 bases; sum-of-contigs estimation.
*NOTE: This is a 'working draft' sequence. It currently
*consists of 7 contigs daps between the contigs
*are represented as runs of N. The order of the pieces
*is believed to be correct as given, however the sizes
*of the gaps between them are based on estimates that have
*provided by the submittor.

*This sequence will be replaced
*by the finished sequence as soon as it is available and
*the accession number will be preserved.

*56175 56274; gap of unknown length
*100975 113127; contig of 44600 bp in length
*11328 118190; cantig of 44600 bp in length
*11328 118290; gap of unknown length
*11328 118290; gap of unknown length
*118291 119694; contig of 1404 bp in length
*113291 119694; contig of 1404 bp in length
*113298 123397; contig of 3503 bp in length
*113298 123397; contig of 55074 bp in length
*113298 123397; contig of 55074 bp in length
*113291 119694; contig of 1404 bp in length
*113291 119694; contig of 150740 bp in length
*113298 123397; contig of 150740 bp in length
*113298 12397; contig of 2266 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Project Information
Center Project Name: 369535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: CIT-HSPC_480B11
                                                                                                                                                                                                                                                                                                                     42561 a
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                              /clone_lib="CalTech human BAC library C" 26309 c 27580 g 48609 t 600 others
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                   /clone-"CTC-480B11"
                                                                                                         15.0%; Sur
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Qualifiers
                                                                                                                                                         Score 23;
Pred. No.
                                                                                                                           Mismatches
                                                                                                                                                     DB 2; Length 145659; 0.021;
                                                                                                                           0; Indels
                                                                                                                           0; Gaps
                                                                                                                           0;
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Search completed: August 3, 2002, 01:42:44 Job time: 40734 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Exsting first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_032802:*
1: /SIDS1/gcgdata/hc
2: /SIDS1/gcgdata/hc
3: /SIDS1/gcgdata/hc
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67.3
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2: \SIDSI_gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT: *
3: \SIDSI_gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1736436 seqs, 858457221 residues
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153
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                       Length DB
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AAT42751
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Chick CHD-1A gene
Chicken CHD-1A gen
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Chicken CHD-W gene
Great tit CHD-W gene
Mouse CHD-1 gene (
Altered telomere r
Human polypucleoti
Human lung tumour
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ALIGNMENTS

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RESULT
AAT42757
(ISIS-) ISIS INNOVATION LTD
                                                                                                                                    misc_difference 52..81
                                                                                                                                                                   Gallus sp.
                                                                                                                                                                                                                Chick CHD-1A gene fragment.
                                                                                                                                                                                                                                                      AAT42757;
                                                                                                                                                                                                                                                                        AAT42757 standard; DNA; 153 BP.
                         06-JUN-1995;
                                            05-JUN-1996;
                                                                                                                                                                                    CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                             Bird; sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                  12-MAR-1997 (first entry)
                                                                                 WO9639505-A1.
                                                              12-DEC-1996.
                                                                                                                                                                                                                                                                                           _
                         95GB-0011439
                                             96WO-GB01341
                                                                                        /*tag= a
/note= "bases 52-81 are a repeat of bases 22-51
/note= "bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
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RESULT ANTI-2751 ID ATT-2751 ID ATT-2751 ID ATT-2751 ID ATT-275 ID
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avian
birds
Avian chromodomain-helicase-DNA binding genes determine sex in
                                                        WPI; 1997-043127/04.
                                                                                                         Griffiths R,
                                                                                                                                                                                                                06-JUN-1995;
                                                                                                                                                                                                                                                                    05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chicken CHD-1A gene
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                                                                                                                                                             (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex determination; chromodomain-Helicase-DNA binding 1 Avian;
chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                             INNOVATION
                                                                                                         Tiwari B;
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                                                                                                                                                                                                                                                                    96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
228..5390
/*tag= a
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No. 4.6e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 153;
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RESULT
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Best Local
                                                                  WPI; 199
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4160 taaagaccttgcaagaaaggaagcacaaaggcttgctggtgca 4202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4100 caagaaaccccaggcaaagcagctacagacccgtgcagactacctcattaaattactgaa 4159
 Claim
                           Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                   Bird; sex determination; chromodomain-Helicase-DNA binding CHD-lA; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Chick CHD-W gene fragment.
                                                                                                         Griffiths R,
                                                                                                                                                                 06-JUN-1995;
                                                                                                                                                                                            05-JUN-1996;
                                                                                                                                                                                                                       12-DEC-1996
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                                                                                                                                                                                                                                                                                                                                  misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             birds - used for sex determn. and
                                                                                                                                     (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 TAAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGGTGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 CAAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAAATTACTGAA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                  1997-043127/04.
DB; AAW08148.
8; Fig 3; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                        for sex determn.
                                                                                                                                     INNOVATION LTD
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                                                                                                          Tiwari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
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                                                                                                                                                                                                                                                                         "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153
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Pred. No.
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Query Match
Best Local
           Matches 47;
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                                                                                                                                                                                                                                                                                                                                                                                      The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a trade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in Maral 146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT40754-55) genes determine sex in birds and can be used to identify the sex of an embryo, for the characteristic sex of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT42754;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                           Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAAGCACA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 tacctcattaaattactgaataaagaccttgcaagaaaggaagcaca 137
                                                    Local Similarity
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47; Conservative
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-GB01341.
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Pred. No.
                                                                DB 18;
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RESULT

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                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                 AAT42756 standard; DNA; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
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                                                                                                                                                                                                                                                      91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACA 137
                                                                                                                                                                                           91 tacctcattaaattactgaataaagaccttgcaagaaa 128
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                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHD-W; W chromosome; ss
                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                          24.8%; Score 38; DB 18; 100.0%; Pred. No. 3.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                           Length 153;
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AAT42756;

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Best Local S
Matches 25
                                                                                                                                                                                                                                                                                Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1a (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW48146-49. The CHD-IA (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                      Avian
birds
                                                            14-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Griffiths R,
                  ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                      Altered telomere repeat binding factor 1 gene.
                                                                                 AAV59280;
                                                                                                     AAV59280
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHD-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                         74
                                                                                                                                                                              74 TACAGACCCGTGCAGACTACCTCAT 98
                                                                                                                          7
                                                                                                                                                         tacagacccgtgcagactacctcat 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                   chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex determination; chromodomain-Helicase-DNA binding
CHD-W; W chromosome; ss.
                                                                                                                                                                    8; Fig 3; 76pp; English.
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW08146
                                                                                                                                                                                                                                                      153
                                                                                                     standard;
        ageing; ataxia telangeictasia;
                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                      вP;
                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tiwari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                     CDNA;
                                                                                                                                                                                                                                                      Ą
                                                           entry)
                                                                                                                                                                                                            16.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
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                                                                                                                                                                                                           Score ?
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                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                        DB
                                                                                                                                                                                                                                                      0 other;
       Down's syndrome; tumour;
                                                                                                                                                                                                            в 18;
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                                                                                                                                                                                                   0;
                                                                                                                                                                                                                     Length 153;
                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g. for expression of recombinant proteins or where intended for subsequent transpared to the statement of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, heteror-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-1998;
13-FEB-1997;
                                                                  Homo sapiens
                                                                                                                                                                              tissue
                                                                                                                                                                                                               vaccine;
                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI80568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1311 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The altered vertebrate telomere repeat binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW59280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-480769/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplant or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 TACAGACCCGTGCAGACTACCTCAT
                                                                                                                                                                                                                                                                                                                   polynucleotide
                                                                                                                                                                      cytokine; cell proliferation; cell differentiation; gene the; peptide therapy; stem cell growth factor; haematopoiesis; growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIND
                                                                                                                                         system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for testing, eliminating
                                                                                                                                         disorders; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0018628
97US-0800264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            441 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA;
                                                                                                                                                                                                                                                                                                                   SEQ ID NO 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
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Pred. No.
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                                                                                                                                            inflammation; ss
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0.0021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein (A-TRF) has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1311;
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                                                                                                                                                                                                                                                therapy;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 401 BP; 113 A; 87 C; 108 G; 93 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, Liu C, Drmanac RT;
              30-JUN-1999;
15-OCT-1999;
                                                                                                                                                                                       Human; lung cancer; lung tumour; lung tumour protein; gene therapy; lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine; cytostatic; antisense inhibition; ss.
                                                                                                                                                                                                                                                                                                                      AAF68219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 628; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
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                                                             30-JUN-2000; 2000WO-US18061
                                                                                                                           WO200100828-A2.
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                    Human lung tumour protein related nucleotide sequence SEQ ID NO:137.
                                                                                                                                                                                                                                                                                      12-APR-2001
                                                                                                                                                                                                                                                                                                                                                  AAF68219 standard; cDNA; 552 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                304 CAGACAAGAAACCCCAGG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 CAGACAAGAAACCCCCAGG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                    (first entry)
99US-0346492.
99US-0419356.
99US-0466867.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 401; 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAs) that encode them.
CC (I) have cytostatic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAs and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC especially lung cancers. For example, the NAs may be administered to
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC triat affect the activity of the protein by expressing inactive proteins
CC or to supplement the patients own production of (I). Additionally, the
CC NAs may be used to produce the lung-tumour associated protein, according
CC molecules may be administered to down regulate protein expression by
CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as NAA probes in diagnostic
CC assays to detect and quantitate the presence of similar NA sequences in
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC AAP76848 to AAP76878 represent human lung tumour protein related
CC CAAP76848 to AAP76878 represent human lung tumour protein related
CC CAAP76848 to AAP76878 represent human lung tumour protein related
CC CAAP76848 to AAP76878 represent human lung tumour protein related
CC CAAP76848 to AAP76878 represent human lung tumour protein related
CC CAAP76848 to AAP76878 represent human lung tumour protein related
CC CAAP76848 to AAP76878 represent human lung tumour protein related
RESULT 10
AAV49574
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Best Local :
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06-MAR-2000); 2000US-0519642.
22-MAR-2000); 2000US-0533077.
10-APR-2000); 2000US-0546259.
27-APR-2000); 2000US-0560406.
05-JUN-2000); 2000US-0589184.
                                                                              Transmembrane domain; human; nutrition; cytokine; cell proliferation; differentiation; immune system; stimulator; suppressor; regulator; heamatopoiesis; activin; inhibitor; chemotactic; chemotactic; receptor; haemostatic; thrombolytic; ligand; anti-inflammatory; tumour; ds.
                                       Homo sapiens
                                                                                                                                                                                           Human lymphoma cell line U937 clone HP10136 cDNA #1.
                                                                                                                                                                                                                                        21-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                AAV49574 standard; cDNA to mRNA; 1409 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 552 BP; 220 A; 118 C; 69 G; 144 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 193; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lung tumor-associated proteins and the nucleic acids that encode them useful for preventing, diagnosing and treating lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-071488/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           492 attaaattactgaataaa 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 ATTAAATTACTGAATAAA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WW,
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bangur CS, L
W, Mannion J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 22; Length 552; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Key

Location/Qualifiers

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Best Local
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       Wang
                                                                           06-MAY-1999
                                                                                                                             diagnosis; ss
                                                                                                                                    autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein having transmembrane research and nutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                        (UYSH-) UNIV SHANGHAI SECOND MEDICAL
                                         29-OCT-1997;
                                                          29-OCT-1997;
                                                                                           W09921988-A1
                                                                                                           Homo sapiens
                                                                                                                                             Human; vesicle trafficking
                                                                                                                                                              Human CBFBBA01
                                                                                                                                                                              16-JUL-1999
                                                                                                                                                                                               AAX56240;
                                                                                                                                                                                                                                                                                                                                    Sequence 1409 BP;
                                                                                                                                                                                                                                                                                                                                                           haematopolesis regulating, tissue growth, activin/inhibin, chemotactic/chemokinetic, haemostatic and thrombolytic, re
                                                                                                                                                                                                                                                                                                                                                                          AAV49550-V49599 are cDNA sequences which encode human proteins containing a transmembrane domain. These proteins can be used for, e.g. research and nutrition, and may have cytokine and cell proliferation/differentiation, immune stimulating/suppressing,
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-1998
                                                                                                                                                                                                                AAX56240 standard;
                                                                                                                                                                                                                                                                                                                                                    anti-inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9821328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SAGA
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SAGAMI CHEM RI
                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                       Page 153-155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kobayashi M,
                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                              (first entry)
                                                                                                                                                             vesicle trafficking protein SEC22b gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHEM RES CENTRE
                                         97WO-CN00115
                                                          97WO-CN00115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96JP-0301429
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/*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                    377 A;
                                                                                                                                                                                                                                                                                                                                                    or tumour inhibition activity.
                                                                                                                                                                                                                cDNA;
                                                                                                                                                                                                                                                                                       11.8%; 5c.
100.0%; Pr
                                                                                                                                     diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                     205pp;
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                                                                                                                                                                                                                                                                                                                                   278 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "transmembrane
                                                                                                                                    protein; SEC22b;
es mellitus; mult:
                                                                                                                                                                                                                                                                                                  Score
Pred.
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                                                                                                                                                                                                                                                                                                                                    325
                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamaguchi T;
                                                                                                                                                                                                                                                                                                   . 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                    G;
                                                                                                                                   multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                    429
                                                                                                                                                                                                                                                                                                  9. DB
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                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                              CBFBBA01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
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                                                                                                                                                                                                                                                                                                                                    other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       containing
                                                                                                                                                                                                                                                                                                          Length 1409;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               for,
                                                                                                                                             cancer;
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RESULT 1
AAV20467/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                         The present sequence represents an oncogene from the present invention. The present invention describes a composition which comprises two antisense oligonucleotides. The first oligonucleotide is specific for cytoplasmic oncogene or proto-oncogene selected from ras, raf, EGF-1, c-fms, C-ros, C-kit, c-met, C-trk, c-src, C-bbl, bor-abl, c-fgr and c-fms, C-ros, C-kit, c-met, C-trk, c-src, C-bbl, bor-abl, c-fgr and c-fms, C-ros, C-kit, c-met, C-trk, c-src, C-bbl, bor-abl, C-fgr and c-fms, C-ros, C-kit, c-met, C-trk, c-src, C-bbl, bor-abl, C-fgr and c-fms, C-ros, C-kit, c-met, C-trk, c-src, C-bbl, bor-abl, C-fgr and c-fms, C-ros, C-kit, c-met, C-trk, c-src, C-bbl, bor-abl, C-fgr and c-fms, C-ros, C-kit, c-met, C-trk, c-src, C-bbl, bor-abl, C-fgr and C-fms, C-ros, C-kit, C-met, C-trk, c-src, C-bbl, bor-abl, C-fgr and C-fms, C-ros, C-kit, C-met, C-trk, C-src, C-bbl, bor-abl, C-fgr and C-fms, C-ros, C-kit, C-met, C-trk, C-src, C-bbl, bor-abl, C-fgr and C-fms, C-ros, C-kit, C-met, C-trk, C-src, C-bbl, bor-abl, C-fgr and C-fms, C-ros, C-kit, C-met, C-trk, C-src, C-bbl, bor-abl, C-fgr and C-fms, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes CBFBBA01, which is a protein homologous to murine vesicle trafficking protein sec22b. CBFBBA01 is a cytoplasmically orientated integral membrane protein, located in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-312961/26.
P-PSDB; AAY09512.
                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                    Anticancer
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-229882/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human c-myb oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               826
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                                                                                                                                                                                                                                                                                                                   targetting
c-ros, c-kit, c-met, c-trk,
The second oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page
                                                                                                                                                                                                                                                 Column
                                                                                                                                                                                                                                                                                                               composition comprising two anti-sense oligo:nucleotide(s)
ing cytoplasmic and nuclear oncogene(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JEFFERSON THOMAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0306691
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                                                                                                                                                                                                                                                 131-134;
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proto-oncogene; n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.8%;
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                                                                                                                                                                                                                                              92pp;
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                                                                                                                                                                                                                                              English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neoplastic disease; anticancer;
e; c-myb; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 18;
c-src, c-abl, l
is specific for
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   oncogene
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RESULT 13
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proto-oncogene selected from myc, jun, c-ets, c-fos, c-myb, B-myb, c-rel, c-vav, c-ski, c-spi, cyclin Dl, PML/RAR alpha, AML1/MYG8, E2A/prl and ALL-1/AF-4. The composition is used for treating cance: The combination of antisense oligonucleotides has synergistically enhanced ability to inhibit growth of cancer cells.
                                                                                                                                                       capable of detecting 1000 or more genes from Drosophila. The inventuaseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher entaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABD16176-ABL30511), expressed DNA sequences (ABD16176-ABL30511), expressed DNA sequences (ABD16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2662 ATTAAATTACTGAATAAA 2645
                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/jpublished_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 40958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL15492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL15492 standard; cDNA; 59967 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3225 BP; 975 A; 687 C; 698 G; 865 T; 0 other;
                                                                                Sequence 59967 BP; 17305 A; 12463 C; 12291 G; 17908 T; 0 other;
                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent and or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 40958; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                  interactions
                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY.
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                    Local
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)B; ABB71389.
                                                                                                                                                                                                                                                                                                                                               solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signalling and cell-cell
                    Similarity
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                    100.0%;
                  11.8%; Score 18; 100.0%; Pred. No.
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Pred. No.
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                  9.7;
                               DB 23; Length 59967;
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                                                                                                                                                                                                                                        The invention relates to a mammalian PG1 gene and protein, and a set of PG1 biallelic markers. The PG1 polynucleoride and biallelic markers are used in a hybridisation assay, a sequencing assay, or in an allele-specific amplification assay for determining the identity of a nucleotide at a PG1-related biallelic marker. The methods can be used to detect and to assess the risk of developing cancer or prostate cancer. Barly-stage diagnosis of prostate cancer relies on prostate specific antigen (PSA) dosage. However, the effectiveness of this is limited due to its inability to discriminate between malignant and non-malignant affections of the organ. A need exists for both a reliable diagnostic procedure which would enable early-stage diagnosis, and for preventative and curative treatments of the disease. The PG1 gene can be used for detection of prostate cancer, and the risk of developing it in the future, and can also be used to determine therapies for the disease.
                                                                                                                                                                                                                 Sequence 19 BP; 9 A; 6 C; 3 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 368; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of a prostate cancer associated gene and biallelic markers derived from it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blumenfeld M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-1998;
22-DEC-1997;
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                                                                            3 aaagcagctacagacca 19
                                                                                                                                                      ocal
                                                                                                                                                      Similarity
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                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0099658
97US-0996306
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                                                                                                                                                    Score 17;
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                                                                                                                                       Mismatches
                                                                                                                                                    DB 20;
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                                                                                                                                       0,
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AAZ01079 standard; DNA; 47 BP

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Search completed: August
Job time: 32192 sec
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                                                                                                                           Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 313; 385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a prostate cancer associated gene derived from it
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22-DEC-1997;
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                                                                                                                                                                                                   Sequence 47 BP; 17 A; 10 C; 10 G; 10 T; 0 other;
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe for human PG1
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                                                                    AAAGCAGCTACAGACCA 52
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100.0%; Pr
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             2002, 01:50:07
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29;
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
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Match Length DB
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294.307 Million cell updates/sec
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Gapop 60.0 , Gapext 60.0
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153
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Copyright (c) 1993 - 2000 Compugen Ltd.
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ALIGNMENTS

		TITLE JOURNAL COMMENT	AUTHORS	SOURCE ORGANISM REFERENCE	ACCESSION VERSION KEYWORDS	RESULT I BB155356 LOCUS DEFINITION
Fax: 81-45-503-9216 Email: genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh. M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cloNas to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura	COntact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922	ragamity. Ragawa,A., Takanashi,F., Takeda,F., Tahaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001) On Jun 29, 2000 this sequence version replaced gi:8811286.	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,	house mouse. Mus musculus Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 619)	musculus cDNA clone A130024L16 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence. BB155356 BB155356.2 GI:16268254 EST:	BB155356 619 bp mRNA linear EST 18-OCT-2001 BB155356 RIKEN full-length enriched, 16 days neonate thymus Mus

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RESULT
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Division of Experimental Animal Research in Riken contributed to
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Normalization and subtraction of cap trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
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1 (bases 1 to 660)
Arakawa, T., Carninci, P., Fukuda, S., Furuno,
Hiramoto, K., Hori, F., Ishii, Y., Ito, M.,
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Konno,H., Fukunishly, Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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On Jul 21, 2000 this sequence version replaced gi:9356558
Contact: Yoshihide Hayashizaki
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Please visit our web site (http://genome.gsc.riken.go.jp/)
further details.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                               transcriptase and subsequently enriched for full-length by
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/lab_host="DH10B"
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                                                                                       263 CAGACCCGTGCAGACTACCTCAT 285
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25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Am Klopferspitz 18a D-82152 Martinsried, Germany
This 1s the 5 sequence of the Cone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by GBF (Mational Research Centre for Biotechnology Ltd.
Braunschweig/Germany) within the cDNA sequencing consortium of th
                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone (DKFZp313J1040) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wiemann,S.)
Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
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DREZED313J1040_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DKFZp313J1040 5′, mRNA sequence.
    вв830730
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                                                                                                                                                                                                                                                                /lab_host="DH10B"
/note="Vector: priplEx2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
a 81 c 86 g 100 t
                                                                                                                                                                                                                                                                                                                              /clone="DKFZp3131040"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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343 TACAGACCCGTGCAGACTACCTC 365
                                                             74 TACAGACCCGTGCAGACTACCTC 96
                                                                                                                                                                    Local
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y. Hayatsu,N. Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayyshizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNNs to
prepare full length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S. Inoue,K. Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y., da Companya, Matsuura
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Jyg-MC(B) cDNA Mus musculus cDNA clone G930013K04 3', mRNA
sequence.
BB830730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno-H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 further details
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                           15.0%; Score 23; DB 9; Length 438; llarity 100.0%; Pred. No. 0.071; Conservative 0; Mismatches 0; Indels
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RCB-0527 Jyg-MC(B) CDNA"
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/cell_line="RCB-0527 Jyg-MC(B)"
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74 TACAGACCCGTGCAGACTACCTC 96
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa
, A., Takahashi, T., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
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RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
wayashirayi v
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"
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1 99 c 108 g 100 t
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                                               15.0%; Scc
100.0%; Pr
                                                                                Score 23;
; Pred. No.
                                                           Mismatches
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                                                                                   0.072;
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Insert Length: 1924 Std Error: 0.00
                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_lib="NCI_CGAP_Uft2"
/clone_lib="NCI_CGAP_Uft2"
/tissue_type="moderately-differentiated endometrial
adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 821)
NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 678.
Location/Qualifiers
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.lludwig.org.br/scripts/gethtml2.pl?tl=&t2=Qv3-BN0047-150
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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CDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 CAGACCCGTGCAGACTACCTCAT 55
                                                                                                                                            Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                  1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                                                                                     Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 866)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
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o,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
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/clone=lib="NMGE:4133129"
/clone=lib="NMGE:4133129"
/clone=lib="NMGE:4133129"
/clone=lib="NMGE:4133129"
/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
/note="Organ: bone marrow; Vector: pDNR-LIB (Clonted);
/note="Organ: bf11 clonting as follows: 5"
/note="Organ: bf11 clonting as follows: 5"
/note="Organ: bf11 clonting as follows: 5"
/note="Organ: bf11 clontech by CR. This library was enriched for full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."
                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                     Location/Qualifiers
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/db_xref="taxon:9606"
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/clone_lib="NT2RM4"
                         /clone="NT2RM4002061"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai, T.)
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RESULT 1
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                                                                                                        176 CAGACCCGTGCAGACTACCTCAT 198
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                                                                                                                                      76 CAGACCCGTGCAGACTACCTCAT 98
                                                          11
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         AZ570983
281PvC04
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Plate: LLAM9753 row: h column: 16
High quality sequence stop: 488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1028)
NIH-MCC http://mcc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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601436060F1 NIH_MGC_72
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23; Conservative
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                     387
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                                                                                                                                                                                                                                                                     b
                                                                                                                                                                                                                                                                /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."

1 205 c 238 g 198 t
           Pv MBN #30 Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pME18SFL3; mRNA from uninduced
precursor cells"
149 c 196 g 207 t 2 others
                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:3921087"
/clone_lib="NIH_MGC_72"
                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                   125 GAAAGGAAGCACAAAGGCTTG
                                                                                                                                                                         BH351821

CH230-160016.TV CHORI-230 Segment

CH230-160016, DNA sequence.
              Norway rat.
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                BH351821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 664)
Carlton,J.M.-R. and Dame,J.B.
The Plasmodium vivax and P. berghei gene sequence tag projects
Parasitol. Today 16 (10), 409 (2000)
Rattus
                                                                                                                    SSD
                                                                                                                                       вн351821.1
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Dept. of Pathobiology, College of Veterinary Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malaria parasite P. vivax. Plasmodium vivax
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2015 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA
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352 392 9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xfel="Laxon:9030"
/clone_lib="pv MBN #30"
/clone_lib="pv MBN #30"
/dev_stage="asexual blood forms"
/lab_host="Saimiri boliviensis"
/lab_host="Saimiri boliviensis"
/note="vector: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP; Site_1: EcoR V; Site_2: EcoR V;
Host leukocytes were extracted from P. vivax infected blood using the following methods: first, infected blood was activated by the addition of 0.5 ml of ADP (40mg/ml) per 10 ml blood. Then blood was passed over a column of acid washed 0.1 mm glass beads, then through a Plasmodipur filter, followed by passage through a column of pre-wet Whatman CF11 powder (1:2 ratio volume of blood to CF11), and finally centrifuged through a 50% percoll density cushion. Purified DNA was digested with mung bean nuclease in the presence of 44% formamide at 50cC as described (Vernick, K.D., Imberski, R.B., and McCutchan, T.F. 1988. Nucleic Acids Research 16:6883-6896). Digested DNA was blunt-ended using T4 DNA Polymerase and size fractionated over a Sepharose CL-2B column. Fractions in the size range 500bp-4kb were ligated into the Eco RV site of pBluescript SK(+), and E. coli XL-10 Gold transformed with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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1 Rattus
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COMMENT

TITLE

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REFERENCE
AUTHORS
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ACCESSION
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JOURNAL
                                                                                                                       TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                       AUTHORS
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Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de Jong, P. and Fraser, C.M.

Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)

Other_GSSs: CH230-160016.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conservative
Direct Submission
Submitted (02-ANG-2001) Asao Fujiyama, The Institute of Physical
Submitted (Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-Chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG128961
AG128961.1 GI:16658126
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG128961 838 bp DNA linear GSS 04-NOV-200 Pan troglodytes DNA, clone: PTB-140E13.F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 160 row: O column: 16
                                                                                                                                                                                   2 (bases 1 to 838)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                         Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Matanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes
Eukaryota; Meta:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library clone:PTB-140E13.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .a; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong"
a 147 c 158 g 103 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .693
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/clone="CH230-160016"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Female
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%; score 20; DB 12; Length 693; 100.0%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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AUTHORS
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AQ453778
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Best Local :
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                                                                                                                                                                                                                 High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: Jwallacedu washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleteredejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
plate: 746 row: G column: 3
Seg primer: T7
Class: BAC ends
                                                                                                                                                 High quality sequence stop: 505
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
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Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
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Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
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Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9110, Fax:81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 505)
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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/clone_lib="PTB Chimpanzee Male BAC Library"
1 276 c 177 g 44 t 55 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="PTB-140E13.F"
/sex="male"
                                          /organism="Homo sapiens" (
/db_xref="taxon:9606"
            /clone="Plate=746 Col=3 Row=G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pan troglodytes"
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ORIGIN

FEATURES

Length 838;

0, Gaps

0,

GSS 21-APR-1999

RESULT 1 AG128961

SOURCE VERSION POCOR. ₽

/clone_lib="RPCI-11 Human Male BAC Library" /sex="male"

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RESULT 15
AZ486207/c
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KEYWORDS
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ORGANISM
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0314 row: M column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 527)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ486207 527 bp DNA linear GSS 05-OCT-200100314M02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0314M02 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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a 77 c 107 g 119 t 5 others
                   (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="TUGCIM0314M02"
                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                       /sex="Male"
                                                                                                                                                                                                                                                                                                             /clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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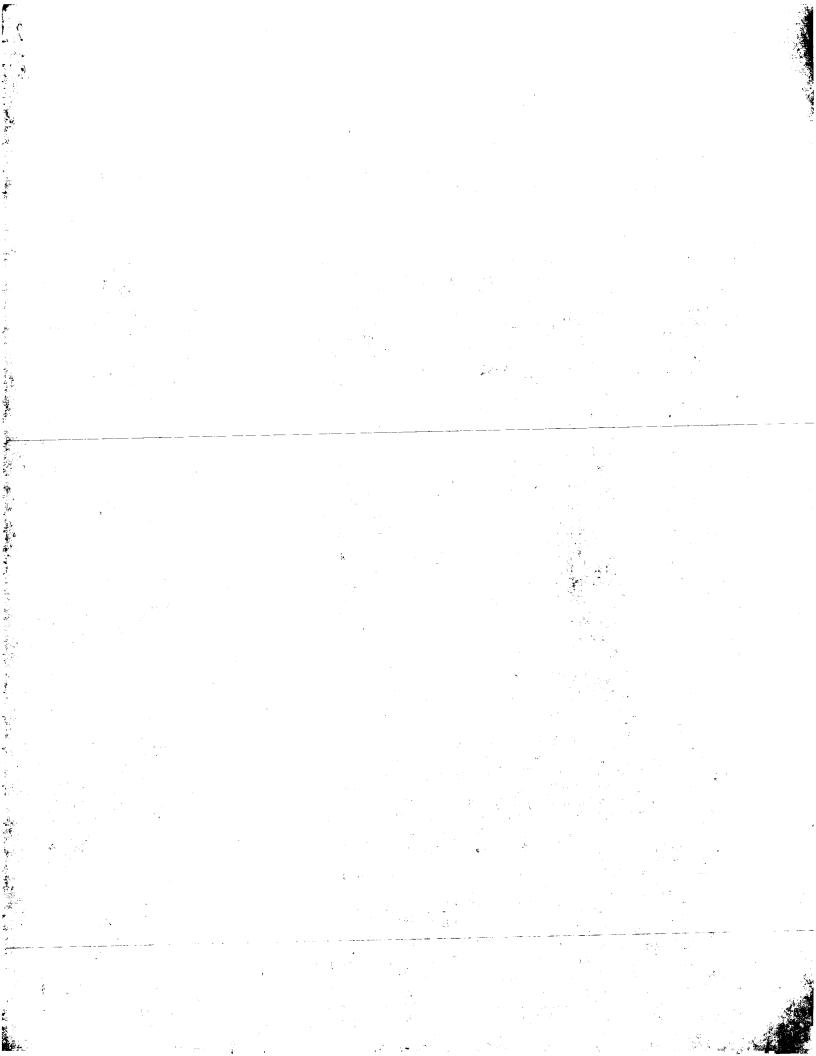
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BASE COUNT
ORIGIN
                       Query Match
Best Local
                                                                                                                                              174 a
                                                                                                                                      electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114/gb)AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLJO-Gold (Stratagene) cells and selected for ampicillin resistance."
                       100.0%;
                                                 12.4%;
                       Score 19;
Pred. No.
                       DB 12; Length 527; 11;
0;
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밁 QΥ Matches 404 GAAGCACAAAGGCTTGCTG 386 130 GAAGCACAAAGGCTTGCTG 148 Local Similarity nes 19; Conserv Conservative 0; Mismatches Indels 0; Gaps

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COCUS

Search completed: August Job time: 30152 sec 2 2002, 22:41:37



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em_ba:*
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Sequence 5 from Patent W09639505.
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                                                                                                                                                                                                                                                                                                            1 (bases 1 to 153)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unidentified.
                                                                                                                                                                                                                                             Patent: WO 9639505-A 5 12-DEC-1996;
                                                                                                                                                                                                                                                                                          BIRDS
                                                                                                                                                                                                                                                                                                                                                                                                             unclassified.
                                                                                                                                                                                  Other publication AU 5906996 961224
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/db_xref="taxon:32644"
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A58685 Sequence 4
A58686 Sequence 3
A58681 Sequence 10
AF004397 Gallus 9a
U91538 Mus musculu
BC001364 Homo sapi
AC016280 Homo sapi
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AC016281 Homo sapi
AC01672 Homo sapi
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AC016372 Homo sapi
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AC025131 Homo sapi
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Y98276 A. thaliana
U69138 Arabidopsis
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Result No.

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Sequence 15 from Patent
A58696
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                      Patent: WO 9639505-A 15 12-DEC-1996; ISIS INNOVATION (GB) Other publication AU 5906996 961224.
                                                                                                                             unidentified
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224
Location/Qualifiers
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                                                                                                                           Archosauria; Aves; Neognathae; Craniata; Vertebrata; Eute
Phasianinae; Gallus.
1 (bases 1 to 2292)
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Gallus gallus
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Sequence 3 from Patent W09639505
A58684
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47; Conservative
                     Funahashi, J., Sekido, R., Murai, K., Kamachi, Y. and Kondoh, H. Delta-crystallin enhancer binding protein delta EF1 is a zinc finger-homeodomain protein implicated in postgastrulation
                                                                        Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Cancer, Tohoku Univ.; 4-1 Seiryo-machi, Aoba-ku, Sapan (Tel:022-272-9499, Fax:022-272-3982)
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ORF2.
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Other publication AU 5906996
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
              embryogenesis
                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other publication AU 5906996 961224.
Location/Qualifiers
1. .6608
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Griffiths, R. and Tiwa
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Sequence 10 from Patent WO9639505.
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3 (bases 1 to 2292)
Funahashi, J.
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AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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/Product="ORE2"
/Product="ORE2
                                                                                                                                                                                                                                                                                                                                       /organism="unidentified"
/db_xref="taxon:32644"
1207 c 1459 g 165:
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LLVGITEYAYGSWQCKVNGSRSQLNTEILPDDPDRTPRQNSYRPVQTTSLNY"
1385 c 546 g 534 t
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HN fragment of delta-crystallin enhancer."
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/tissue_type="lens"
/clone_lib="lambda gtl1"
/dev_stage="13 day embryo"
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                                                                                                                                                                                                           Length 6608;
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AF004397
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TITLE
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A CHD1 gene is Z chromosome linked in the chicken Gallus domesticuene 197 (1-2), 225-229 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF004397 6872 bp mRNA linear VRT 08-OCT-19 Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-Z) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 6872)
Griffiths, R. and Kor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus
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                                                              CKVLKQ.RETEVALK.KQ.SY.TG.HESLELED.YOL.MG.LIM.KAK.QXALDE.F.SKNQ.SK.11.F.K.

KTI.QTI.STLNYL.FHEHQLY.QF.F.LLRV.PL.STLT.SWQ.REI.QTWA.PQNNAVVYLGDITS.RN

KT.RT.BWHHPOYR.K.E.K.F.NILLTY.YEILLK.DS.F.GGLMAR.PT.GVDEAHREK.NDD.SLL.V

RTIL.IDTK.SN.H.R.L.IT.GT.PL.QNS.L.K.F.LAGS.L.H.F.T.MPEK.F.SSR.DEDEEEHGK.GREY.GY.A.S

LIKELEPPLL.RRV.C.C.N.CY.L.I.K.P.DD.NB.F.Y.NK.QEAL.QH.L.R.S.GS.C.L.I.L.D.KLL.I.R.T.

ERGARV.L.I.F.SQWVR.M.D.I.A.EY.L.K.Y.G.F.F.F.Q.R.D.GS.T.K.GEL.K.R.AL.D.K.L.S.K.G.S.K.G.

ERGARV.L.I.F.SQWVR.M.D.I.A.EY.L.K.Y.G.F.F.F.Q.R.D.GS.T.K.GEL.K.R.AL.D.H.F.NA.EG.S.E.D.F.C

FLL.ST.R.G.G.L.G.I.M.A.S.D.TYV.I.F.D.SDMWRP.OND.D.AQ.A.R.H.R.I.G.OK.O.V.NI.Y.R.L.Y.K.G.

VEEDI.L.EBAK.K.M.V.L.D.H.D.Y.Q.R.D.T.G.K.F.V.L.H.G.S.F.P.S.S.T.F.R.NA.EEL.S.A.I.K.F.G.A.E.

LEPERN.SKWWEEL I.F.SQ.R.RRI EEEEER.Q.K.L.EE.I.Y.M...P.R.NINCEAL.S.A.I.K.F.G.A.E.

LEPERN.SKWWEEL I.F.SQ.R.RRI EEEEER.Q.K.L.EE.I.Y.M...P.R.NINCEAL.S.A.I.K.F.G.A.E.

SRXYSGS.DS.D.S.T.T.E.K.R.F.K.R.G.R.F.T.I.F.R.E.N.I.K.G.S.S.D.A.F.I.K.F.I.S.Y.K.F.G.G.F.E.R.D.

SRXYSGS.DS.S.T.T.E.K.R.F.K.R.G.F.F.F.T.I.F.R.F.N.L.F.R.S.F.K.F.G.F.R.F.S.Y.K.F.G.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.F.R.G.
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1. .6872
KEYTNPEQIKQWRKNLWIFYSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
THVIRNPDVERLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERII
AHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALIAKKFQARIDEYFSRNQSKTTPFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDDEDYDKRGSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTEEDEFETIEKFMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
/codon_start=1
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/db_xref="taxon:9031"
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RESULT
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Matches 38
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                                                                                                                                                                            Local Similarity
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BC009024 1339 bp mRNA linear ROD 12-JUL-20 Mus musculus; SEC22, vesicle trafficking protein (S. cerevisiae)-like 1, clone MGC:5885 IMAGE:3481731, mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 959)
Hay,J.C., Chao,D.S., Kuo,C.S. and
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
U91538
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                                                                                                                                                                                                                                                /translation="MYLLTMIARVADGLPLAASMQEDEQSGRDLQQYQSQAKQLFRKL
NEQSPFRCTLEAGAMTEHYI ERGVCYLVLCEAAFPKKLAFAYLEDLHSEEDEGHGKK
VPTVSRPYSFIEFDTETQKTKKLYLDSRARRNLGSINTELQDVQRIMVANIEEVLQRG
EALSALDSKANNLSSLSKKYRQDAKYLMNRSTYAKLAAVAVFFIMLIVYVRFMML"
219 c 261 g 238 t
                                                                                                                                                                                                                                                                                                                     /product="vesicle trafficking protein sec22b"
/protein_id="AAC53130.1"
/db_xref="GI:1907386"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
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1223 c 1520 g
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/gene="CHD-Z"
                                                                                                                                                                                                                                                                                                                                                                              note="similar to Sec22"
                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       959 bp mRNA linear RO vesicle trafficking protein sec22b mRNA,
                                                                                                                                                                           13.7%;
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                                                                                                                                                             0;
                                                                                                                                                                            Score 21;
; Pred. No.
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Pred. No.
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1683
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7.7e-09;
                                                                                                                                                                           4.1;
                                                                                                                                                                                          DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scheller, R.H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Cellular Physiology,
Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ťä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      longer variant mRNA of CHD-2"
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                                                                                                                                                            0;
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                                                                                                                                                                                       Length 959;
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NA, complete cds.
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                              ROD 12-JUL-2001
                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
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AUTHORS
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SOURCE
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Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNI at: http://image.lln1.gov Series: IRAK Plate: 6 Row: k Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 1907385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk
A.M., Holloway, M., Telford, B, Hodgson, A.,
Muzny,D.M., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hump
cDNA Library Preparation: Life Technologles, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-MAY-2001) National Institutes of Hea
Gene Collection (MGC), Cancer Genomics Office, Nat
Institute, 31 Center Drive, Room 11A03, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC009024
BC009024.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                              347
                                                                                         Conservative
                                                                                                                                                                                                                 /protein_id="AAH99024.1"
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/db_xref="GI:14290512"
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/translation="MVLITMIARVADGLPLAASMQEDEQSGRDLQQYQSQAKQLFRKL
NEQSPTRCTLEAGAMTFHYIIEQGVCYLVLCEAAFPKKLAFAYLEDLHSEFDEQHGKK
VPTVSRPYSFIEFDTFFJQXTKKLJUSSRARRNLGSINTELQDVQRIMVANIEEVLQRK
VPTVSRPYSFIEFDTFJQXTKKLJUSSRARRNLGSINTELQDVQRIMVANIEEVLQRK
EALSALDSKANNLSSLSKKYRQDAKYLNIRSTYAKLAAVAVFFIMLIVYVRFWWL"
3 291 c 344 g 357 t
                                                                                                                                                                                                                                                                                                                                                                               /product="SEC22, vesicle trafficking protein
cerevisiae)-like 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: 82. .729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Mammary tumor.
old, gross tissue."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="MGC:5885 IMAGE:3481731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="LocusID:9554"
                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
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                                                                                                              13.7%;
100.0%;
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Pred. No.
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3.9
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hodason, A., Bouck,
                                                                                                                                  10;
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ı, W.,
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Homo sapiens, SEC cerevisiae)-like

1491 bp mRNA linear PRI SEC22, vesicle trafficking protein (S. ike 1, clone MGC:1960 IMAGE:3051087, mRNA,

PRI 12-JUL-2001

BC001364

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ACCESSION
VERSION
RESULT 11
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                                                                                                                      111 TAAAGACCTTGCAAGAAAAGA 131
                                                                        889 TAAAGACCTTGCAAGAAAAGA 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Gaithersburg, Maryland:
Gaithersburg, Maryland:
Gaithersburg, Maryland:
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Legaspi,R.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.B., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Submitted (I2-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov Series: IRAL Plate: 4 Row: c Collumn: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 3335139.
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                                                                                                                                                                                                     Similarity
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1491)
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                                                                                                                                                                                                                                                                                                                              428
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                     /Product="SEC22, vesicle trafficking protein (S. cerevisiae)-like 1"
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NFTVSRFYSFIEEDTFIQKTKKLYIDSRARRNLGS:NTELQDVGRINVANIEEVLQRG
EALSALDSKANNLSSLSKKYRODAKYLMMRSTYAKLAAVAVFFIMLIVYVRFWML"
a 289 c 342 g 432 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="MGC:1960 IMAGE:3051087"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B_R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="LocusID:9554"
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                                                                                                                                                                                                  13.7%;
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nisc_mgc@nhgri.nih.gov
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                                                                                                                                                                0;
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Pred. No.
                                                                                                                                                                          Mismatches
                                                                                                                                                                                                  3.8;
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25083 TAAAGACCTTGCAAGAAAAGA 25103
                                        111 TAAAGACCTTGCAAGAAAAGA 131
                                                                                                                                                                                 Local Similarity
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On Sep 14, 2001 this sequence version replaced gi:13897376.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >-
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one Mi3 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl RP11-944024 is from the library RPGI-11.2 constructed by the group of Pleter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RP11-544024 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP11-544024 is at 1 in this sequence. The true left end of clone RP4-646P11 is at 85737 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL359758 85836 bp DNA linear PRI 13-SEP-2001 Human DNA sequence from clone RP11-544024 on chromosome 1, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. B-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 85836)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                           /note="Single clone region. Assembly confirmed by restriction digest data." 25942 a 1696 c 16876 g 26032 t
                                                                                                                                                 13.7%; Solitarity 100.0%; For Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-544024"
/clone_lib="RPCI-11.2"
30369...30381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                          Score 21; DB 9; 
; Pred. No. 1.9;
                                                                                                                                                      Mismatches
                                                                                                                                                                                                                     Length 85836;
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COMMENT

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 56% of reads
Chemistry: Dye-terminator ET-amersham; 43% of reads
Chemistry: Bose at least Q40
Consensus quality: 86114 bases at least Q40
Consensus quality: 91633 bases at least Q20
Consensus quality: 91633 bases at least Q20
Insert size: 9378; sum-of-contigs
Insert size: 125478; 4.5% error; agarose-fp
Quality coverage: 3.24x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Sanger Centre
Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence so soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Oct 7, 2000 this sequence version replaced gi:10040155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 95178)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL391556

95178 bp DNA linear HTG 10-JUL-2001
Homo sapiens chromosome 1 clone RP4-630J2 map q21.1-21.3, ***
SEQUENCING IN PROGRESS ***, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coverage: 2.64x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: dJ630J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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be preserved.
                                50595 50594: gap of 100 bp 50695 53352: contig of 2658 bp in le 53353 53452: gap of 100 bp 53453 61187: contig of 7735 bp in le 61188 61287: gap of 100 bp 61288 65069: contig of 3782 bp in le 65170 65169: gap of 100 bp 65170 69334: contig of 4165 bp in le 69335 69434: ran of
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3064 3163: gap of 100 bp
3164 6176: contig of 3013 bp in length
6177 6276: gap of 100 bp
6277 933: contig of 3057 bp in length
9334 9433: gap of 100 bp
18624: contig of 9191 bp in length
18625 18724: gap of 100 bp
18725 18724: gap of 100 bp
27068: gap of 100 bp
37152: contig of 10084 bp in length
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37253 443
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  69434: gap of
77503: con
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44300: contig of 7048 bp in
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79965 84018: contig of 4054 bp
84019 84118: gap of 100 bp
84119 86596: contig of 2478 bp
86597 86696: gap of 100 bp
86697 92135: contig of 5439 bp
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86697. 92135
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                                                                                                                        note="assembly_fragment:00514'
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13.7%; 100.0%;

Score 21; Pred. No.

DB 2; 1.9;

Length 95178;

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REFERENCE
AUTHORS
TITLE
JOURNAL
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E 2 (Dases 1 to 144979)

E 3 (Dases 1 to 144979)

E 3 (Dases 1 to 144979)

E 4 (Dases 1 to 144979)

E 5 (Dases 1 to 144979)

E 6 (Dases 1 to 144979)

E 7 (Dases 1 to 144979)

E 8 (Dayley R., Boguslavkiy L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy L., Boukhgalter, B., Gooke, P., Dewar, K., Domaino, M., Donelan, L., Doyle, M., Collins, S., Granto, M., Donelan, L., Doyle, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Hebwald, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., Magurk, A., McKernan, K., McLaughlin, J., Marquis, N., McEwan, F., Maylor, J., Roy, A., Santos, R., Severy, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Peterson, K., Subrananian, A., Talamas, J., Stange-Thomann, N., Stojanovic, N., Subrananian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Namer, S., Severy, P., Stange-Thomann, N., Stojanovic, N., Subrananian, A., Talamas, J., Talamas, J., Talamas, J., Talamas, J., Talamas, J., Zimmer, A., and Zody, M., Wheeler, J., Wu, X., Namer, S., Shange-Tshminston
                                                                                                                                                                                                                                                    * NOTE: This record contains 138 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
871. Continued to the property of the preserved.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens; Clone Rpl1-20N19
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144979 bp DNA linear HTG 13-JUL-2000
HOMO sapiens clone RP11-20N19, LOW-PASS SEQUENCE SAMPLING.
ACO16280
ACO16280.3 GI:9123976
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17928 contig of 902 bp in length

17928 contig of 912 bp in length

18810 1890; gap of

18810 1890; gap of

1988 contig of 882 bp in length

1988 1980 contig of 882 bp in length

1988 1980 contig of 879 bp in length

1988 2079; contig of 910 bp

1988 contig of 910 bp

1988 contig of 910 bp

1988 2079; contig of 910 bp

21829; contig of 930 bp;

22837 contig of 900 bp;

133 23912; gap of

133 23912; gap of

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24897; cr
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1776: gap of 903 b
39679: contig of 903 b
9779: gap of 100 br
40654: contig of 875
40754: gap of 100 b
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63476: contig of 843 bp i
3576: gap of 100 bp
64458: contig of 882 bp ii
1558: gap of 100 bp
165442: contig of 884 bp in
542: gap of 100 bp
6645: contig of 894 bp in
542: gap of 100 bp
6645: contig of 913 bp in
5746: gap of 100 bp
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43575: contig of 916 bp
3675: gap of 100 bp
44570: contig of 895 bp
4670: gap of 100 bp
45577: contig of 907 bp
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54528: contig (
1628: gap of
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50511: contig of 0
10611: gap of 10
51543: contig of 0
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HTG.
                                                                                         Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6 On Jan 9, 2002 this sequence version replaced gi:14165368
                                                                                                                                                    4 (bases 1 to 14 Waterston, R. Direct Submission
                                                                                                                                                                                                           Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                      Genome Res. 8 (11),
99063792
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Sulston, J.E. and Waterston, R.
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               Contact: sapiens@watson.wustl.edu
Center project name: H_NH0470J24
                                                              Center: Washington
Center code: WUGSC
                                              Web site: http://genome.wustl.edu/gsc
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sapiens BAC clone RP11-470J24
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Eutheria; Primates;
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(1998)
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from 2,
                                                                                                                         St. Louis, Missouri 63108,
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                                                                                                                                                                                                                    Louis,
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. NOTICE:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Mo. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc ו D. et. Louis

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) SOURCE INFORMATION: The RPCI-11 human B NEIGHBORING SEQUENCE INFORMATION: pBACe3.6

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clone sequenced
clone sequenced to the left is RP11-310K15, to the right is RP11-156A1, 2000 2000 g b overlap; overlap.

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AAAGACCTTGCAAGAAAAGAA 136793

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9685. .9973
 /rpt_family="Alu"
9974. .10197
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                                                                                                                                 rpt_family="L1"
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   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact:hgc@igtp.ac.cn.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
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Xu,S., Zhao,Y., Lin,W., Dong,H., Wan,M.,
Jia,J., Wu,C., Lu,G., Zhong,M., Zhou,Y.,
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http://www.genomics.org.cn
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human.
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                                length
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Ъ
                  Qy
                                                                                      BASE COUNT
ORIGIN
                                     Query Match
Best Local Similarity
Matches 21; Conserv
45301
                                     13.7%; Solitarity 100.0%; If Conservative 0;
                                                                                              /chromosome="3"
/clone_lib="542j23"
a 29770 c 31151 g
                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                      Score 21; DB; Pred. No. 1.7
0; Mismatches
                                                                                                44136
                                                DB 2;
1.7;
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                                                        Length 150436;
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0;

Search completed: August Job time: 40768 sec

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2002, 01:43:18

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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Word size :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being prir and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                  Query
Match
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4: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT: *
5: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT: *
6: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT: *
7: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT: *
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1: /SIDS1/qcqdata/
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Gapop 60.0 , Gapext 60.0
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153
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Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTTACCTGATGACCCAGA.....TGCAAAGACTTACTGGTGCA 153
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AFT-1 interacting 
Arabidopsis thalia
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9 19 AAV49574 Human lymphoma cel		3 18 AAT42758 Chick CHD-W gene f	3 18 AAT42759 . Great tit C		h DB ID Description			SUMMARIES		lysis of the total score distribution.	equal to the score of the result being printed
oma cel PR		 -			xx	FT	FT	FT	FT		ted, FH
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	AAQ70192	15	699	10.5	16	45	
Sequence encoding	AAQ47363	14	699	10.5	16	44	
Encodes human beta	AAQ20236	13	699		16	43	
~	AAQ20237	13	696		16	42	
	AAQ70191	15	690	10.5	16	41	
	AAQ70209	15	690	•	16	40	
	AAQ47362	14	690		16	39	
	AAQ70201	15	681	•	16	38	
Sequence encoding	AAQ47369	14	681	•	16	37	
Q.	AAS93365	23	634		16	36	
Sequence encoding	AAQ70199	15	630	10.5	16	35	
Sequence encoding	AAQ47367	14	630		16	34	
Human cDNA clone r	AAK93548	22	594		16	ω ω	
	AAK91625	22	594	10.5	16	32	
#9746	AAI41060	22	537	•	16	31	O
Human bone marrow	AAK35347	22	537	•	16	30	O
(D)	AAK09455	22	537	•	16	29	C
	ABA61160	22	537	•	16	28	C
2	AAT95097	18	453	•	16	27	
uman polyn	AAF67429	22	385	•	16	26	
Partial sequence o	AAQ45230	14	351	•	16	25	O
Staphylococcus aur	AAV78976	18	196	10.5	16	24	C
d fragi	AAQ74182	15	136	٠	16	23	
	AAT81515	17	17	•	16	22	C
	AA163751	22	5647	•	17	21	
đ	AAI99401	22	5647	11.1	17	20	
thali	AAC43194	21	2395	11.1	17	19	C
Escherichia coli f	AAZ56344	21	1788	11.1	17	18	
secreted pr	AAC09900	21	165	11.1	17	17	C
	AAV20467	19	3225	:	18	16	C
homo	AAF89129	22	1580		18	15	
Human lung tumour	AAF68219	22	552	11.8	18	14	
DNA encoding pyrid	AAS20000	24	44861		19	13	
	AAI58977	22	2532		19	12	
gene	983	21	2580	13.1	20	11	
Arabidopsis thalia	AAC34655	21	16	13.1	20	10	

ALIGNMENTS

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RESULT

AAT42759

ID AAT47

XX AAT4

AC AAT4

XX AT12-M

XX II2-M

XX B1rd

KW B1rd

KW CHD-

XX Paru
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                                                                                                                                                                                                                                                                                           Bird; sex determination; chromodomain-Helicase-DNA binding 1; CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                      Great tit CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   AAT42759;
                                                                                                                                                                                                                                                                                                                                                                                                                               AAT42759 standard; DNA; 153 BP.
            (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                               Parus major.
                                       6-JUN-1995;
                                                                     5-JUN-1996;
                                                                                                 .2-DEC-1996.
                                                                                                                             09639505-A1.
                                                                                                                                                                                                    Location/Qualifiers
visc_difference 52..81
    /*tag= a
                                       95GB-0011439
                                                                     96WO-GB01341.
                                                                                                                                                       /note= "bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
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ARESULT AAT42758
ID 42758
ID 27758
AC AAT4
AC 
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Best Local Similarity
Matches 138; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translatted amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) genes determine sex in birds and can be used to identify the sex of an embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian
birds
                       Griffiths
                                                                                                               06-JUN-1995;
                                                                                                                                                           05-JUN-1996;
                                                                                                                                                                                                                                                  WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                    misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chick CHD-W
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                                                                   (ISIS-) ISIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene fragment.
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                       Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Σ
                                                                                                               95GB-0011439
                                                                                                                                                           96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76pp; English.
                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                        /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 C;
                                                                                                                                                                                                                                                                                                               "bases 52-81 are
and are ignored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153
                                                                                                                                                                                                                                                                                     and are ignored in the translated acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 T;
                                                                                                                                                                                                                                                                                                               a repeat of bases in the translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.6e-60;
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Best Local
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            The chicken CHD-W gene (AAT42754) acting alone or in conjunction wit the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a hiral control characteristic control can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a hiral can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to control the sex of progeny of a can be used to can be used to control the sex of progeny of a can be used to                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avian
birds
                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene (AAT42757), to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid and the great tit cHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken
                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                          Griffiths
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT42754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT42754 standard; cDNA; 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 153 BP; 56 A; 36 C; 31 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW08148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1996
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- used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                     chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex determination; chromodomain-Helicase-DNA binding 1 chromodomain-Helicase-DNA binding on the W chromosome; \label{eq:chromodomain}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHD-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        ₽,
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                                                                                                                                                                                                                                                     8; 76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INNOVATION
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                                                                                                                                                                                                                                                                                                                                                                                                                        Tiwari
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100.0%;
                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; : 2.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                            Query Match
Best Local
                                                                                                                                                                                            Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chick CHD-1A gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key Location/Qualifiers misc_difference 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bird; sex determination; chromodomain-Helicase-DNA binding
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                                                                                                                                                         Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW08147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS INNOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
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91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAA 128
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al Similarity 100.0%;
47; Conservation
                                                                               Similarity
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                            24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB 18;
Pred. No. 2.9e-14;
                                                                            Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                               DB 18; Length 153;
                                                                               le-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                          Indels
                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                         RESULT
ANT42751
INT 4472751
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XX Bir
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                                                                                                                  RESULT
AAV49574
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                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chicken CHD-1A gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT42751;
                  21-OCT-1998
                                                          AAV49574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT42751 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 tacctcattaaattactgaataaagaccttgcaagaaa 128
                                                                                                                                                                                                                                                                         Local Similarity les 38; Conserv
                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                              Conservative
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8099
                                                                                                                                                                                                                                                                              0;
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4140 tacctcattaaattactgaataaagaccttgcaagaaa 4177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or 2 chromosome. Probes based on CHD-W and CHD-1A give a W chromosome specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
AAV49574 standard; cDNA to mRNA; 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                            91 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 228..5390
                                                                                                                                                                                                                                                                                                                                                                                                            24.8%; Score 38; DB 18; Length 6608; 100.0%; Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                               0;
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AAX56240
ID AAX5
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                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                      AAV49550-V49599 are cDNA sequences which encode human proteins containing a transmembrane domain. These proteins can be used for, e.g. research and nutrition, and may have cytokine and cell proliferation/differentiation, immune stimulating/suppressing, haematopoiesis regulating, tissue growth, activin/inhibin, chemotactic/chemokinetic, haemostatic and thrombolytic, receptor/ligand, anti-inflammatory or tumour inhibition activity.
                                                   Human; vesicle trafficking protein; SEC22b; CBFBBA01; cancer; autoimmune disease; diabetes mellitus; multiple sclerosis; diagnosis; ss.
          WO9921988-A1
                                                                                                   Human CBFBBA01
                                                                                                                                                 AAX56240;
                                                                                                                                                                        AAX56240 standard;
                                                                                                                                                                                                                                                                                                                                     Sequence 1409 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 153-155; 205pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane domain; human; nutrition; cytokine; cell proliferation; differentiation; immune system; stimulator; suppressor; regulator; heamatopolesis; activin; inhibitor; chemotactic; chemokinetic; recept haemostatic; thrombolytic; ligand; anti-inflammatory; tumour; ds.
                                                                                                                        16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human protein having transmembrane domain - research and nutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kato S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09821328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human
                               Homo sapiens
                                                                                                                                                                                                                                842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAGA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROT-)
                                                                                                                                                                                                                                                     111 TAAAGACCTTGCAAGAAAAGA 131
                                                                                                                                                                                                                                                                             Local Sin
                                                                                                                                                                                               7
                                                                                                                                                                                                                              1998-297932/26
DB; AAW64546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lymphoma cell line U937 clone
                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEGENE INC.
SAGAMI CHEM RES CENTRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kobayashi M,
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                        (first entry)
                                                                                                vesicle trafficking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96JP-0301429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-JP04056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 82..729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "transmembrane domain containing protein"
                                                                                                                                                                                                                                                                                                                                  377 A; 278 C; 325 G; 429 T; 0 other;
                                                                                                                                                                        cDNA;
                                                                                                                                                                                                                                                                                      13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sekine S,
                                                                                                                                                                        1462
                                                                                                                                                                                                                               862
                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                       Score 21;
Pred. No.
                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamaguchi
                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HP10136 cDNA
                                                                                                                                                                                                                                                                                                  DB 19;
                                                                                                                                                                                                                                                                                       0.38;
                                                                                                 SEC22b gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for,
                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                  Length 1409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor;
                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                           0;
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RESULT
AAT11338
DЪ
                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     murine vesicle trafficking protein sec22b. CBFBBA01 is a cytoplasmically-orientated integral membrane protein, located in the endoplasmic reticulum and golgi membranes. CBFBBA01 polynucleotide (I), vectors containing (I) and recombinant host cells are useful for recombinant production of CBFBBA01. Both (I), CBFBBA01 and antibodies against CBFBBA01 are useful as research reagents, for screening assays and in diagnostic assays, especially for cancer, autoimmune disease, diabetes mellitus and multiple sclerosis. Antagonists and agonists of CBFBBA01 can be used to inhibit or enhance, respectively, the activity of CBFBBA01 or expression of (I). Anti-CBFBBA01 antibodies and CBFBBA01 or its fragments can be used in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CBFBBA01
diabetes
                                                                                                                                 CDS
                     22-JUN-1995;
                                             24-JAN-1996
                                                                    EP693554-A1
                                                                                                                                                                    Arabidopsis
                                                                                                                                                                                                        signal
                                                                                                                                                                                                                              Arabidopsis fourteen-three-three 1; AFT1; Cruciferae; regulation;
                                                                                                                                                                                                                                                    AFT-1 interacting protein (partial ascorbate peroxidase) cDNA
                                                                                                                                                                                                                                                                              05-SEP-1996
                                                                                                                                                                                                                                                                                                      AAT11338;
                                                                                                                                                                                                                                                                                                                             AAT11338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes CBFBBA01, which is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 21; 29pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-312961/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-1999
                                                                                                                                                                                                                    transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYSH-) UNIV SHANGHAI SECOND MEDICAL.
                                                                                                                                                                                                                                                                                                                                                                                      826 taaagaccttgcaagaaaaga 846
                                                                                                                                                                                                                                                                                                                                                                                                              111 TAAAGACCTTGCAAGAAAAGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100. Local Similarity 100. Local Similarity
                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                        transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY09512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W.
                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein useful in treating cancer, mellitus and multiple sclerosis
                                                                                                                                                                    sp.
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                    activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 419 A;
                      95EP-0109669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-CN00115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-CN00115
                                                                                           /*tag= a
/product= partial_ascorbate_peroxidase
/note= "plant defence related protein"
                                                                                                                                 Location/Qualifiers
2..370
                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                             cDNA;
                                                                                                                                                                                                        defence
                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                             557
                                                                                                                                                                                                                   gene expression modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 21;
Pred. No.
                                                                                                                                                                                                      response; gene
                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>ଜ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       autoimmune
                                                                                                                                                                                                     therapy; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                    cruciter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease
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23-JUN-1994;

94US-0266451

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RESULT

AACA TACA

AC AAC

AC 
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Best Local
     25-FEB-1999
05-MAR 1999
09-MAR 1999
23-MAR 1999
25-MAR 1999
29-MAR 1999
01-APR 1999
06-APR 1999
08-APR 1999
11-APR 1999
11-APR 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMT11338 encodes a partial ascorbate peroxidase, a plant defence-related protein (PDRP). AMT11338 and other CDNA molecules encoding PDRPS were isolated using a LexA, AFT1 33-194 fusion protein i.e. AFT1 (Arabidopsis 14-3-3 1) protein residues 33-194 fused to LexA, a DNA binding protein, in an interaction trap assay. AFT1 is a transcriptional activator protein and may be used to enhance, control or modify plant gene expression, e.g. in the regulation of plant storage components (esp. naplin, legumin or phaseolin). AFT1 can also be used to modulate signal transduction events involved in plant defence responses to pathogens such as fungi, nematodes, and the plant defence responses to pathogens such as fungi, nematodes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant transcriptional activator AFT-1 - isolated from Arabidopsis and useful for modifying gene expression and modulating plant defence responses to pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID NO: 54126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC47521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC47521 standard; DNA; 1157 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 557 BP; 164 A; 110 C; 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 21; 47pp; English.
                                                                                                                                                                                                                                                                                                                    25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                    06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bacteria and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP.

(MASS-) MASSACHUSETTS GEN HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 caggcaaagcagttgcagac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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DB; AAR89746.
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.l Similarity 100.0%; 1
20; Conservative 0;
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                                                                                                                                                                                                                                                                                                                  2000EP-0301439
  990S-0121825
990S-0123180
990S-012548
990S-0125788
990S-0125785
990S-0126785
990S-012785
990S-012714
990S-0128714
990S-0128714
990S-0128075
990S-0128045
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                         The invention relates to isolation of coding sequences and/or genes involved in tolerance to environmental stress in plants. The sequences (AAZ98305-Z98365) are useful for producing a transgenic plant having enhanced tolerance or resistance to environmental stress conditions such as anaerobic, flooding, cold, dehydration, drought, heat stress or salinity. This is useful for producing improved yield, growth, development and productivity under environmental stress conditions, and also provides growth of crops in areas where they cannot grow without the induced osmotolerance. Sequences AAZ98305-365 represent polynucleotide sequences from A. thaliana that are involved in
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                           system, such as peripheral nervous injuries, peripheral neuropathy localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                   Tang
Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                    Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI58977;
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                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leukaemia; ss.
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                                                                                                                                                                                                                                                 2001-442253/47.
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            for receptor
                                                                                                                                                                                                                                                                                                                       HYSEQ
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                                                                                                                                                                                                                                                                       Wang Z,
Zhou P,
                                                                                                                                                                             SEQ ID NO 1180;
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2000US-0598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
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Wehrman
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                                                                                                                                                                                                                                                                        Goodrich R,
           activity,
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                                                                                                                                                                            10078pp; English
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Xu C,
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Pred. No.
            arthritis and
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Ku C, Xue
Drmanac F
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a AJ,
RT;
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                                                                                                                                                                                                                                                                                  Qian >
Yang
                                                                                                                                                                                                              for treating disorders
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             leukaemias
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                                                                                                                                                                                                                                                                                     J.
                                                                                                                                                                                                                                                                                              Wang
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ET VALIACION				FT intron	exon	T intron	T exon	T Variation	T intron	T exon			TH Key The variation	Homo		DE DNA encoding		20000;	RESULT 13 AAS20000	Qy 9 TGATGAC Db 1776 tgatgac	Matches	i t	Q Sequence 2532	CC Note: The se
replace(Jabos,A) /*tag= m /standard_name= "Single nucleotide polymorphism"	/*tag= 1 /*tag= 1 /*tag= 1 /*tag= 1 /*standard_pame= "Single nucleotide polymorphism"	/ ABOUG . 304/6 /*tag= k /*tag= k //outber= 4 //outber= 4	2852228605 /*tag= j /number= 4	7657028521 7657028521 74:ag= 1 74:ag= 1	26465. 26569 24465. 26569 24489- h	آ ۾ کي آ	. 1	נה מו	/number= 1 4180: 18866 /*tag= d	ecifically claimed in claim 27"	yridoxine, vitami	<pre>/*tag= a /standard_name= "Single nucleotide polymorphism" 409340861</pre>	Location/Qualifiers replace(3930,G)		Pyridoxal kinase; pyridoxine; vitamin B6; PDXK autoimmune polyglandular disease type 1; transgenic animal; gene therapy; chromosome 21q22.3; ds.	pyridoxal (pyridoxine, vitamin B6) kinase (PDXK).	(first entry)	standard; DNA; 44861 BP.		TGATGACCCAGATAAGAAA 27 	0; Mismatch	12.4%; Score	2 BP; 648 A; 654 C; 688 G; 542 T; 0 other;	Note: The sequence data for this patent did not form part of the printed specification.
F F F	1 1 1 1	1 F F F	FT	# # # # # # # #	1 11 11 11	1 7 7 7	# # # # # # # #	7 F F	7 F F F	F # F	F F T T	FTTT	3 3 3	FT	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	ŋ ŋ ŋ	7 F F	FT FT	FT FT	F F F F	H H H	1 F F 7	7 F F	FT
variation	exon	variation	intron	variation	exon	variation	intron	exon	variation	variation	variation	intron	exon	variation	variation		intron	variation	variation	variation	exon	variation	intron	exon
/number= 10 replace(40516,C) /*tag= ak	2002		/standard_name= "Single nucleotide polymorphism" 38518.40495 /*tag= ah	/*tag= ar /number= 9 replace(38397,T) /*tag= ar	/*tag= ae /*standard_name= "Single nucleotide polymorphism" 383238517	e SF	/ ruy		6 1	<pre>/standard_name= "Single nucleotide polymorphism" replace(37287,A) /*tag= a=</pre>	יים פ	٠ ٦	/standard_name= "Single nucleotide polymorphism" 3530135343		replace(33922,G) /*tage v /standard_name= "Single nucleotide polymorphism"	/number= 6 /number= 6	- 100	e (<pre>/standard_name= "Single nucleotide polymorphism" replace(3331,G) /*tag= s</pre>	/*tag= q /number= 6 replace(33801,A) /*tag= r	<pre>/*rag= p /*rag= p /standard_name= "Single nucleotide polymorphism" 3379333880</pre>	/_cay= 0 /number= 5 replace(33776,C)	. н	3087730923 /*tag= n

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The invention describes an isolated human pyridoxal (pyridoxine, vitamin CC B6) kinase, (PDXK) polynucleotide. The polynucleotide is useful in CC studying the expression and function of PDXK, and in expressing PDXK CC protein for use in screening for candidate drugs to treat PDXK related CC diseases and for therapeutic purposes. A transgenic animal is useful for CC studying expression of the PDXK isogenes in vivo, for in vivo screening CC and testing of drugs targeted against PDXK protein, and for testing the CC efficacy of therapeutic agents and compounds for autoimmune polyglandular CC disease type 1. The polypeptide is useful for studying the effect of the CC variation on the biological activity of PDXK and the binding affinity of CC andidate drugs targeting PDXK for the treatment of autoimmune CC polyglandular disease type 1. Genotyping and haplotyping is useful for CC improving the efficacy and reliability of several steps in the discovery and development of drugs for treating disease associated with PDXK CC as a candidate agent for treating a specific condition or disease CC predicted to be associated with PDXK activity, and in the design of CC clinical trials of candidate drugs. This sequence (located on chromosome CC 21922.3) encodes human pyridoxal (pyridoxine, vitamin B6) kinase (PDXK) and forms the reference sequence on which the isoforms AdUll92 and CC AMUll93 are based, described in the method of the invention.
                                                             Query Match
Best Local s
Matches 19
1832
                                                                                                                                              Sequence 44861 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated human pyridoxal (pyridoxine, vitamin B6) kinase polyNts useful for therapeutic purposes, for studying the expression and function of the polyNt, and for expressing pyridoxal protein -
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ccaagaaaccacaggcaaa 1850
                              CCAAGAAACCACAGGCAAA 68
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                                                                19;
                                                                              Similarity
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                                                             Conservative 0;
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replace(40875,C)
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/*tag= am
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replace(40521,T)
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                                                                                                                                              A; 12297 C;
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                                                                                           Score 19;
                                                                              Pred.
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                                                                               No.
                                                                                                                                             13398 G;
                                                                              3.8;
                                                                                             DB 24;
                                                                                                                                              10125
                                                             0;
                                                                                           Length 44861;
                                                                                                                                             T; 0 other
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                                                             Gaps
                                                             0;
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Дb Qy

RESULT

Query Match
Best Local Similarity

11.8%; Score 18; 100.0%; Pred. No.

DB 22; 13;

Length 552; Indels

Sequence

552

BP;

220 A;

118

ç; 69

G; 144

Η,

1 other

Matches

Conservative

0;

Mismatches

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Gaps

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AAF68219
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                                                                                   CC associated proteins (I) and the nucleic acids (NAS) that encode them.

CC (I) have cytostatic activity and can be used in gene therapy, antisense conhibition and in vaccines. The NAS and the lung tumour-associated proteins they encode may be used in the prevention, treatment and concers. For example, the NAS may be administered to treat diseases by rectifying mutations or delections in a patient's genome that affect the activity of the protein by expressing inactive proteins cor to supplement the patients own production of (I). Additionally, the CC NAS may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NA complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar NA sequences in cassays to detect and quantitate the presence of similar NA sequences in cassays to identify modulators (agonists and antagonists) of the captesion and activity of the protein. AAF6808 and antagonists) of the concert inventor sequences which have a satigens in the production of antiboddes and in assays to identify modulators (agonists and antagonists) of the concert inventor sequences which are used in the exemplification of the concept inventor of the protein related the protein related the protein related.
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17-DEC-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang T, Ba
Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes immunogenic portions of lung tumour-
associated proteins (I) and the nucleic acids (NAs) that encode them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lung tumor-associated proteins and the nucleic acids that encode them, useful for preventing, diagnosing and treating lung cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2000;
22-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 193; 436pp; English.
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99US-0468867.
99US-0476300.
2000US-0519642.
2000US-0560406.
2000US-0589184.
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                                                                   invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fanger GR, Vedvick TS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
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AAF89129
                                                        Query Match
Best Local Si
Matches 18;
                                                                                                                                                           The present invention provides the protein and coding sequences of human homoglutamine-rich factor 56 (HQRE). This is useful in the treatment of cancer, anglocardiopathy, nervous system diseases, immune diseases and phlogosis. The present sequence is the homoglutamine-rich factor 56
                                                                                                                                                                                                                                                           Homo (human) glutamine(Q)-rich factor 56 applicable in diagnosis and treatment of cancer, angiocardiopathy, nervous system diseases, immune diseases and phlogosis \,\cdot\,
                                                                                                                                                                                                                                  Claim 6; Page 21-22; 29pp; Chinese.
                                                                                                                                                                                                                                                                                                                  WPI; 2001-281976/29.
P-PSDB; AAB83299.
                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-2000; 2000WO-CN00310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; homoglutamine-rich factor 56; HQRF; cancer; angiocardiopathy; nervous system disease; immune disease; phlogosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human homoglutamine-rich factor 56 coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF89129 standard; DNA; 1580 BP
                                                                                                                      Sequence 1580 BP; 463 A; 444 C; 346 G; 327 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                          Mao Y, Xie Y;
                                                                                                                                                                                                                                                                                                                                                                                                             10-OCT-1999; 99CN-0116946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200127148-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
coding sequence.
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                                                    . Match 11.8%; Score 18; DB 22; Length 1580; Local Similarity 100.0%; Pred. No. 13; conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 27..1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "homoglutamine-rich factor 56"
                                                      0;
                                                      Gaps
                                                      0;
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Search completed: August 3, 2002, 01:50:11 Job time: 32196 sec

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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               nucleic search, using sw model
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Match Length
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Gapop 60.0 , Gapext 60.0
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153
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTTTACCTGATGACCCAGA.....TGCAAAGACTTACTGGTGCA 153
                                                                                                                                                                                                                                                                                                                      em_gss_hum: *
em_gss_inv: *
em_gss_pln: *
em_gss_vrt: *
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gb_htc:*
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                     BEB43996 MR4-ST024
A335413 EST63335
BF289372 EST453963
A190276 QV-BT011-
AA234796 Zr78c05 L
AA24796 Zr78c05 L
AA24796 Zr78c05 L
AA45685 aa14 f05 r
BG666575 DRABNG04
BG573124 602594129
AW464549 BP230016A
BE198540 Ug79905 y
AW579514 MR0-HT016
BM28157 K0256B07
AM412999 EST241229
AM579516 G01773364
AW9922861 RC2-BN003
                                                                                                                                                                                                                  Description
              BF690915 602246933
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AUTHORS
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                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR4-ST0240-240
700-013-e10&t3=2000-07-24&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 26
High quality sequence stop: 167.
Location/Qualifiers
1. 167
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 167)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bah,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                              ввич 2996
MR4-ST0340-240700-013-e10 ST0240 Homo sapiens cDNA,
BE842996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                    Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                      Contact: Simpson A.J.G.
                                                                                                                                                                                                                    20202663
                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                               Simpson, A.J.
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1. .167
/organism="Homo sapiens
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AW958448
D BM229259
AW992919
AW993201
AW993283
AW993467
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AI599376
AW993481
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AW992101 PC2-BN003
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AW993201 PC2-BN003
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                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Shirley, R., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA354813
314 bp mrNA linear EST 21-APR-199
EST6335 Jurkat T-cells V Homo sapiens cDNA 5' end, mrNA sequence.
AA354813
AA354813.1 GI:2007319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 314)
                                                                                                                                                                                              For clone availability, addi
                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_ESTs: THC180658
                                                                                                                                          Seq primer: M13 Reverse.
                                                                                                                                                              Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                    Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                               Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                              Medical Center Drive, 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                  arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: stomach; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue mRNA and cDNA amplification were performed under low stringency conditions."
42 c 29 g 58 t
/organism="Homo sapiens"
/db_xref="ATCC (inhost):155260"
/db_xref="taxon:9606"
                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST453963 Rat Gene Index, normalized rat, Rattus norvegicus cDNA clone RGIHE60, mRN. BF289372 BF289372.1 GI:11220442
AI902726 355 bp mrNA linear EST 30-QV-BT011-101198-028 BT011 Homo sapiens cDNA, mrNA sequence AI902726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nhlee@tigr org
This clone is available through the ATCC,
tel#703-365-2700 for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sultana, R., Tsai, J., White, J., Quackenbush, J. and Lee, N.H. Generation of ESTs from Normalized Rat Embryo, Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Malek,R.L., Cho,J., Lee,Y., Karamycheva,S., Parvizi,B., Pe Sultana,R., Tsai,J., White,J., Quackenbush,J. and Lee,N.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
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                                                                                                                                                                                                                                                          /note="Vector: pT3T7Pac; Site_1: EcoR1; Site_2: Not1; Combination of ROV, RBR, RXI, RLI, RPL, RLU, REM, RMU, RHE, RPC, RPN"

3 71 c 80 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-;
                                                                                                                                                                                                                                                                                                                      /tissue_type="mixed tissue"
/lab_host="DH5-alpha"
                                                                                                                                                                                                                                                                                                                                                   norvegicus cDNA"
                                                                                                                                                                                                                                                                                                                                                               /organism-"Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RRIHE60"
/clone_11b-"Rat_Gene Index, normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                         Cocation/Qualifiers
                                                                                                                                                                                  13.7%;
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1.3;
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1.3;
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                                 EST 30-MAR-2000
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                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                           438 bp mRNA linear EST 06-AUG-11-2178c05.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:669512 5', mRNA sequence.
AA234796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: +55-11-2/V/V/L
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 355)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baha, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 438)
1 (bases 1 to 438)
1 (bases 1, Dowles, L., Dubque, T., Geisel, G., Jost, S., Hillier, L., Allen, M., Bowles, L., Lennon, G., Marra, M., Martin, J., Moore, B. Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Woore, B. Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer:
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                          AA234796.1 GI:1859289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.ludwig.org.br/seq/gethtml.pl?tl=QV&t2=QV-BT011-028.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
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/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196. 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

a 66 c 80 g 102 t
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1. .355
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism⇔"Homo sapiens"
/db_xref⇒"taxon:9606"
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Pred. No. 1.4;
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                         Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le. N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

Washu-Marck EST project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T., Waterston,R. and Wilson,R. WashU-Merck EST Project 1997 Unpublished (1997) Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                              Ammalia: Entheria; Primates; Catariata; Vertebrata; Euteleostomi; Mammalia: Entheria; Primates; Catarinia; Vertebrata; Euteleostomi; Mammalia: Entheria; Primates; Catarinin; Homonidae; Homo.

1 (bases 1 to 461)
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA456385.1 GI:2178961
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         est@watson.wustl.edu
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/db_xref="GDB:5563479"
/db_xref="taxon:9606"
/clone="IMAGE:669512"
/clone_lib="Soares_NHHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart,
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                                                                                                                                                                                                                                                                                            Distinct gene expression profiles of rat induced by peripheral nerve axotomy Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BG666575
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DRABNG04 Rat DRG Library
                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 474)
Xiao, H.S., Han, Z.G.,
                                                                                            This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Pudong New Area, P.R.China. Please contact with Zhang Xu
                                                                                                                                                                                           Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
                                                                                                                                                                                                                                                        Contact: Zhang Xu
Laboratory of Sens
                                                                                                                                                                                                                                                                                                                                                   Zhang,
                        BACKWARD: T7
                                                              PCR PRimers
                                                                                                                                                           Email: xu.zhang@ion.ac.cn
                                                                                                                                                                               Fax: 86-21-64713446
                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                          FORWARD: T3
                                                                            (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
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Guo,C., Yan,Q., Jin,S.X., Zhu,Z.D., Xu,X.R.,
primer: T3
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pregnant uterus"
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/db_xref="GDB:6044159"
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Please contact with Zhang Xu
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R., Li,N.G.,
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; Murinae;
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ne DRABNG04 5',
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3., Chen, Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                               http://image.llnl.gov
Plate: LLCM1577 row: j column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                   //uswref="taxon:you
/db_xref="IMAGE:4721382"
/clone=lib="NHH_MGC_79"
//lab_host="DH10B (TI phage-resistant)"
//lab_host="DH10B (TI phage-resistant)"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
/site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTTGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTTGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for fill-length clones and was constructed by Clontech
                     136
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRABNG04"
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/db_xref="taxon:9606"
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116 c 125 g
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                            111 TAAAGACCTTGCAAGAAAAGA 131
403 TAAAGACCTTGCAAGAAAAGA 423
                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 217 333 5998
Fax: 217 244 5617
Email: h-Lewin@uiuc.edu
Email: h-Lewin@uiuc.edu
Email: h-Lewin@uiuc.edu
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
Sequences submitted are vector free and at least 200 bp in length.
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTAACGACTCACTATAGG
BACKWARD: ATTAACCCCTCACTATAGG
BACKWARD: ATTAACCCCTCACTATAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 489 Std Error: 0.00 Plate: BP230016A10 F. E COlumn: 9 Seq primer: AGCGGATAACAATTTCACACAGGA High quality sequence stop: 489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW464549 489 bp mRNA linear EST 24-FEB-BP230016A10E9 Soares normalized bovine placenta Bos taurus cDNA clone BP230016A10E9 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 489)
Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
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148 а
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                                                                      Conservative
                                                                                                                                                                                   /note-"Organ: placenta; Vector: pT7T3Pac; Site_1: ECORI; Site_2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. "

a. B. (1996), Genome Research 6(9): 791-806. "
                                                                                                                                                                                                                                                                                                    /clone="BP230016A10E9"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                    13.7%; Score 21; DB 9;
100.0%; Pred. No. 1.4;
1tive 0; Mismatches
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/db_xref="taxon:10090"
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AW579514 515 bp mRNA linear
MRO-HT0164-070100-013-f05 HT0164 Homo sapiens cDNA,
AW579514 AW579514.1 GI:7254563
HCGP http://www.ludwig.org.br/ORESTES.
The FARESF/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                           Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalla: Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases 1 to 515)
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/clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="mammary gland"
/lab_host="DH10B"
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=MRO&t2=MRO-HTO164-
070100-013-f05&t3=2000-01-07&t4=1)
Seq.primer: puc 18 forward
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Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0256 row: B column: 07
Seq primer: -21M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                   /organism="Mus musculus"
/strain="CS7BL/6J"
/db_xref="niaEST:K0256B07-3"
/db_xref="taxon:10090"
/clone="K0256B07"
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/db_xref="taxon:9606"
/clone_lib="HT0164"
                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
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RESULT 13
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Best Local :
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                                                                                                                                                                                       Unpublished (1998)
Contact: Lee, NH
Contact Center Genomic Research
The Institute for Genomic Research
9712, Medical Center Drive, Rockvi.
Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp. Rattus sp.
                                                                                                                                     Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AI412929.1 GI:4256433
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EST241229 Normalized rat kidney,
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/organism="Rattus sp."
/db_xref="taxon:10118"
/db_one="REG55"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNAs were amplified by long range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The CDNAs were digested with Sal1 and NotI enzymes and cloned into Sal1/NotI site of pSPORTI plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA)."
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/note="Vector: pSI
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                                                                                                                        Location/Qualifiers
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100.0%;
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                                                         Query Match
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111 TAAAGACCTTGCAAGAAAAGA 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=RC2-BN0033-180
200-014-f04at3-2000-02-18c44-1)
Seq_primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chorddta; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 594)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
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21; Conservative
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                                     Conservative
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                                                                                                                                             /note="Organ: breast_normal; Vector: puc18; Site_1: SnaI; Site_2: SmaI; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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/db_xref="taxon:9606"
/clone_lib="BN0033"
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                                                    13.7%; Score 21; DB 9; Length 594; 100.0%; Pred. No. 1.4;
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Job time: 30155 sec
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Query Match
Best Local :
417 TAAAGACCTTGCAAGAAAAGA 437
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9911 row: o column: 16
High quality sequence stop: 585.
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Tissue Procurement: Gilbert Smith, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:3994215"
/clone=lib="NCI_CGAP_Lu29"
/clone=lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
/tissue_type="spontaneous tumor, metastatic                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="CZECH II (feral)"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                13.7%; Score 21; DB 10; Length 597; 100.0%; Pred. No. 1.4;
                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                        Mismatches
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2, 2002, 22:41:40

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9b_In:DROCHDIA

9b_htg:AC01985

9b_In:AC007765

9b_In:AC0092187

9b_In:AC0092187

9b_In:AF006514

9b_htg:AC087641

9b_htg:AC087641

9b_htg:AC074383

9b_DY:AF181825

9b_OV:AF181825

9b_OV:AF181825

9b_OV:AF181826

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9b_DV:AC026108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_ro:MUSCHD1x
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Database sequences: 1797656
Database length: 1873333701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search information block:
Query: US-08-973-363-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: Aug 3, 2002 7:08 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search time (sec): 4908.870000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -MODEL-frame+_p2n.model -DEV=x1h
-MODEL-frame+_p2n.model -DEV=x1h
-Q=/cgn2_1/USPRO_Sp001/US08973361/runat_01082002_080123_19828/app_query.fasta_1.638
-DB=GenEmbl -OpMT=fastap -SUEFIX=01ip2n.rge -GAPOp=4.500
-GAPEXT=0.000 -MINMATCH=0.100 -LOOPCI=0.000 -LOOPEXT=0.000
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCI=0.000 -VGAPEXT=60.000
-GAPOP=6.000 -GAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-FGAPOP=6.000 -FELEXT=7.000 -YGAPOT=1 -MATRIX=01ip0
-TBLNG=10.000 -DELEXT=7.000 -START=1 -MATRIX=01ip0
-TBLNG=10.000 -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US08973563_eGRAll_1.4551 -NOPU=6 -1CPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of: US-08-973-363-6 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
        . 6e-22

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2 8e-22

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3 8e-22

3 1e-21

7 6e-11

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5.7e-33 53
5.3e-27 15
1.4e-23 59
                                                                                             153 i A58684 Sequence 3 from Patent W
153 i A58685 Sequence 4 from Patent W
153 i A58686 Sequence 5 from Patent W
153 i A58686 Sequence 5 from Patent W
154 i AF060702 Struthio camelus clone
202 i D14316 delta-crystallin enhanogas
202 i D14316 delta-crystallin enhanogas
202 i L77907 Drosophila melanogas
204 i AC019885 Drosophila melanogas
204 i AC019885 Drosophila melanoga
204 i AC02187 Drosophila melanoga
204 i AC02188 Drosophila melanoga
204 i AC02188 Drosophila melanoga
204 i AF06514 Homo sapiens CHDD mRN
205 i AC028764 Homo sapiens Chromo
207 i AC028764 Homo sapiens Chromo
207 i AC013394 Homo sapiens chromo
207 i AF181825 Aegolius funereus chr
207 i AF181826 Gallus gallus chromos
204 i AF181826 Gallus gallus chromos
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204 i AF181826 Gallus gallus chromos
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5349 | L10410 Mouse DNA-binding prote
153 | A55683 Sequence 2 from Patent W
15947 | AF006513 Homo sapiens CHD1 mak
                                                               AF181826 Gallus gallus chromo:
AC026108 Homo sapiens 12 BAC
AC079625 Homo sapiens chromo
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JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS MUSCHD1X
DEFINITION Mouse DNA-bir
ACCESSION L10410 X66028
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gb_pat:AX083550
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gb_pat:AX027892
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gb_in:PARSP51A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced g1:293322.

Location/Qualifiers
1. 5349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 5349)

Delmas, V., Stokes, D.G. and Perry, R.P.
Delmas, V., Stokes, D.G. and Perry, R.P.
A mammalian DNA-binding protein that contains a chromodomain and SNF2/SWIZ-like helicase domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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DCRYGRKGATGATTIYAVEANGDDRAGGERNKEDGDIQYLIKKKGWSH HINTWETEE
TLKQONVERCHKKLDNIKKKKODETKERKLKNASEDDEVSYKYQQBELTDLLHKQYQIYERI
I AHSNQKSAAGLPDYYCKWGGLPYSECSWEDGALISKKFQTCIDEYFSRNOSKTIPFK
DCKYLKQRPREYALKKODEYIGGHEGLELRDYYQLNGLNWLAHSKCKGWSCIHADEMGL
KYTIQTISETSLNYLEHBIOLYGPFLLVPLSTILTSWQRELGTWASQNNAVYVLIGDINSR
INITTHEWMHPQTKRLKFNILLTTYEILLKDKAFLGGLNWAFIGVDEAHRLKNDDSLL
YKTLIDFKSNHRLLTGTPLONSLKELWSLLHFIMERFSSWEDEEBEHGKGREKGYA
SLIHKELEFELLRFYKKDVEKSLPAKYEOLIKHEWMSALGKGSKGVIHLLKLIRL
KGCNUCHCYLIREDDNUNETYNKOBALOHLIRSKGLHIRLANGSGEDF
CFLLSTRAGGIGINLASADTYVIFDSDWWFQNDLQAQARAHRIQALDHFNAEGSEDF
CFLLSTRAGGIGINLASADTYVIFDSDWWFQNDLGAGARSKSTPRKKQALDHFNAEGSEDF
CFLLSTRAGGIGINLASADTYVIFDSDWWFQNDLGAGARAHRIQAKKQVNIYRLVTKG
SYEEDILERAKKKWLDHLJIQRWDTGAGTSGAFSSSTPPKREELSALLKRGAE
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GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLHKIKKHAIKKRQESQQNSDQNSNVATTHVIRNPDMERLKENTNHDDSSRDSYSSDRHLS
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ELBEERNSKNWEEI I FEEQORRLEEEROKLEET MILPMANCAGZISFNGSEGRS
RSRRYGGSDSISSEKREKKRGRPFI PERBIKGFSDAEIRREIKSYKKFGGPLERL
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VQVNAKLVIAHEDELIFLHKSIESDFERKQYTIFCHFRANFDIDMGKEDDSNLLIG
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QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK
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/gene="CHD-1"
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/db_xref="taxon:10090"
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69 | M38556 Paramecium aurelia :
36 | AF202165 Turbatrix aceti 18
52 | AX027892 Sequence 20 from P
66 | BC022041 Homo sapiens, clon
54 | M65163 P.tetraurelia 51A su
664 | AX083550 Sequence 15 from
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alignment_scores:
Quality: 34.00
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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Location/Qualifiers
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Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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GLGKTIQTISTLNYLFHEHQLYGPFLLVVPLSTLTSQRENIQTWASQMNAVYYLGDIN
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SKGSTSGFLNIMMELKKCCNUCYLIKPDDNNEFYNKQEALQHLITSGGKILLDKILI
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DFCFILLSTRAGGLGINLASADTYVIFDSDWNPQNDLQAQARAHRIGGKKQVNIYRLVT
KGSVEDDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSAPSSTPFNKEELSAILKFG
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DIELEPERGEGEPQEMDIDELIKRAETHENEFGPLTVGDELLSQFKVANFSNMOED
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YHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHRDWDHYKQDSRYYSDREKHRKLDDH
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GLSEREQLEHTRQCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKFTEFDARKLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
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HOMO sapiens chromosome 5 clone RP11-58M12,
AC092372 GI:17402768
                                                                                                                                                                                                                                                                                                                                      NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624. The number of bases overlapped is 90404.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101220)
DOB Joint Genome Institute and Stanford Human Genome Center.
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1. 101220
                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9806"
/db_cref="tone"=5"
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a 18862 c 17827 g 30409 t
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seq_name: gb_htg:AC021449
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US-08-973-363-6 x AC012624
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                                        26882 CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAA 26837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases I to 134365)
3 (bases I to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases I to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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AC012624.6 GI:14993679
HTG.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 134743 bases at least Q40 Consensus quality: 139227 bases at least Q30 Consensus quality: 140814 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 4.6 in Q20 bases; agarose-fp Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: 58_M_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name:
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38921 404:
                                                                                    40412 40511:
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920: gap of 100 bp 40411: contig of 1491 bp in length 511: gap of 100 bp 43279: contig of 2768 bp in length
                                                                                                                                                                                                                                                                           38820: contig of 38820 bp in length
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alignment_block:
US-08-973-363-6 x AC021449
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Quality:
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ORIGIN
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                          CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAA 116242
                                                                                                                                                                                      gb_htg:AC008531
                    Homo sapiens chromosome 7 ordered pieces.
AC008531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43971
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106510 143079: contig of 36570 bp in length
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51931    62619
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40512. .43279
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43380. .46905
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106510. .143079
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47006. .51830
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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75509. .92516
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26246 c 26678 g
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Gaps: 0
Percent Identity: 100.000
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contig of 13793 bp in
ap of 100 bp
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                          alignment_block:
                                                                                                         alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
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                                                                     Quality: 32.00
Ratio: 1.000
Percent Similarity: 100.000
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US-08-973-363-6 x AC008531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 139128 bases at least 040
Consensus quality: 142556 bases at least 020
Consensus quality: 142744 bases at least 020
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in 020 bases; pulse field gel estimation
Quality coverage: 6.4 in 020 bases; sum-of-contigs estimation.
**NOTE: This is a 'working draft' sequence. It currently
**consists of 7 contigs caps between the contigs
**are represented as runs of N. The order of the pieces
**is believed to be correct as given, however the sizes
**of the gaps between them are based on estimates that have
**provided by the submittor.
**This sequence will be replaced
**by the finished sequence as soon as it is available and
**the accession number will be preserved.
**100975 110127: contig of 44600 bp in length
**101975 110127: contig of 44600 bp in length
**11328 118190: contig of 12153 bp in length
**11328 118190: gap of unknown length
**11328 118291 119694: contig of 4404 bp in length
**113291 119694: contig of 3503 bp in length
**113298 123397: gap of unknown length
**113298 123397: gap of unknown length
**113298 123397: contig of 3503 bp in length
**12398 123597: contig of 3503 bp in length
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Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center Project Name: 369535
Center clone name: CIT-HSPC_480B11
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DDE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.jgi.doe.gov
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                                                                                                                                                                                                                                                                          /clone="CTC-480B11"
/clone_lib="CalTech human BAC library C"
/ 26309 c 27580 g 48609 t 600 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .145659
                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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Align seg 1/1 to: AC008531 from: 1 to: 145659
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Consensus quality: 180259 bases at least 030
Consensus quality: 180259 bases at least 020
Consensus quality: 1804175 bases at least 020
Estimated insert size: 204509; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in 020 bases; sum-of-contigs estimation
Quality coverage: 5.79 in 020 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the places
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Homo sapiens chromosome 5 clone RP11-36012,
PROGRESS ***, 33 unordered pieces.
AC091946
AC091946.1 GI:14333882
HTG: HTGS_PHASE1.
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Center Code: JGI
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Submitted (99-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Center clone name: RPCI-11_36012
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DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                        8: contig of 1358 bp in length
8: gap of unknown length
7: contig of 1209 bp in length
7: gap of unknown length length
3: contig of 1056 bp in length
3: gap of unknown length
1: contig of 1997 bp in length
1: contig of 1474 bp in length
4: contig of 1474 bp in length
4: gap of unknown length
6: contig of 1502 bp in length
6: gap of unknown length
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/clone_lib="RPCI human BAC library 11"
35252 c 37061 g 60360 t 3202 others
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/db_xref="taxon:9606"
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seq_documentation_block:
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                                                                                                                                                     29732 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC
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                                                                                                              17
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                                                                                                                                                                       1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                         CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAA 29637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Porive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:13677045.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-MAR-2000) production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459 (bases 1 to 195433)
DOE Joint Genome Institute and Stanford Human Genome Center.
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WI-13675 G23101
SHGC-58345 G38487
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195433)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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a 37302 c 37040 g 58329
                                                                                                                                                                                                                                                                                                                         100.000
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1. .195433
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ne 5 clone CTC-428I11, complete sequence.
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Gaps:
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-973-363-6 x AC022121/rev
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VERSION
                                                                  seq_documentation_block:
                                                                                                                 seq_name: gb_htg:AC092382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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         LOCUS AC092382 276181 bp DNA linear HTG 03-JUL-2001
DEFINITION Homo sapiens chromosome 5 clone RP11-75H1, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
DEFINITION
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                          89400 CCGTGCAGACTACCTCATCAAATTACTTAGTAGAGATCTTGCAAAA 89355
                                                                                                                                                                                                                                                                               89450 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 89401
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                                                                                                                                                                                                                                                                                                               1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu ouality: Phrap Quality >-40 99.8% of Sequence; Estimated Total Number of Errors is 0.4.
STS Content:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
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SHGC-103595 G57841.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DDE Joint Genome Institute and Stanford Human Genome Center.
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AC022121.6 GI:15375145
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DOE Joint Genome Institute.
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3 Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism "Homo sapiens"
/db_xref "taxon:9806"
/db_xref "taxon:9806"
/chromosome "5"
/clone= "CTD-2007H13"
t 42062 c 40933 g 64309 t
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1. .219258
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Percent Identity: 100.000
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Consensus quality: 256163 bases at least Q20
Consensus quality: 256163 bases at least Q20
Consensus quality: 256163 bases at least Q20
Consensus quality: 256193 bases at least Q20
Estimated insert size: 174820; agarose-fp estimation
Estimated insert size: 174820; agarose-fp estimation
Quality coverage: 8.62 in Q20 bases; agarose-fp estimation
Quality coverage: 5.55 in Q20 bases; sum-of-contigs estimation.
Quality coverage: 5.55 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a "working draft' sequence. It currently

* consists of 47 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
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Center clone name: RPCI-11_75H1
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Submitted (03-UUL-2001) Production Sequencing Facility, DOE Joint Submitted [03-UUL-2001) Production Sequencing Facility, DOE Joint Sequencing Facility, DOE Joint Submission
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DOE Joint Genome Institute.
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DDE Joint Genome Institute.
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AC092382
AC092382.1 GI:14589571
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                                                                                                                                              15361
15461
16668
16768
18391
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11199
11299
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1162
2828
2928
                                                                                                                                                                                                                                                                                                                                                                           1061: contig of 1061 bp in length
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2827: contig of 1666 bp in length
2927: gap of unknown length
4227: contig of 1300 bp in length
4327: gap of unknown length
5618: contig of 1300 bp in length
5618: contig of 1291 bp in length
5718: gap of unknown length
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6983: contig of 1265 bp in length
6983: contig of 1365 bp in length
8422: contig of 1339 bp in length
8522: gap of unknown length
9771: contig of 1249 bp in length
9871: gap of unknown length
11198: contig of 1327 bp in length
11298: gap of unknown length
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13906
6: gap of unknown length
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gap of unknown length
contig of 1207 bp in length
gap of unknown length
contig of 1623 bp in length
contig of 1635 bp in length
contig of 1051 bp in length
gap of unknown length
contig of 1051 bp in length
contig of 1515 bp in length
                                                                                                                                                                                                                                                                            gap of unknown length
contig of 1292 bp in length
gap of unknown length
contig of 1454 bp in length
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BASE COUNT
ORIGIN
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126798
126898
135115
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146714
146814
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157895
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102125
102125
109906
110006
116738
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201688
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80662
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32481
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26485
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                                                                                                                           Location/Qualifiers
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201787:
231268:
231368:
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US-08-973-363-6 x A58696
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    Quality:
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US-08-973-363-6 x AC092382/rev
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Ratio: 1.000
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Ratio: 1.000
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                                                                                                                          gb_pat:A58691
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unidentified.
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unclassified.
                                          Sequence 10 from Patent W09639505.
A58691
A58691.1 GI:3714250
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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Sequence 15 from Patent W09639505.
A58696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified unidentified
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US-08-973-363-6 x A58691
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LOCUS AF004397
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Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked in the chicken Gallus domesticus
Gene 197 (1-2), 225-229 (1997)
97473516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF004397 mRNA linear VRT 08-OCT-15 AF004397 mRNA linear VRT 08-OCT-15 Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-Z) mRNA, complete
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
Direct Submission
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Gallus gallus
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                                                                                                                                                                                                                                                                                                        Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8QQ, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF004397.1 GI:2501845
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1207 c 1459 g 165.
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Location/Qualifiers
                                                          /product="chromo-helicase-DNA-binding on the Z chromosome
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/note="CHD protein with hydrophilic domain"
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Ratio: 1.000
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1 (bases 1 to 1311)
de Lange,T., Steensel,Bvan. and Bianchi,A.
Altered telomere repeat binding factor
Patent: US 5859183-A 3 12-JAN-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    Sequence 3 from patent US
AR029026
                                                                                                                                                                                                                                                                                                                       AR029026.1 GI:5940999
                                                                                                                                                                                Unclassified
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KTIQTI SFINYLEHEIGLYGEPLLRVPLSTLTSWORELGTWARDMINAVYLLGD ITSRI
MIRTHEWHIPOYRKLK PILLTTYE ILKDKSFLGGLINWAF LOVDBAHRLKINDSLLY
RTLIDFKSNHRLLITGTPLONSLKELMSLLHE INDEKESSMEDDFEEBERGKREVGYAS
LIKEELEPFLLRRVKDVEKSLPAKVEQILRAMBALOKOY YKWILTRNYKALSKGSKG
STSGFLNIMMELKKCCHCY YLIKPDDMEFYNNOBALOKOY YKWILTRNYKALSKGSKG
STSGFLNIMMELKKCCHCY YLIKPDDMEFYNNOBALOKOY YKWILTRLWKALSKGSKG
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FLLSTRAGGIGI MLASADIYVLTFOSMWANDONLOLAORARHETGOKKOYNYT RLYYKGS
VEEDILERAKKKMYLDHLVJORNDTTGKTYVLHTGSTPSSSTFFNKEELSAILKFGAEE
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LEPERNSRMEEIIPESORRRIEDEEROKELEEITMLFRRHNCAKOISFNOSEGRRSR
SRRYSGSDSDSTTERKRPKKRGPRTITERENIKGFSDAEIRREIKSYKKFGGPLERLD
AVARDAEITERKRPKKRGPRTITERENIKGFSDAEIRREIKSYKKFGGPLERLD
AVARDAEITERKPENLOELVHNGCIKALIKDUSSGCRASH
OVANKLVISHEDELAELTSTENFENLOELVHNGCIKALIKDUSSGCRASH
VENGYSGERMIKMDEDLSTOKTIPEDDEKKRYVIPCHKAAHFDIGNEKSEDSKLILKOLARKEAO
RIAGASNKRRKTRNKKNKMKASKIKEEIKSDSSPOPESKSDEDDEEEDNKDEIVSYK
HLHKIKIKTEKBNEEKEPDJGIKKEAEBKRFTVERKNKREKKEKEDKKELKEKD
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKKQQQQQKAASSDSGSEEDSSSSEDSADDSSSETKKKKHKDEDWQMSGSGSVSGTGS
DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNGHSDEESVRNSSGESSRSDDDSGSASGSGSGSGSSSGSSSDGSS
SQSGSSDSESGSESGSQSESESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NKEKRENKVKESTQKEKEVKEEKVNEMKSENKEKSKKIPLLDTPVHITATSEPVPISE
ESEELHQKTFSVCKERMRPVKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CHD-Z"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 26
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 29-SEP-1999
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REFERENCE AUTHORS JOURNAL FEATURES

ACCESSION VERSION KEYWORDS

SOURCE

ORGANISM

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WARN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
Query: US-08-973-363-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Date: Aug 3, 2002 7:18 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM of: US-08-973-363-6 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    search time (sec): 521.050000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query length: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MODEL-frame+_p2n.model -DEV-x1h
-MODEL-frame+_p2n.model -DEV-x1h
-MC-Crgn2_1/USP70_spool/US08973353_runat_01082002_080123_19849/app_query.fasta_1.638
-DB-N_Geneseq_032802 -QFMT=fastap -SUFFIX=011p2n.rng
-CAPOP-4.500 -GAPEXT=0.050 -MINMATCH-0.100 -LOOPECT=0.000
-CAPOP-4.500 -GAPEXT=0.050 -MINMATCH-0.100 -YGAPOP-60.000
-XGAPEXT=60.000 -GAPOP-6.000 -FCAPEXT=7.000 -YGAPOP-60.000
-YGAPEXT=60.000 -DELOP-6.000 -DELEXT=7.000 -START=1
-MATRIX=011g0 -TRANS-human40 cdi -LIST=45 -DOCALIGN=20
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-NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-20000000
-USER-US08973363_CGM1_1.186 -NCPU-6 -ICPU-3 -LONGLOG
-USCH-US08973363_CGM1_1.186 -NCPU-6 -ICPU-3 -LONGLOG
-USCH-US08973363_CGM1_1.186 -NCPU-6 -ICPU-3 -LONGLOG
-USCH-US08973363_CGM1_1.186 -NCPU-6 -ICPU-3 -LONGLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  out_format : pfs
alignment_block:
US-08-973-363-6 x AAT42756
                                                                                                              alignment_scores:
                                                                         Percent Similarity: 100.000
           Align seg 1/1 to: AAT42756
                                                                                      Quality:
Ratio:
                                                                                      34.00
1.000
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AC AAT42756;
XY
AC AAT42756;
XY
AC AAT42756;
XY
AC AAT42756;
XY
Mouse CHD-1 gene (bases 3855-977)
DE Mouse CHD-1 gene (bases 3855-977)
XX
Mus sp.
XX
Mus sp.
XX
Mus sp.
XX
AC Mus sp.
XX
AC Mus sp.
XX
AC Mus sp.
XX
AC Mus sp.
XX
AC Mus sp.
XX
AC Mus sp.
AC Claim 8; Fig 3; 76pp; English.
AC Mus sp.
AC Claim 8; Fig 3; 76pp; English.
AC Mus sp.
AC Claim 8; Fig 3; 76pp; English.
AC Mus sp.
AC Claim 8; Fig 3; 76pp; English.
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AC Claim 8; Fig 3; 76pp; English.
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AC Claim 8; Fig 3; 76pp; English.
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AC Claim 8; Fig 3; 76pp; English.
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AC Mus sp.
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                                                                                                                                                                Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42758) and the great fit region are provided in Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.00 117.84
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7.00 117.78
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7.00
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7.00 118.24
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117.95
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from: 1

to: 153

Percent Identity: 100.000

27 G; 28 T; 0 other;

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alignment_block:
                                                                                                                      alignment_scores:
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ID AAT42754 standard;
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                        Align seg 1/1
                                                US-08-973-363-6 x AAT42754
                                                                                    Percent
                                                                                                                                                                                          The chicken CHD-W gene (AAT42754) acting alone or in conjunction wit the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102
                                                                                                                                                          Sequence 1316 BP;
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                      Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chicken CHD-W gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT42754;
                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 CG 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         la 41
IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                                                                                                                                                                                                                                                                        chromodomain-helicase-DNA binding genes det - used for sex determn. and to control sex
                                                                                                           Quality:
                                                                                              Ratio:
                        to: AAT42754
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                                                                                                                                                                                                                                                                                                                                                                                                        Tiwari
                                                                                  26.00
1.000
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-GB01341.
                                                                                                                                                          492 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA; 1316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                        В;
                                                                                                                                                          208 C;
                         from:
                                                                                    Percent
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Gaps:
Identity:
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sex of progeny
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seq_documentation_block:
ID AAT42751 standard; cC
XX
AAT42751;
AC AAT42751;
XX
DT 12-MAR-1997 (first e
.XX
Bird; sex determinati
KW Bird; sex determinati
KW CHD-W; chromodomain-H
XX
Gallus sp.
XX

XX

W09639505-A1.
XX

XX

VA

ICCAT
FH Key 12-DEC-1996.
XX

XX

O5-JUN-1996; 96WO-G
XX

O6-JUN-1995; 95GB-G
XX

XX

(ISIS-) ISIS INNOVATI
XX

PD 12-DEC-1996.
XX

XX

(ISIS-) ISIS INNOVATI
XX

PD 12-DEC-1996.
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Claim 1; Fig 5; 76pp:
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Claim 1; Fig 5; 76pp:
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The chicken CHD-W ger
CC the closely related of female development in CC
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CO
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CC the
                                                                                                                                                                                                                                                                                                      alignment_scores:
    Quality:
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US-08-973-363-6 x AAT42751
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                                                                                                                                                                                                                                              Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                             Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-043127/04.
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1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INNOVATION LTD
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                                                                                                AAT42751
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                                                                                                                                                                                                                                                                                                                                                                                                                               2289 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA; 6608
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                                                                                                from:
                                                                                                                                                                                                                                                                                                                                                                                                                               1207 C;
                                                                                                                                                                                                                                                 Percent Identity:
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100.000
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seq_documentation_block:
ID AAV59280 standard; cDNA; 1311 BP.
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alignment_block:
US-08-973-363-6 x AAV59280
                                                                        alignment_scores:
                                  Percent Similarity: 100.000
                                                                                                                               The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atheroscierosis, tumours and viral (including human immune deficiency virus) infection. Cells expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4080 ATTTTACCTGATGATCCAGACAAGAAACCCCAGGCAAAGCAGCTACAGAC 4129
                                                                                                                                                                                                                                                                                                         Nucleic acid encoding altered telomere repeat binding protein and related vectors 'transformants, hetero-dimers and antibodies, us to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV59280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-1998;
13-FEB-1997;
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                                                                                                                                                                                                                                                                                    Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            Bianchi A, De Lange T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Altered telomere repeat binding factor 1 gene.
                                                                                                          Sequence 1311 BP; 441 A; 257 C; 316 G; 297 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-480769/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGTGCAGACTACCTCATTAAATTACTG 4157
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                                                 Quality:
Ratio:
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/product= "A-TRF"
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1..1311
                                                 25.00
1.000
                                                                                                                                                                                                                                                                                                                                                                                                            Van Steensel B;
                        Length: 25
Gaps: 0
Percent Identity: 100.000
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 alignment_block:
US-08-973-363-6 x AAT42759
                                                                                                          AAT42759;
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42759
                                                                                                        alignment_scores:
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          Quality: 19.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1237 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1287 CCGTGCAGACTACCTCATCAAACTA 1311
                                                                                                                                                                                                                                                Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                  Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Great tit CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT42759 standard; DNA; 153 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-043127/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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and are ignored in the translated amino
acid sequence given in Fig 3"
Length: 19
Gaps: 0
Percent Identity: 100.000
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alignment_scores:
Quality:
alignment_block:
US-08-973-363-6 x AAT42757
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                                Percent Similarity:
                                                                                                                    Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW88146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT4275-5) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chick CHD-1A gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy
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                                                                                                                                                                                                                                            chromodomain-helicase-DNA binding genes determine sex - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex determination; chromodomain-Helicase-DNA binding
                                            Ratio:
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us-08-973-363-6 x AAT42758
                                                    alignment_scores:
    Quality:
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ID AAT42758 standard;
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                                                                                                                   Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT47758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                Sequence
                                                                                                                                                                                                                       Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                             P-PSDB; AAW08148
                                                                                                                                                                                                                                                                                         WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                             Griffiths R,
                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chick CHD-W gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1997
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                                                                                                                                                                                                                                            chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex determination; chromodomain-Helicase-DNA binding
A; CHD-W; W chromosome; ss.
                                                                                                153 BP;
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and are ignored in the translated
acid sequence given in Fig 3"
                                                                                                56 A;
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                                                      19.00
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alignment_block:
US-08-973-363-6 x ABL06443
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ID ABL06443 standard; cDNA; 6240 BP
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Align seg 1/1 to: ABL06443 from: 1
                                                                                        Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and inequivalent cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG10511), expressed DNA sequences (ABLIG1640-ABLIG1615) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
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11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811
                                                                                                                                                                                                        Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-656860/75.
                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL06442 standard; cDNA; 9933 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000\ \mathrm{or} more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                9 LysProGlnAlaLysGlnLeuGlnThrArgAla 19
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Gaps: 0
Percent Identity: 100.000
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chronic colitis;
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29-SEP 2000
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendictis, Hirschisprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - \,
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05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 421 BP; 148 A; 78 C; 127 G;
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                                                                                                                                            19-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
 31-JAN-2000; 2000US-0179065
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DB; AAM93109.
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Percent Identity: 100.000
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01-NOV-2000;
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08-NOV-2000;
Isolated polypeptide disorders related to and also for testing
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                                        2001-457727/49.
DB; AAM38625.
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2000US-0246611

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2000US-0249245

2000US-0249245

2000US-0249265

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2000US-0251868

2000US-0251479

2000US-0251868

2000US-0251868

2000US-0251868

2000US-0251989

2000US-0251999

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2000US-0241781
2000US-0241785
2000US-0241787
2000US-0241808
2000US-0241809
2000US-0241826
2000US-0246617
2000US-0246475
2000US-0246477
2000US-0246477
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2000US-0239937
                                                                                        GENOME
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  the
and
                                                                                        SCI INC
 treating, preventing and/or prognosing colon and rectum including colorectal c detection e.g. diagnosis -
                                                                    SM;
           colorectal cancers
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e.g. diagnosis

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seq_name:
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US-08-973-363-6 x AAI57603
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    Quality:
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               une invention.
                                                                                                                                                                                                                                                                       Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antipreumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; pathological condition; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzhelmer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published not sequence.
                       used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        number of colorectal cancer antigens. These are shown in AAI57547-AAI57619 and AAM35569-AAM3641. These can be used diagnosis, prevention and treatment of cancer of the colon The present sequence is a colorectal cancer antigen coding
 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                   Isolated nucleic acid
                                                                                                        Rosen
                                                                                                                                                       13-MAY-1999;
                                                                                                                                                                              11-MAY-2000; 2000WO-US12788
                                                                                                                                                                                                      23-NOV-2000
                                                                                                                                                                                                                             WO200070042-A1
                                                                                                                                                                                                                                                                                                                                                                                             Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-2001
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                                                                                                                                (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGCAGCTACAGACCCGAGCGGATTACTTG
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                                                                                                                                                                                                                                                  sapiens.
                        in
                                                                      2000-679828/66.
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                                                           AAB56081
                       preventing,
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Page 858; 1065pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                             Ruben SM,
Florence KA,
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                                                                                                                                                                                                                                                                                                                                                                                           protein gene 5 SEQ ID
                                                                                                                                                       99US-0134068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA;
                       treating
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                       reating or
                                                                                                                                SCI INC
                                                                                             Moore PA, Y, Soppet DR;
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Percent Identity:
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                      encoding a hur ameliorating
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                       human secreted protein ing a medical condition
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ormat directly from WIPO
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seq_documentation_block:
ID AASS6223 standard; cDNA; 1973 BP.
XX
AC AASS6223;
XX
DE Human bone marrow tissue polynucleo
XX Human; bone marrow; central nervous
KW peripheral nervous system disorder;
KW lymphoid cell disorder; osteoarthri
KW periodontal disease; cerebrovascula
KW periodontal disease; cerebrovascula
KW hyperproliferative disorder; cognit
KW inflammatory disorder; tumour; colo
KW inflammatory disorder; tumour; colo
KW inflammatory disorder; tumour; colo
KW inflammatory tissue regeneration;
XX
PN W0200179447-A2.
XX
PD 25-OCT-2001.
XX
18-APR-2000; 2001W0-US12607.
XX
18-APR-2000; 2000US-0522929.
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US-08-973-363-6 x AAC99822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:AAS96223
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                            Human; bone marrow; central nervous system disorder; haematopolesis; ss; peripheral nervous system disorder; myeloid cell disorder; osteoporosis; lymphoid cell disorder; osteoparthritis; bone degenerative disorder; stepperiodontal disease; cerebrovascular disorder; viral infection; cancer; bacterial infection; fungal infection; autolimune disorder; pancreas; hyperproliferative disorder; cognitive disorder; depression; stomach; inflammatory disorder; tumour; colon; liver; bladder; prostate; kidney; ovary; brain; skin; bone; cartilage; tendon; ligament; nerve; tissue growth; tissue regeneration; wound; burn; incision; ulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow tissue polynucleotide #9.
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Gaps:
Identity:
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0
100.000
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seq_documentation_block:
ID AAA/1645 standard; DNA; 2(
XX
AC AAA/1645;

XY
DT 14-DEC-2000 (first entry)
XX
DE Human aspartate protease; neuror
XX
Aspartate protease; neuror
XX
Aspartate protease; psl 5
XX
Alzheimer's disease; psl 5
XX
PN WO200043505-A2.
XX
PN WO200043505-A2.
XX
PD 27-JUL-2000.
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Quality:
Ratio:
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US-08-973-363-6 x AAS96223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotides encoding bone marrow CC tissue polypeptides. The sequences of the invention can be used in the CC treatment of central nervous system disorders such as Parkinson's CC disease, Alzheimer's disease, Huntington's disorders and amyotrophic CC lateral sclerosis, peripheral nervous system disorders such as peripheral CC neuropathy, haematopoiesis, myeloid and lymphoid cell disorders, periodontal CC disease, cerebrovascular disorders such as stroke, viral infections, disease, cerebrovascular disorders such as stroke, viral infections, activities, bone degenerative disorders, periodontal CC disease, cerebrovascular infections, autoimmune disorders such as CC rheumatoid arthitis, multiple sclerosis, asthma and eczema, inflammatory CC disorders such as Crohn's disease and nephritis, hyperpoilferative CC disorders such as Crohn's disease and nephritis, hyperpoilferative CC covary, kidney, brain and skin). The sequences, depression and cancer (e.g. tumours of the stomach, colon, pancreas, liver, bladder, prostate, CC ovary, kidney, brain and skin). The sequences are also useful in bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration and healing of wounds, burns, incisions and ulcers. Sequences as assigned to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAS96223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1683 TCTAGGGATCTAGCAAAGCGAGAG 1706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polynucleotides encoding bone marrow tissue polypeptides, useful preventing, diagnosing and treating osteopathic diseases \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-OCT-2000; 2000US-0695783; 30-NOV-2000; 2000US-250583P; 26-JAN-2001; 2001US-0770160.
                                                                                                                                                Aspartate profease; neuroprofectant; nootropic; gamma-secretase activity; amyloid precursor profein; APP; beta-amyloid; cleavage; Notch; Irel; Alzheimer's disease; psl 5; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1973 BP; 604 A; 338 C; 352 G; 679 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerArgAspLeuAlaLysArgGlu 34
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT;
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seq_documentation_block:
ID AAK84450 standard;
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US-08-973-363-6 x AAA71645/rev
                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                            seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK84450
                                                                                                                                                                                                                                                                                           Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AAA71645
                                                                                                                                                                                                                                                                                                                                                                                                  amyloid precursor protein (APP) to beta-amyloid, and also in cleavage of other membrane proteins such as Notch (implicated in development of the nervous system). *Terminal signal peptides: C-terminal propeptides; generation of peptides for presentation in the context of major histocompatibility complex molecules, and cleavage of the endoplasmic reticulum stress sensor protein Irel. (1), also nucleic acid (II) that encodes it, and its inhibitors and antibodies (Ab) are used to treat or diagnose diseases that are associated with cleavage of amyloid precursor protein, especially Alzheimer's disease, aberrant breakdown of hydrophobic signal peptides, or accumulation of unfolded proteins in the endoplasmic reticulum. They can also be used to modify presentation of hydrophobic peptides by histocompatibility complex molecules, in cases of e.g. viral infection, cancer and transplant rejection. This sequence method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JAN-1999;
08-JUN-1999;
24-JUN-1999;
                                                                                                                                                                                      959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel protease (I) that has two aspartate residues in a catalytically active structure. The aspartate residues are present in motifs of formulae X_1GX_2GD and X_3X_4DX_5 both present in a transmembrane region. The products of the invention have neuroprotective and nootropic activity. (I) represent the previously unidentified gamma-secretase activity that is involved in conversion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 31-32; 32pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New protease that cleaves amyloid precursor protein, useful e.g. for treating Alzheimer's disease, and related nucleic acid, inhibitors and antibodies \,
             cytostatic; gene therapy; vaccine; metastasis;
                                                 Human
                                                                          07-NOV-2001
                                                                                                  AAK84450;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 2052 BP;
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                          Human; immune;
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99DE-1025946.
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                         haematopoietic; immune/haematopoietic antigen; cancer;
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PR 29-SEP-2000; 2000US-0235369.
PR 29-SEP-2000; 2000US-0237038.
PR 20-CCT-2000; 2000US-0249960.
PR 20-CCT-2000; 2000US-0241785.
PR 20-CCT-2000; 2000US-0241785.
PR 20-CCT-2000; 2000US-0241786.
PR 20-CCT-2000; 2000US-0241809.
PR 20-CCT-2000; 2000US-0241819.
PR 20-CCT-2000; 2000US-02441819.
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PR 20-CCT-2000; 2000US-02441819.
PR 20-CCT-2000; 2000US-0244677.
PR 20-CCT-2000; 2000US-0244652.
PR 20-CCT-2000; 2000US-024465.
PR 20-CCT-2000; 2000US-024465.
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XX
PI Rosen CA, Barash SC, Ruben SM;
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WPI; 2001-483426/52.
XX
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis.

Disclosure; SEQ ID NO 39262; 3071pp + Sequence Listing; English.
XX
PS Disclosure; SEQ ID NO 39262; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression by rectifying mutations or deletions in a patient's genome
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic related diseases, especially
CC concers and cancer metastases of haematopoietic antigen genomic
CC sequences from the present invention. AAK54921 to AAK8793 and AAW82169
CC represent sequences used in the exemplification of the present invention.
XX
Sequence 5271 BP; 1866 A; 897 C; 951 G; 1757 T; 0 other;
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gb_est1:BB155356
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gb_est1:AL601246
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-Q-/Gg72_1/USF90_spoi/USG08973563/runat_01082002_080123_19814/app_query.fasta_1.638
-Q-/Gg72_1/USF90_spoi/USG08973563/runat_01082002_080123_19814/app_query.fasta_1.638
-DB-EST -ORMT-fasta_ -SUFFIX-vol1p3n.rst -GAPOP=4.500
-GAPEXT-0.000 -MINMATH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-GGAPOXT-0.050 -MARATY-0.100 -YGAPOP=60.000 -YGAPEXT-60.000
-GGAPOP=4.500 -GGAPEXT-7.000 -YGAPOP=60.000 -YGAPEXT-60.000
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-01169
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-01169
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -TRR_SCORE-quality
-THR_MIN-1 -ALIGN-15 -MODE-LOCAL -OUTEMT-pfs -NORM-ext
-HEAPSIZE-500 -MINLEN-0 -MAXLEN-20000000
-USER-USG0873363_GCG11_1_2938 -NCPU-6 -ICPU-3 -LONGLOG
-USCR-USG073363_GCG11_12938 -NCPU-6 -ICPU-3 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -NO_XLPXY -WAIT -THREADS-1
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Carninci, P., Shibata, Y., Hayatsu, M. and Hayashizaki, Y., Nonco, P., Carninci, P., Shibata, Y., Hayatsu, M., Sugahara, Y., Shibata, K., Itoh Carninci, P., Shibata, Y., Hayatsu, M. and Hayashizaki, Y., Muramatsu, M. and Hayashizaki, Y., Muramatsu, M. and Hayashizaki, Y., Nuramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

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RIKEN Mouse ESTs (Arakawa, T., et al. 2001)

Unpublished (2001)

On Jun 29, 2000 this sequence ...

Contact: Yoshihia-...
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)
17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                         further details.

Further details.

Genome Exploration Research Grogenomic Sciences Center and Genome Science Laboratory is
Division of Experimental Animal Research in
                                                                                                                                                                                                                                                 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with suman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
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mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
(bases 1 to 619)
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6 | AW422113 fi57b02.y1 Sugano K
4 | BG994052 PMO-HT0913-125021-0
1 | BG999049 PMO-HT0913-250401-0
2 | AA427958 Zw50a01.r1 Soares_t
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alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-973-363-6 x BB155356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 100.000
                                                                                                                                                                                                                   ORGANISM
                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                489 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 539 CCGTGCAGACTACCTCATCAAACTACTTAGCAGAGATCTTGCAAAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 luAlaGlnArgLeuCysGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rArgAlaAspTyrLeuIleLysLeuLeuSerArgAspLeuAlaLysArgG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGCTCAGAGACTTTGTGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est1:BB461065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                            BB461065 RIKEN full-length enriched, 12 days embryo spinal ganglion Mus musculus cDNA clone D130070B13 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
                   Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 660)
Tagami, M.,
                                                                                                                                                                                                                                                                                       BB461065.2 GI:16426612
                                                                                                                                                                                                                                                                                                                BB461065
                                                                                                                                                                                                                                         house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB155356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGAGCCCCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from I
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/clone_lib="RIKEN full-length enriched, 16 days neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
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  Tagawa, A., Takahashi, F., Takeda, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611
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  Tanaka,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   588
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  Toya, T.,
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KEYWORDS SOURCE

alignment_scores:

Quality: Ratio:

41 0

VERSION. ACCESSION

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FEATURES
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ORIGIN
                                   BASE COUNT
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It,
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KOndo,S., Shinagawa,A., Salto,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Mouse ESTs
Unpublished (2001
On Jul 21, 2000 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Jul 21, 2000 this sequence version replaced gi:9356558
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki,Y
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                                211
                                                         was cleaved with BamHI and XhoI. Vector: a pBluescript KS(+) after bulk excision from
                                                                                                                                                             prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                  prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D130070B13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, 12 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: Sall; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="spinal ganglion"
/dev_stage="12 days embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contributed to
                                                                    modified
Lambda Fl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsuura
                                                                    FLC I.
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EST 07-MAR-2000

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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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US-08-973-363-6 x BB461065
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alignment_block:
US-08-973-363-6 x AL601246
                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                        BASE COUNT
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LOCUS AL601246
                                                                                        Quality: 32.00
Ratio: 1.000
Percent_Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGCTCAGAGACTTTGTGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5 sequence of the Clone insert
Clone from 5. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemannédkfz-heidelberg.de;
sequenced by GBF (Mational Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL601246 430 bp mRNA linear EST 14-AUG-2001 DK72p313J1040_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone DK72p313J1040_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No sl sequence available.

This clone (DKF2p31371040) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Bloecker H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
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                                                                                                                                                                                                                                                                                                                            /clone="DKFZp3131040"

/clone=lb="313 (synonym: hlcc2)"

/dev_stage="adult"

/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                    Length: 32
Gaps: 0
Percent Identity: 100.000
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US-08-973-363-6 x AI890775/rev
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LOCUS AI890775
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378 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 329
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                                1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

C1 (bases 1 to 547)

RS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Tumor Gene Index

AL Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: Cgapbs-Temail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1924 Std Error: 0.00

Seq primer: -400F from Gibco

High quality sequence stop: 418.

Location/Qualifiers

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similar to SW:CHD1_HUMAN 014646
PROTEIN 1 ;, mRNA sequence.
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AI890775.1 GI:5595939
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sapiens cDNA clone IMAGE:2443725 3'
546 CHROMODOMAIN-HELICASE-DNA-BINDING
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alignment_scores:
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LOCUS AU125712
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                             TATGAlaASPTYTLeuIleLySLeuLeuSerArgAspLeuAlaLys 32
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AU125712
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HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
 601436060F1 NIH_MGC_72 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genomicselri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing:
Research Institute; cDNA library construction: Department
Virology, Institute of Medical Science, University of Toky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics Lawring institute
Helix Research Institute
Time Venez. Kisarazu, Chiba
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1 (bases 1 to 866)
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                   BE89513
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Location/Qualifiers
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Tel: 81-438-52-3951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito, K., Yamamoto, J., Naki, Y., Sugano, S., Isogai, T.)
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                                                                                                                                                                                                                                                               AU125712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pME18SFL3; mRNA from uninduced
precursor cells"
a 149 c 196 g 207 t 2 others
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/clone_lib="NT2RM4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="teratocarcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
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nRNA linear EST 20-OCT-2000 CDNA clone IMAGE:3921087 5',
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US-08-973-363-6 x BE895133
                                                  REFERENCE
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                                                                                                                                                                                                             mRNA sequence.
BF239967
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1 (bases 1 to 1028)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                        601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129
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BE895133
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 821)
                                                                                                                  Homo sapiens
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Plate: LLAM9753 row: h column: 16
High quality sequence stop: 488.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
Technologies."
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Percent Identity:
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US-08-973-363-6 x BF239967
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Ratio: 1.000
Percent Similarity: 100.000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
1. (bases 1 to 593)
Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
Sanger Centre
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plate: LLCM1033 row: k column: 18
High quality sequence stop: 562.
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                    western clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                   AL659353.1 GI:17672995
                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345
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//Clone_lib="NIH_MCC_54"
//Clone_lib="NIH_MCC_54"
//Lissue_type="from Chronic myelogenous leukemia"
//Lab_host="DH10B (T1 phage-resistant)"
//note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
//note="Organ: bone marrow; Vector: pDNR-LIB (Clontech
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/db_xref="taxon:9606"
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Gaps: 0
Percent Identity: 100.000
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TNeu045e20 5',
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                           source
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Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
                                                                                                                                                  Sequencing primer: PlC
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                   Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_ESQUENCE_ID: L1E1d12.plc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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EST.
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
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/clone_lib="XGC-neurula"
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/lab_host="scherischia coli DH10B"
/note="Vector: pCS107; Site_1; EcoRI; Site_2; NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end."

a 134 c 114 g 226 t
/organism="Silurana tropicalis"
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/clone="L1E1d12"
                                                                                               Location/Qualifiers
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Gaps: 0
Percent Identity: 100.000
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US-08-973-363-6 x AL644594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   686 bp QV3-BN0047-150400-152-c03 BN0047 AW997058
                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150 400-152-c03&t3=2000-04-15&t4=1)
Seq_primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                             Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simpson, A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Fammmalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                   Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                    quality sequence start: 19 quality sequence stop: 678 Location/Qualifiers
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was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
a 125 c 156 g 141 t 1 others
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0047"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTTAGTAGAGATCTTGCAAAAAGA
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I (bases 1 to 337)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Nagai,M.A., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Jongeneel,C.V., O'Hare Brunstein,A., deOliveira,P.S., Bubher,P., Jongeneel,C.V., O'Hare M.T. Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QV3-BN0047-230200-102-d03 BN0047 Homo sapiens cDNA, AW996787
                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed sequence tags % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simpson, A.J.
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                                                                                                                                                                                                                                                            Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                    (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-23&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                            quality sequence start: 2 quality sequence stop: 337. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue mRNA and cDNA amplification were performed under low stringency conditions." 154\ c \qquad 126\ g \qquad 241\ t
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="BN0047" /dev_stage="Adult"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 rArgAlaAspTyrLeuIle 23
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Email: genome-reseges.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci,P., Shibata,Y., Hayatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 438)

1 (bases 1 to 438)

1 (bases 1 to 438)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Ug-MC(B) CDNA Mus musculus CDNA clone G930013K04 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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Gaps: 0
Percent Identity: 100.000
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    FEATURES

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VERSION
KEYWORDS
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                               TITLE
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BB834922 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) cDNA Mus musculus cDNA clone G930033J21 3', mRNA
                                                                                                                                                                                                                                    1 (bases 1 to 446)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Imotani, K., Ishii Hayatsu, N., Hiramoto, K., Hiraoka, T., Konno, H., Kouda, M., Matsuyama, T., Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kodada, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Salto, R., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB834922.1 GI:17013165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse
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/clone_lib="RIKEN full-length enriched, mammary gland
/close_527 Jyg-MC(B) cDNA*
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
g6 c 108 g 96 t
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/db_xref="taxon:10090"
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alignment_block:
US-08-973-363-6 x BB834922
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ORGANISM
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                                                                                                                                                                                                               VERSION
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    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCCAAACAGTTACAGAC 358
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AL286261
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URL:http://genome.gsc.riken.go.jp,
Carninci.p. Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                              CNS04DVG 856 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 103K08 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                       AL286261.1 GI:8024707
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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RIKEN integrated sequence analysis (RISA) system--384-format
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Fax: 81-45-503-9216
1 (bases 1 to 856)
Roest-Crollius, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e mouse tissues.
                                             Tetraodontidae;
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/clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) CDNA"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
a 99 c 108 g 100 t
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/db_xref="taxon:10090"
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                                      Tetraodon.
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  Jaillon, O.,
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  Dasilva,C.,
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Fizames, C., Fisher, C
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SOURCE
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LOCUS BF881342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est2:BF881342
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US-08-973-363-6 x CNS04DVG/rev
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TITLE
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                                                                                                                  Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovigenome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                         BF881342 129 bp PM0-ET0208-031200-001-f12 ET0208
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Proc. Natl. A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius, H., Jaillon, O., Dasilva, C., Boundernot, A., Fizames, C., Wincker, P., Brottler, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the confreshwater pufferfish Tetraodon nigroviridis
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Weissenbach,J.
                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                     Simpson, A.J.
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                               Homo sapiens
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Contact: Simpson A.J.G.
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Lubbratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rus Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2707001
Email: asinpsonelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-PMO&t2-FMO-ET0208-
031200-001-f12&t3-2000-12-03&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 22
High quality sequence start: 22

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gb_pat:A58691
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Query: US-08-973-363-7
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183658 | AC013394 Homo sapiens chromos

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2754 | AF181827 Nymphicus hollandicus

2754 | AF181828 Nymphicus hollandicus

2754 | AF181828 Nymphicus hollandicus

2754 | AF181826 Gallus gallus chromos

252 | AR044113 Sequence 5 from patent

649 | G51024 SHGC-80650 Human Homo sa

3315 | U69109 Rattus norvegicus calci
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101220 | AC022372 Homo Sapiens Chromd
134365 | AC012624 Homo Sapiens Chromd
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21921 | D14316 Geltar-Crystallin enhanc
1311 | AR023026 Sequence 3 from paten
153 | AS6633 Sequence 2 from Patent W
348 | AF066702 Struthio Camelus Clone
1320 | D14316 Geltar-Crystallin enhanc
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I A58685 Sequence 4 from Patent
I A58686 Sequence 5 from Patent
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A58691 Sequence 10 from Patent
AF004397 Gallus gallus chromo-
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AUTHORS
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SOURCE
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                              6608 bp
Sequence 10 from Patent WO9639505.
A58691 A58691.1 GI:3714250
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Sequence 15 from Patent W09639505.
A58696
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Griffiths, R. and Tiw.
             Patent: WO 9639505-A 10 12-DEC-1996; ISIS INNOVATION (GB)
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/db_xref="taxon:32644"
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1188 TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG 1237
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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Gaps: 0
Percent Identity: 100.000
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I AR058775 Sequence 2 from pa
U33284 Human protein tyrosi
AF063890 Rattus norvegicus
Seposta related adhesion foc
U45854 Rattus norvegicus mR
L49207 Homo sapiens (clone
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VERSION
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US-08-973-363-7 x A58691
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LOCUS AF004397
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Ratio: 1.000
Percent Similarity: 100.000
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TITLE
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Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked
Gene 197 (1-2), 225-229 (1997)
97473516
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AF004397.1
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6872 bp mRNA linear VRT 08-OC' Gallus gallus chromo-helicase-DNA-binding on the Z chromosome protein, variant with hydrophilic domain, (CHD-Z) mRNA, comple
                                                                                                                                                                                                                                                                                        Glasgow
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Griffiths, R. and Korn, R.M.
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                                                                                                                                                                                                                                                                                                            Submitted
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Location/Qualifiers
                                                                                                                                                                                                                                                                                        ed (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, G12 8QQ, UK
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/db_xref="taxon:32644"
1207 c 1459 g 165
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SQSGSSDSESGSESGSQSESESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
                                                                                                                  /function="role in chromatin archite/note="CHD protein with hydrophilic
                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                   /product="chromo-helicase-DNA-binding
                                                                                                                                                                                                                       /organism="Gallus gallus"
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                                                                                                  codon_start=1
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Sequence 3 from Patent W09639505
A58884
1 (bases 1 to 153)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
                                                                                                    unidentified unclassified
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ERGNRYLIFSOMVRMLDILAFYLKYROPPFORLDGSIKGELKROALDHENAEGSEDFC
FLLSTRAGGLGINLASADTVVIFDSDMNPQNDLQAQARAHRIGOKKQVNIYRLVTKGS
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LFKEPEGEEQEPQEMDIDEILKRAETRENEPGPLTVGDELLSOFKVANFSNMDEDDIE
LEPERNSRNWEEIIPESQRRIEEEERQKELEEIYMLDRANKCGISRGSRSR
SRRYSGSDSSITERKREPKKRGRPFTIPRENIKTKGFSDAEITRRFIKSYKKFGGPLERLO
AVARDAELVDKSETDLRRLGELVHNGCIKALKNNSSGOERAGGRLGKVKGPTFRISGV
OVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSNLLVGI
OVNAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSNLLVGI
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RLAGAQNSKRKTRNKKNKMKASKIKEIKKSDSPQ-SSKSDEDDEEEDNKDEIYSYK
RLAGAQNSKRKTRNKKNKMKASKIKEIKKSKSPG-SSKSDEDBEEDNKDLIKSYK
HLHKKIKTERENEDEKREPDIGIKKAABEKRETKEKENNRELKREKKEKEDKELFEDY
LISE
NKEKRENKYKESTQKEREVKEERVNEMKSENKEKSKKIPLLDTPVHITATSEPVPISE
ESEELHQKTPSVCKERMRPVKAALKQLDRPEKGLSERFQLEHTRQCLLKIGDHTTECL
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MIRTHEWMHPQTKRLKFNILLTTYEILLKDKSFLGGLWAF GYDEAHRLKNDOSLLY
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LHKELEPFLLRRYKKDVEKSLPAKVEQILRMEMSALQKQYYKWILTRNYKALSKGSKG
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SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
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CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
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DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
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VERSION KEYWORDS

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SOURCE

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US-08-973-363-7 x A58685
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ACCESSION
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                                                       Align seg 1/1 to: A58685 from: 1 to: 153
                                                                                                                               Quality: 34.00 Length: 34 Ratio: 1.000 Ratio: 1.000 Percent Similarity: 100.000 Percent Identity: 100.000
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Quality:
Ratio:
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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A58685
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/db_xref="taxon:32644"
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US-08-973-363-7 x A58686
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Ratio:
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                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Rodentia; Sciurognath1; Muridae; Murinae; Mus. 1 (bases 1 to 5349)

Delmas, V., Stokes, D.G. and Perry, R.P. A mammalian DNR-binding protein that contains a chromodomain and an SNF2/SWIZ-1ike helicase domain Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                         Mus musculus
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Perry, R.P.
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TITLE

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US-08-973-363-7 x MUSCHD1X
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ORIGIN
      seq_documentation_block:
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Ratio: 1.000
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                                                                                                                                                            CCGTGCAGACTACCTCATCAAACTACTT 4103
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01 Burholme Avenue, Philadelphia, PA 19111, USA
01 Burholme 16, 1994 this sequence version replaced gi:293322.
Location/Qualifiers
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GSTSGFLNIMMELKKCCNHCYLIKPPDNNEFYNKQEALQHLIRSSGKLILLDKLLIRL
RERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGSEDF
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GKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQRELQTWASGMNAVVYLGDINSR
NMIRTHEMMHPQTKRLKFRILLTTYEILLKDKAFLGGLWAFIGVDEAHEKKNDDSLL
YKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYA
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QYHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHREWDHYRQDSRYYSDREKHRKLDD
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QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK
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DAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSGTERAGGRLGKVKGPTFRISG
VQVNAKLVIAHEDELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLLIG
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SDSESEEERDKSSCDGTESDYEPKNKVRSRKPQNRSKSKNGKKILGQKKRQIDSSEDE
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/protein_id="AAB08486.1"
/db_xref="GI:455015"
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/db_xref="taxon:10090"
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Noodage, T., Basrai, M.A., Basevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins

Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SOGGSSDSDGSEGGSOSESESDTSRENKVOAKPFKVDGAEFWKSSPSILAVORSAIL
KKQQQQQQQQAGASSNSGSEEDSSSSEDDSSSEVKRKKHKDEDWQMSGSGSPSOS
GSDSSEEEREKSSCDETESDYEFKNKKKSKFKONRSKILIQKKRQIDSSEE
DDDEEDYDNDKRSSRRQATVRVSYKEDEEMKTDSDDLLEVCGEDVPQPEEEEFFT IER
FMDCRIGRKGATGATTTIVAVEADGDPNAGFEKNKEPGEIQYLIKMKGWSHIHNTWET
EETLKQQNVROMKKLDNYKKKDQETKRRLKNASPEDVETYNCQOELTDDLHKQYQIVG
RIIAHSNQKSAAGYPDYYCKWQGLFYSECSWEDGALISKFQACIDEYFSRNQSKTP
FKDCKYLKORPRFVALKKQPSYIGGHEGLELDDYQLMGLAWLAHSWCKGNSCILADEM
GLGKTIQTISFLNYLEHHENQLYGFFLLVVELSTLTSWQREIQTWASQMNAVYLGDIN
SRNMIRTHENTHHOTKRLKFNILLTTYEILLKDKAFIGGKHAMAFIGVEBAHRLKNDDS
LLYKTLIDFKANRKLKGCNICYLIKPPDNNEEFYNKOBALGKQYYKWILTTNYKALSKG
YASLHKELDFPLLRYWKDVERSLPAKVEQILEMEMSALGKQYYKWILTTNYKALSKG
SKSSTSGFLNIMMELKKCCNICYLIKPPDNNEEFYNKOBALGKQTYKWILTDNKLLI
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AEELFKEPEGEEQEPOEMDIDEILKRAETHENEPGPLTVGDELLSQFKVANESNNDED
DIELEPERNSKNWEEIIPEDQRRKLEEDEEROKELEEIYMLPRMRNCAKQISFNGSEGR
RSRSRRYSGSDSDSISEGKRPKKRGRPRTIPREMIKGFSDAEIRRFIKSYKKFGGPLE
RLDAIARDAELVDKSETDLRRLGELVHNGCIKALKDSSSGTERTGGRLGKVKGPTFRI
                                                                                                                                                                 RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWQMDH
RASSSGPRSPLDQRSYGSRSPFEHSVEHKSTPEHTWSSRKT"
                                                                                                                                                                                                                                                                                                   ERSKKSSYSDAPVHITASGEPVPISEESEELDQKTFSICKERMRPVKAALKQLDRPEK
GLSEREQLEHTRQCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKFTEFDARKLH
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DFCFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVT
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164. .5293
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                                                                                                                                                                                                                                                                        KLYKHAIKKRQESQQNSDQNSNLNPHVIRNPDVERLKENTNHDDSSRDSYSSDRHLTQ
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/db_xref="GI:2645429"
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/product="CHD1"
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1. .5947
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/db_xref="taxon:9606"
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alignment_block:

Percent Similarity: 100.000

Percent Identity:

100.000 26 0

Quality:

26.00 1.000

Ratio:

365 bp DNA linear PRI 21-JUL-clone CTD-2082I17, complete sequence

PRI 21-JUL-2001

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alignment_block:
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ORIGIN
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LOCUS AC092372
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                            Align seg 1/1 to reverse of: AC092372 from: 1 to: 101220
                                                                                                                                                                                         US-08-973-363-7 x AC092372/rev
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                                            4075 CCGTGCAGACTACCTCATCAAATTACTT 4102
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17 rArgAlaAspTyrLeuIleLysLeuLeu 26
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-shgc.stanford.edu
www-shgc.stanford.edu
quality: Phrap Quality >=40 100% of Sequence;
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
Location/Qualifiers
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases 1 to 101220)
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-58M12"
34122 a 18862 c 17827 g 30409 t
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/db_xref="taxon:9606"
/chromosome="5"
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Gaps:
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                                            ACCESSION
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AUTHORS
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US-08-973-363-7 x AC012624
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ORIGIN
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LOCUS AC021449
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LOCUS AC012624
DEFINITION Homo sapiens
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                                                                                                                     DEFINITION
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                                                                                                                                                                                                                                                                                                         17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.

1. 134365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134365 bp
Homo sapiens chromosome 5 clone
AC012624
AC012624.6 GI:14993679
HTG.
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
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1 (bases 1 to 134365)
                                                                                                             ACU21449 143079 bp
Homo sapiens clone RP11-58M12, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (bases 1 to 134365)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 134365)
DOE Joint Genome Institute.
human.
                   HTG; HTGS_PHASE1; HTGS_DRAFT
                                          AC021449
AC021449.3 GI:10047806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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1.000
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/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="CTD-2082I17"
24497 c 25503 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 100.000
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JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS TITLE

SOURCE

KEYWORDS VERSION

ACCESSION

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

JOURNAL

FEATURES

P DNA linear HTG 10-SEP-2000 WORKING DRAFT SEQUENCE, 10 unordered

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COMMENT
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Choepelly, Colangelo, Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
Pierre, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 143079)
Birren,B., Linton,L., Nusbaum,C.
Homo sapiens, clone RP11-58M12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                 be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 143079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L5154
Center clone name: 58_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                    51931
                                                                                                                                                                                                40512
                                                                                                                                                                                                                                        1 38820: contig of 38820 bp in length
38821 38920: gap of 100 bp
38921 40411: contig of 1491 bp in length
                                                                                                                                                                                                                       40412 40511:
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                                                                        51831 51930:
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62719: gap of
75408: contig
                                                                                                                                       43279: contig of 2768 bp in length 379: gap of 100 bp
005: gap of 100 bp 51830: contig of 4825 bp in length 930: gap of 100 bp 62619: contig of 10689 bp in length 719: gap of 100 bp 75408: contig of 12689 bp in length
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ORIGIN
  REFERENCE
AUTHORS
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US-08-973-363-7 x AC021449
                                                                                                                                                                  ACCESSION
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                                                                                                                   SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                          CCGTGCAGACTACCTCATCAAATTACTT 116224
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                                                                                                                                                                                                                                           Homo sapiens chromosome 5 clone
                                                                                                 Homo sapiens
                                                                                                                                              HTG; HTGS_PHASE2;
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                                                                                                                                                                  AC008531.3 GI:12830078
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92617 1064
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92617. .106409
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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26246 c 26678 g
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116147 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 116196
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 145659)
DOE Joint Genome Institute.
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106410 106509: gap of 100 bp
106510 143079: contig of 36570 bp in length.
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REFERENCE
AUTHORS
TITLE
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US-08-973-363-7 x AC008531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                   Quality: 26.00
Ratio: 1.00
Percent Similarity: 100.000
                                                                                                                                                                                           Align seg 1/1 to: AC008531 from: 1 to: 145659
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                                                              source
17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 139128 bases at least 040
Consensus quality: 142556 bases at least 020
Consensus quality: 142744 bases at least 020
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in 020 bases; sum-of-contigs estimation
Quality coverage: 6.4 in 020 bases; sum-of-contigs estimation.
NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
fit he gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * the accession number will be preserved.

1 56174: contig of 56174 bp in length

56175 56273: gap of unknown length

56275 100874: contig of 44600 bp in length

100875 113127: contig of 44600 bp in length

110975 113127: contig of 12153 bp in length

113128 11327: gap of unknown length

113128 11329: gap of unknown length

113128 118190: contig of 463 bp in length

118191 118290: gap of unknown length

118191 11949: gap of unknown length

119695 119794: gap of unknown length

119795 123297: contig of 303 bp in length

123298 123397: gap of unknown length

123298 123397: gap of unknown length

123398 145659: contig of 32262 bp in length.
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Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing of Human Chromosome 5 Unpublished
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DOE Joint Genome Institute.
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/clone_lib="CalTech human BAC library C"
a 26309 c 27580 g 48609 t 600 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                   Length: 26
Gaps: 0
Percent Identity: 100.000
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AUTHORS
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AUTHORS
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LOCUS AC091946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 157767 bases at least Q40 consensus quality: 180259 bases at least Q30 consensus quality: 180259 bases at least Q30 consensus quality: 184175 bases at least Q30 consensus quality: 184175 bases at least Q30 consensus quality coverage: 204590; agarose-fp estimation guality coverage: 5.38 in Q20 bases; agarose-fp estimation quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the places is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Direct Submission
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Submission
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Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING
PROGRESS ***, 33 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence 
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Joint Ge
Center Code: JGI
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19346)
DOE Joint Genome Institute.
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AC091946.1 GI:14333882
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Unpublished
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Joint Genome Institute.
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: Joint Genome Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1358: contig of 1358 bp in length 1458: gap of unknown length 2667: contig of 1209 bp in length 2767: gap of unknown length 3823: contig of 1056 bp in length 1956 bp in length
                                                   3: gap of unknown length
0: contig of 1997 bp (1997 bp)
4: contig of 1474 bp in length
4: contig of 1474 bp in length
6: gap of unknown length
6: contig of 1502 bp in length
6: contig of 1504 bp in length
0: contig of 1564 bp in length
0: contig of 1564 bp in length
0: contig of 2100 bp in length
0: contig of 2100 bp in length
0: contig of 2100 bp in length
1: contig of 2101 bp in length
1: contig of 2051 bp in length
1: contig of 2051 bp in length
1: contig of 1570 bp in length
                                    length
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alignment_scores:
Quality:
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seq_name:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                           1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                        rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                          ATTCTTCCAGATGATCCCGATAAAAAAACCACAAGCAAAACAGTTGCAGAC
                                     CCGTGCAGACTACCTCATCAAATTACTT
 gb_pr:AC026778
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/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-36012"
/clone_lib="RPCI human BAC library 11"
35252 c 37061 g 60360 t 3202 others
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79895: gap of 1
79895: gap of 1
87511: contig 6
87511: gap of 1
92791: contig 9
2791: contig 9
102794: contig 1
102794: contig 1
102894: gap of 1
11066: contig 0
111966: gap of 1
117571: gap of 1
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193446: contig
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57359:
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ig of 5514 bp in length
if unknown length
ig of 10422 bp in length
ig of 6151 bp in length
ig of 6151 bp in length
if unknown length
ig of 7616 bp in length
ig of 5180 bp in length
ig of 5180 bp in length
ig of 903 bp in length
if unknown length
ig of 9972 bp in length
ig of 6605 bp in length
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f unknown length
g of 10861 bp in
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g of 27465 bp in
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of 24237
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of 4813
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of 3324
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Gaps:
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DEFINITION
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AUTHORS
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AUTHORS
                                                                                    seq_documentation_block:
LOCUS AC022121
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US-08-973-363-7 x AC026778/rev
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Quality:
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ORIGIN
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SOURCE
                                               ACCESSION
                                                                                                                                      seq_name: gb_pr:AC022121
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LOCUS AC026778
                                                                     DEFINITION
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                                                                                                                                                                                                                                                 29732 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAAACAGTTGCAGAC
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                                                                                                                                                                                               17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                                                                                                                                                                                   1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
                                                                                                                                                                            CCGTGCAGACTACCTCATCAAATTACTT 29655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.9% of Sequence; Estimated Total Number of Errors is 0.2.
STS Content:
WI-13675 G23101
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Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 195433)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone CTC-428II1, complete sequence.
AC026778
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                                                 AC02212
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SHGC-103595 G57841.
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Mammalia; Eutheria; Primates; C
1 (bases 1 to 195433)
DOE Joint Genome Institute and
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                                                                    Homo sapiens chromosome 5
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ORGANISM

Homo sapiens

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AUTHORS
TITLE
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89400 CCGTGCAGACTACCTCATCAAATTACTT 89373
                                                                                         source
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Direct Submission

Dive, Walnut Creek, CA 94598, USA

CE 4 (bases 1 to 219258)

DDE Joint Genome Institute, 2800 Mitchell

RS DDE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

AL Submitted (30-AUG-2001) DDE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

On Aug 30, 2001 this sequence version replaced gi:15148108.

Draft Sequence Produced by DDE Joint Genome Institute

WWW-391.doe.gov

Finishing Completed at Stanford Human Genome Center

WWW-stanford.edu

Ouality: Phrap Quality >-40 99.8% of Sequence;

Estimated Total Number of Errors is 0.4.

STS Content:

WI-5811 G04974

WI-1875 G23101
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71954 a 42062 c 40933 g 64309 t
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Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 (bases 1 to 21928)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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Database sequences: 1736436
Database length: 858457221
Search time (sec): 521.050000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60.000
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Query: US-08-973-363-7
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Length: 41
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AC AAR42754;
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DT 12-MAR-1997 (first entry)
XY
DT 12-MAR-1997 (first entry)
XX
Chicken CHD-W gene (partial sequenc XX
Bird; sex determination; chromodoma XX
CHD-W; chromodomain-Helicase-DNA bin XX
OS Gallus sp.
XX
WO9639505-A1.
XX
VO5-JUN-1996; 96W0-GB01341.
XX
VO5-JUN-1996; 95GB-0011439.
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VO5-JUN-1995; 95GB-0011439.
XX
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VOS-JUN-1996; 95W0-GB01341.
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VOS-JUN-1996; 95GB-0011439.
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VOS-JUN-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken CHD-W gene (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.00 124.19
7.00 124.14
7.00 123.24
7.00 123.06
7.00 122.50
7.00 122.00
7.00 121.84
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144
165
165
178
178
189
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alignment_scores:
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ID AAT42751 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name:
                                                                                         alignment_block:
US-08-973-363-7 x AAT42751
                                                                                                                                   Quality: 41.00
Ratio: 1.000
Percent Similarity: 100.000
                                                            Align seg 1/1 to: AAT42751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1188
   4080
                                                                                                                                                                                                                                                      The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD^-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicken CHD-1A gene
                                                                                                                                                                                                                                 Sequence 6608
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT42751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
              1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
ATTTTACCTGATGATCCAGACAAGAAACCCCCAGGCAAAGCAGCTACAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCACAGAGACTTGCTGGTGCA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromodomain-helicase-DNA binding genes determine sex - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gp
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 5; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                 BP; 2289 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tiwari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 228..5390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA; 6608
                                                            from:
                                                                                                                                                                                                                                 1207 C;
                                                                                                                                       Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                      Identity:
                                                            to: 6608
                                                                                                                                                                                                                                 1459 G; 1653 T; 0 other;
                                                                                                                                    41
0
100.000
4129
                              17
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seq_documentation_block:
ID AAT42757 standard; DN
AC AAT42757;

AC AAT4275;

AC AAT42757;

AC AAT427
alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4180
                                                                                                                                                              Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW01476-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bird; sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chick CHD-1A gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGCACAAAGGCTTGCTGGTGCA 4202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tiwari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
                                                                                                        58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA; 153 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SS
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alignment_block: $US-08-973-363-7 \times AAT42757$

Percent Similarity:

Quality: Ratio:

34.00 1.000 100.000

Length: Gaps: Percent Identity:

34 0 100.000

Align seg 1/1

to:

AAT42757

from: 1

to: 153

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seq_documentation_block:
ID AAT42758;
XX
AAT42758;
XX
AC AAT42758;
XX
AC AAT42758;
XX
Chick CHD-W gene fragment.
XX
Bird; sex determination; chromodo KW CHD-lA; CHD-W; W chromosome; ss.
XX
Gallus sp.
XX
Gallus sp.
XX
Key
FH Key
FT misc_difference 52.81
FT //note= "bases 52-
FT //note= True 
                                        alignment_scores:
Quality:
Ratio:
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Quality: 34.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                           Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                     Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW8146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers misc_difference 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 CA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 ATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAAAGGCTTGCTGGTG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 la 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 sLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGlyA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "bases 52-81 are a repeat of bases 22-51
and are ignored in the translated amino
acid sequence given in Fig 3"
             Percent Identity: 100.000
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seq_documentation_block:
ID AAT42759 standard; DNA; 153 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:AAT42759
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US-08-973-363-7 x AAT42758
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                            Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-14 (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Great tit CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 CA 153
Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                           Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                         birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                        Avian chromodomain·helicase-DNA binding genes determine sex in
                                                                                                                                                                                                                                                           P-PSDB; AAW08149
                                                                                                                                                                                                                                                                           WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                       12-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parus major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHD-1A; CHD-W; W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 ATTACTGAATAAAGACCTTGCAAGAAAGGAAGCACAGAGACTTGCTGGTG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 la 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 sLeuLeuAsnLysAspLeuAlaArgLysGluAlaGlnArgLeuAlaGlyA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 AAGAAACCCCAGGCTAAGCAGTTACAGACCCGTGCAGATTACCTCATTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                           Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                         95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                       96WO-GB01341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
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alignment_scores:

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alignment_block:
US-08-973-363-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAT42759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _documentation_block:
AAV59280 standard;
                                                          The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor of dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis,
                                                                                                                                                                                                                 Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, used to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Altered telomere repeat binding factor 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-DEC-1998
tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g. for expression of recombinant proteins or where intended for subsequentransplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                                                                                                                                                       Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-AUG-1998
                                                                                                                                                                                    Claim 14; Page 110-111; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9836066-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
                                                                                                                                                                                                                                                                                                                                                                     (UYRQ ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 sLeuLeuAsnLysAspLeuAlaArgLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTACTGAATAAAGACCTTGCAAGAAAAGAA 132
                                                                                                                                                                                                                                                                                                            1998-480769/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x AAT42759
                                                                                                                                                                                                                                                                                                                                       De Lange
                                                                                                                                                                                                                                                                                                                                                                     ROCKEFELLER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  98US-0018628.
97US-0800264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..1311
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                                                                                                                                                                                                                                                                                                                                         Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A-TRF"
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Identity:
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                 intended for subsequent
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alignment_block: US-08-973-363-7 \times AAV59280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-IA (see also AAT42751) and CHD-W (see also AAT42753) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                                                                                             Griffiths R,
                                                                                                                                                                                                                                                                                                                                     WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bird; sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse CHD-1 gene (bases 3855-977).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1311 BP; 441 A;
                                                                                                                Claim
                                                                                                                                                                                       WPI; 1997-043127/04.
                                                                                                                                                                                                                                    (ISIS-) ISIS
                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                     05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHD-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT42756 standard; DNA; 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGTGCAGACTACCTCATCAAACTA 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42756
                                                                                                               8;
                                                                                                                                       chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHD-W; W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                           AAW08146
                                                                                                               Fig 3; 76pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                           "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
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progeny.

Sequence 153 BP; 61 A; 37

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27 G;

28 T; 0 other;

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seq_documentation_block:
ID ABL06443 standard; cDNA; 6240 BP
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US-08-973-363-7 x AAT42756
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Percent Similarity: 100.000
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                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL10175) and the encoded proteins (ABL01847-ABL10175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 ACTACTT 108
         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811
                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                       Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231.
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                                                                                                                                                                                                                                                       interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 sLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 AAAAAACCACAAGCAAAACAGTTACAGACCCGTGCAGACTACCTCATCAA 101
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                                                                                                                                                                                                                                                                                                                                                                       Adams M,
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2000US-0614150
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18

alignment_scores:

Quality: Ratio:

11.00 1.000

Length:

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seq_documentation_block:
ID ABL06442 standard; cDNA; 9933 BP.
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US-08-973-363-7 x ABL06443
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ0511), expressed DNA sequences (ABLJ0851), expressed DNA sequences (ABLJ0840-ABLJ6175) and the encoded proteins
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  Sequence 9933 BP;
                                                   (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
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11-JUL-2000; 2000US-0614150.
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                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PEKE ) PE CORP NY.
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  2711 A; 2468 C; 2538 G; 2216
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Gaps: 0
Percent Identity: 100.000
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0 other;
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alignment_block:
US-08-973-363-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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        2000US-0189874
2000US-0199874
2000US-0298123
2000US-0299467
2000US-0209467
2000US-02114886
2000US-0211487
2000US-0211487
2000US-0211487
2000US-0214519
2000US-0214519
2000US-0224519
2000US-02252513
2000US-0225268
2000US-0225268
2000US-0225268
2000US-0225758
2000US-0225788
2000US-0225788
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2000US-0184664.
2000US-0186350.
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   Human colorectal cancer antigen cDNA SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 421 BP; 148 A; 78 C; 127 G; 61 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschisprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive nuclear confirmation of the present sequence is a cDNA encoding a digestive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1198; 986pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases - \frac{1}{2}
                                                                                                                                                                   146 AAGCAGCTACAGACCCGAGCGGATTACTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                               system antigen of the invention.
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                                                                                                                                                                                     13 LysGlnLeuGlnThrArgAlaAspTyrLeu 22
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   Homo sapiens.
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PR 29 - SEP - 2000; 2000(S-02376).

PR 20 - CCT - 2000; 2000(S-02376).

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PR 29 - CCT - 2000; 2000(S-02376).

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PR 20 - CCT - 2000; 2000(S-02376).

PR 21 - CCT - 2000; 2000
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OS Homo sapiens.
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PPN US5817479-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-973-363-7 x AAI57603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 200
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding seque number of colorectal cancer antigens. These are shown in AAI37547-AAI57619 and AAM38569-AAM38641. These can be used diagnosis, prevention and treatment of cancer of the colon The present sequence is a colorectal cancer antigen coding the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptide for treating, preventing and/ or disorders related to the colon and rectum including co and also for testing and detection e.g. diagnosis -
                                                                                                                                                                                                                                                                                                       Protein kinase; cell signalling; inflammation; carcinoma; diabetes;
human X-linked agammaglobulinaemia; nonspherocytic haemolytic anaemia;
artherosclerosis; glioma; restenosis; cholera-based septic shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                        (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LysGlnLeuGlnThrArgAlaAspTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCAGCTACAGACCCGAGCGGATTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-457727/49.
DB; AAM38625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:AAV33521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                        Bandman
                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI57603
                                                                                                         96US-0700575.
                                                                                                                                               96US-0700575
                                                                                                                                                                                                                                                                                        tyr kinase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
                                                                                                                                                                                                                                                                                                                                                                            fragment encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67; 522pp + Sequence Listing; English
                                        Ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
                                         Hawkins PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 10
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to:
                                                                                                                                                                                                                                                                                                                                                                            a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
                                         Wilde CG;
                                                                                                                                                                                                                                                                                                                                                                            protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prognosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d in the n and/or rectum. g sequence of
                                                                                                                                                                                                                                                                                                                                                                            homolog.
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seq_documentation_block:
ID ABA61903 standard; DNA; 544 BP.
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US-08-973-363-7 x AAV33521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA61903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAV33521 from: 1
Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human foetal liver single exon nucleic acid probe #10208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA61903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 ANACTGCTCAACAAAGACCTGGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 252 BP; 63 A; 70 C; 72 G; 47 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Columns 29-30; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human kinase poly:nucleotide(s) and recombinant products - useful for identification of modulators of the enzyme, and treatment of diseases associated with abnormal kinase expression
                                                                     (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 LysLeuLeuAsnLysAspLeuAla 31
                                                                                                                                                                                                        2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0632366.
                                                                                                                                      2000US-0236359.
2000GB-0024263.
Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 100.000
    Rank DR;
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Single exon nucleic acid probes for analyzing gene expression in

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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK10214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-973-363-7 x ABA61903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. The present sequence is a single exon nucleic acid whote: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                  Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe SEQ ID NO: 10205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 TACCTGATAAAGTTATTAAATAAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 544 BP; 144 A; 128 C; 88 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 10208; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 TyrLeuIleLysLeuLeuAsnLys 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 100.000
                                                              Rank DR;
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brains

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EX CCCCCCX BX PX P
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US-08-973-363-7 x AAK10214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
    Quality:
  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK36112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                           WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK36112 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 544 BP; 144 A; 128 C; 88 G; 184 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO: 10205; 650pp + Sequence Listing; English
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow
                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                           30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK36112;
                                                     Example 4; SEQ ID NO: 10669; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                               21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrLeuIleLysLeuLeuAsnLys 28
                                                                                                                                                            SG,
                                                                                                                               2001-488900/53.
                                                                                                                                                                                        MOLECULAR DYNAMICS INC.
                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-023659.
2000US-023659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from:
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                                                                                                                                                          Rank DR;
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Gaps:
Identity:
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0
100.000
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SSSSS
                                                                   alignment_block:
US-08-973-363-7 x AAK36112
                                                                                                                                         alignment_scores:
   Quality:
                                      Align seg 1/1 to:
                                                                                                         Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                         samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                Sequence 544 BP;
21 TyrLeuIleLysLeuLeuAsnLys
                                         AAK36112
                                                                                                                                                                                                144 A; 128 C; 88 G; 184 T;
                                         from: 1
                                                                                                            Length:
Gaps:
Percent Identity:
           28
                                         .0
                                           544
                                                                                                            8
0
100.000
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243 TACCTGATAAAGTTATTAAATAAG 266

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gb_est1:AW997058
gb_gss:CNS04DVG
gb_est2:BF881342
gb_est1:AI085785
gb_est2:C84397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9b_est1:AU125712

9b_est2:BE895133

9b_est1:BB830730

9b_est1:BB830730

9b_est1:BB834922

9b_est2:BF239967058
                                                                                                                                                                                    9b_est1:A1915135
9b_est2:BM365726
9b_est2:BM365198
9b_est2:BM365198
9b_est2:BM365756
9b_est2:BM365756
                                                                                                                                                                                                                                                                                                                                                 gb_est1:AA305759
gb_est1:AI870450
gb_est2:H61027
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Database: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WARN: XGAPOP and 1 WARN: XGAPEXT and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database sequences: 13736207
Database length: -1841457050
Search time (sec): 4311.510000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search information block: Query: US-08-973-363-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est2:N49703
                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est2:BM362956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est1:BB155356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est1:AL659353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of: US-08-973-363-7 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        est1:AW168274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5:46 AM
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30.00
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9.6e-19
9.6e-19
9.6e-16
1.0e-14
1.1e-14
2.7e-13
4.9e-10
0.0611
0.0648
0.1514
0.1573
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| AL653353 AL65353 XGC-neurula | AL654594 AL64594 XGC-egg Silux | AL664594 AL644594 XGC-egg Silux | AL6642594 XGC-egg Silux | AL604254 DKFZp313J0140_C-1313 | AL601246 DKFZp313J0140_C-1313 | AL601246 DKFZp313J0140_C-1314 | AL601246 DKFZp313J0140_C-102 | BB815356 BB155356 RIKEN full-le | BB461065 BB461065 RIKEN full-le | BB461065 BB461065 RIKEN full-le | BB839730 BB830730 RIKEN full-le | BB839735 BB830730 RIKEN full-le | BB834922 BB834922 RIKEN full-le | BB834922 BB83200300074 Subtract | RA405754 BS320015100004 Subtract | RA405754 BS320017000047 Subtract | RA405754 BS320017000047 Subtract | BR366124 BS320017000047 Subtract | BR366126 BS320017000049 Subtract | BR366126 BS32001700049 Subtract | BR366126 BS3200170049 Subtract | BR3661
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9b_est1:AM254153
9b_est1:AA427958
9b_est1:BA4278600
9b_est1:BA477856
9b_est1:BF901677
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
ORGANISM
        seq_documentation_block:
LOCUS AL644594
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ORIGIN
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LOCUS AL659353
                                                                      seq_name: gb_est1:AL644594
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US-08-973-363-7 x AL659353/rev
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Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                      source
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Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J. Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TNeu045e20.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Huckle E
Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Silurana tropicalis"
//db_xref="taxon:8364"
//db_xref="taxon:8364"
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//dev_stage="neurula"
//lab_host="Escherichia coli DH10B"
//note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
ECORI NotI cut CDNA was then ligated into pCS107 with
ECORI at the 5' end and NotI at the 3' end."

19 a 134 c 114 g 226 t
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Gaps: 0
Percent Identity: 100.000
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28.41
28.71
34.88
36.10
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        mRNA
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| H88315 yp70c06.rl Soares adu
| AN354153 32640 MARC 2PIG Sus
| AA427958 zw50a01.rl Soares_t
| BH228000 1006143E10.xl 1006
| AA477885 zu34e05.rl Soares o
| AA477887 zu34e05.rl Soares o
        linear
        EST 07-NOV-2001
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REFERENCE
AUTHORS
TITLE
                                                                SOURCE
ORGANISM
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KEYWORDS
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                    REFERENCE
                                                                                                                      VERSION
                                                                                                                                                                               DEFINITION
                                                                                                       KEYWORDS
                                                                                                                                            ACCESSION
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 AUTHORS
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                                                                                                                                                                                                                                                                                  430 bp mRNA
DKFZp313J1040_rl 313 (synonym: hlcc2) Homo
DKFZp313J1040_5', mRNA sequence.
AL601246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huckle, E., Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J Sanger Xenopus tropicalis EST project 2001 (10_2001) Unpublished (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinxton, Cambridgeshire, CB10 1SA, UK Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project
TROPICALIS_SEQUENCE_ID: L1E1d12.plc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL644594 XGC-egg Silurana tropicalis cDNA clone L1E1d12 5', mRNA
Bloecker, H., Boecher, M.,
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                      Homo sapiens
                                                                                                         EST
                                                                                                                         AL601246.1 GI:15164752
                                                                                                                                          AL601246
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                  (bases 1 to 430)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="egg"
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/lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
EcoRI at the 5' end and NotI at the 3' end"
125 c 156 g 141 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Silurana tropicalis"
/db_xref="taxon:8364"
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Percent Identity:
Brandt, P.,
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Mewes, W.,
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                                                                                                                                                                           cDNA clone
                                                   Euteleostomi;
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 and Wiemann
                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                    COMMENT
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                                                                                                                       TITLE
                                                                                                                                        AUTHORS
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                                                                                    JOURNAL
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seq_documentation_block:
LOCUS AI890775
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US-08-973-363-7 x AL601246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est1:AI890775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wm9511.xl NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHD1_HUMAN O14646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1; mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone (DKFZp313J1040) is available at the RZPD in Ber
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dKfZ-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 547)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Promational Cancer Institute, Cancer Genome Anatomy Promational Cancer Institute, Cancer Genome Cancer C
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                                                                                    Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
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CDNA Library Preparation: Life Technologies, CDNA Library Arrayed by: Greg Lennon, Ph.D.
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cDNA-collection"
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/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                     Christopher Moskaluk,
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                                                                                                                                                                                                                                                       TITLE
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Lish Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

CE 1 (bases 1 to 619)

Rarkawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,

Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,

Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Szuuki,H.,

Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,

Muramatsu,M. and Hayashizaki,T., et al. 2001)

On Jun 29, 2000 this sequence version replaced gi:8811286.

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 bp mRNA linear EST 18 BB155356 RIKEN full-length enriched, 16 days neonate thymu musculus cDNA clone A130024L16 3' similar to L10410 Mouse DNA-binding protein (CHD-1) mRNA, mRNA sequence.
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Insert Length: 1924 Std Error: 0.00
Seg primer: -40UP from Gibbo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:2443725"
/clone_lib="NCI_CGAR_UTC"
/clone_lib="NCI_CGAR_UTC"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

Carninci.P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.

.M. Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Thoue,K., Togawa,Y., Tzawa,M., Ohara,E.,

watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura

S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and

Hayashizaki
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) KONGO,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                   194 a
                                                                                                                                                                                                                                                                                                                                                                                                                /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/clone_lib="RIKEN full-length enriched, 16 days neonate
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/db_xref="taxon:10090"
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/dev_stage="16 days neonate"
/lab_host="DH10B"
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koud,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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                                                                                                                                                                                                                                                                                                                                              Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Salto, T., Kiyosawa, H., Yananaka, J., Alzawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Jul 21, 2000 this sequence version replaced gi:9356558 Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 660)
Arakawa, T., Carninci, P., Fukuda, S.,
                                                   prepare mouse tissues
                                                                    Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed t
                                                                                                                                                                                                                                                                                                   ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                       cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                         further details.
                                                                                                                                                                                                                                          Human Genome Sequences Mamm.
                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                Please visit our web site (http://genome.gsc.riken.go.jp/) for
                      Location/Qualifiers
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                                                                                                                             Research Group in Riken
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US-08-973-363-7
                                                                                                                                                             COMMENT
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LOCUS AU125712
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                                                                                                                                                       Contact: Takao
                                                                          1532-3 Yana,
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531 CCGTGCAGACTACCTCATCAAACTACTT 558
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                                                                                                                               Isogai,T.
HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.
saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzu
,Y., Sugano,S., Isogai,T.)
Tel: 81-438-52-3951
Fax: 81-438-52-3952
                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                             Helix Research Institute
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                                                                                      Genomics Laboratory
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/dev_stage="12 days embryo"
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/db_xref="taxon:10090"
                                      Kisarazu,
                                                                                                          Isogai
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US-08-973-363-7 x AU125712
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                        CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plafe: ILMA9753 row b Column: 16
                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1028)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
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/cell_type="reratocarcinoma"
/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"
312 a 149 c 196 ~ ~~~.
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/lab_bost="bl108 [bhage-resistant)"
/lab_bost="bl108 [bhage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
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/db_xref="taxon:9606"
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US-08-973-363-7 x BE895133
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LOCUS AW996787
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                                                                                                                                                                                                                                          mail: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-230
200-102-d03&t3=2000-02-3&t4=1)
Seq primer: puc 18 forward
High quality sequence stor: 2
High quality sequence stor: 37.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW996787 337 bp mRNA linear EST 05-JUN-200
QV3_BN0047-230200-102-d03 BN0047 Homo sapiens cDNA, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson,A.J. \mathcal{S}_{\mathrm{A}}
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Average insert size 2 kb. Library co
Technologies."
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A min1-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
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                                                                                                             /clone_lib="BN0047"
/dev_stage="Adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogaba, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB830730 RIKEN full-length enriched, mammary gland RCB-0527
Jyg-MC(B) cDNA Mus musculus cDNA clone G930013K04 3', mRNA
                                                                                                                                                          Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-360 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                     Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Shibata, K., Itoh, M., Carninci, P., Sugahara
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Jyg-MC(B) cDNA Mus musculus cDNA clone G930033721 3', mRNA
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Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)

Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 446)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                     Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                              Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                  2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
BB834922
                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                    Unpublished (2001)
                                                                                                                                                                                                                                                                                       RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  вв834922.1
                                                                                                        1-7-22 Suehiro-cho, Tsurumi-ku,
                                                                                                                                                                                 Laboratory for Genome Exploration Research Group,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA," /tissue_type="mammary gland" /cell_line="RCB-0527 Jyg-MC(B)" g 6 c 108 g 96 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
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1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 438
                                                                                                        Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                      RIKEN
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US-08-973-363-7 x BB834922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est2:BF239967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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ORGANISM
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309 ATTCTTCCAGATGATCCTGATAAAAAAACCACAAGCCAAACAGTTACAGAC 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                 NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gappbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura, S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF239967 821 bp mRNA linear EST 14-NOV-2000 601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129 5',
                                                                                                                                                                                                                          Ebukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 821)
                                                                                                                                                                                                                                                                                                                                                                                              BF239967.1 GI:11153890
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
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cDNA Library Preparation: CLONETECH Laboratories, Inc cDNA Library Arrayed by: The I.M.A.G.E. Consortium (L
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1. .446
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/db_xref="taxon:10090"
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COMMENT

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US-08-973-363-7 x BF239967
                                                                                             COMMENT
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LOCUS AW997058
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                      MEDLINE
                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)

Dias Neto, E., Garcia. Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW997058 686 bp mRNA linear EST 05-JUN-2000 QV3-BN0047-150400-152-c03 BN0047 Homo sapiens cDNA, mRNA sequence.
Contact: Simpson A.J.G.
Laboratory of Cancer Genetic
Ludwig Institute for Cancer
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Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLCM1033 row: k column: 18
                                                                                                                                                                                                                              sequence tags
                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                            Simpson, A.J.
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/clone_lib="NIH_MCC_54"
/clone_lib="NIH_MCC_54"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="PH10B (T1 phage-resistant)"
/note="0rgan: bone marrow; Vector: pDNR-LIB (Clontech);
/note="0rgan: bone marrow; Vector: 
                                                                                                                                                                           Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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/db_xref="taxon:9606"
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Gaps: 0
Percent Identity: 100.000
                                              Genetics
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS; genome survey sequence.

Tetraodon nigroviridis.

Tetraodon nigroviridis

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostei; Neoteleostei;

Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
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AL286261
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Tetraodon nigroviridis genome survey sequence T7 end of clone
103K08 of library G from Tetraodon nigroviridis, genomic survey
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV3-BN0047-150
400-152-c03&t3=2000-04-15&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                           Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                       Roest-Crollius, H., Jaillo
Bouneau, L., Billault, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL286261.1 GI:8024707
                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodontidae; Tetraodon.
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                                                Roest-Crollius,H.,
                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                        Weissenbach,J
                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 856)
                                                                                                (bases 1 to 856)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue mRNA and cDNA amplification were performed low stringency conditions."
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/db_xref="taxon:9606"
/clone_lib="BN0047"
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    lius,H., Jaillon,O., Dasi
Fizames,C., Wincker,P.,
                                                                                                                                                                                                                                                                                                  Jaillon, O., Dasilva, C., Fizames, C., Fizam
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: Identity:
Dasilva,C., Bouneau,L., Fisher,C.,P., Brottier,P., Quetier,F.,
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KEYWORDS
SOURCE
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LOCUS BF881342
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                                                                                                                                                                                                                   MEDLINE
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1 (bases 1 to 129)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                         Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovi genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Human gene number estimate provided by
Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF881342.1 GI:12271468
EST.
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                                                                       Tel: +55-11-2704922
                                                                                                                     Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                Simpson, A.J.
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                        Email: asimpson@ludwig.org.br
                                                 Fax: +55-11-2707001
                                                                                                                                                                                                                                                                  sequence tags
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/note="103K08"
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/db_xref="taxon:99883"
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-Q-/Cgp2_1/USPTQ_SpOol/US08973363/runat_01082002_080123_19828/app_query.fasta_1.638
-Q-/Cgp2_1/USPTQ_SpOol/US08973363/runat_01082002_080123_19828/app_query.fasta_1.638
-DB-GenEmbl -QFMT=fastap -SUFFIX-olip2n.rge -GAPOP-4.500
-GAPOP-4.500 -VGAPEXT=0.100 -LOOPCC_0.000 -VGAPEXT=0.000
-GAPOP-4.500 -GAPEXT=7.000 -YGAPOP-60.000 -YGAPEXT=60.000
-FGAPOP-6.000 -FGAPEXT=7.000 -YGAPOP-60.000 -YGAPEXT=60.000
-DELOP-6.000 -DELEXT=7.000 -START=1 -MARTIX-Oligo
-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-quality
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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Query: US-08-973-363-8
Query length: 41
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                               5349 | IL10410 Mouse DNA-binding protes 547 | AF006513 Homo sapiens CHD1 mRN 101220 | AC092372 Homo sapiens CHD1 mRN 101220 | AC092372 Homo sapiens chrome 134365 | AC012624 Homo sapiens chrome 143079 | AC021449 Homo sapiens chrome 143079 | AC021449 Homo sapiens chrome 193446 | AC008531 Homo sapiens chrome 193436 | AC026778 Homo sapiens chrome 195433 | AC026778 Homo sapiens chrome 195433 | AC027912 Homo sapiens chrome 276181 | AC092382 Homo sapiens chrome 276181 | AC092382 Homo sapiens chrome 1131 | AC023238 Homo sapiens chrome 276181 | AC023282 Homo sapiens chrome 276181 | AC023282 Homo sapiens chrome 14530 | AC08765 Drosophila melanogaster 14530 | AC019885 Drosophila melanogaster 145
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16 : A58696 Sequence 15 from Patent
168 : A58691 Sequence 10 from Patent
172 : AF004397 Gallus gallus chromo-
173 : A58684 Sequence 3 from Patent
173 : A58685 Sequence 4 from Patent
173 : A58685 Sequence 5 from Patent
174 : L10410 Mouse DNA-binding prote
175 : L10410 Mouse DNA-binding prote
176 : L10410 Mouse DNA-binding Prote
177 : AF006513 Homo Sapiens GHD mRN
177 : AF006513 Homo Sapiens GHD mRN
178 : AF006
! U69109 Rattus norvegicus
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gb_pat:AR058275
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Ratio: 1.000
Percent Similarity: 100.000
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                                            1 (bases 1 to 6608)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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Sequence 10 from Patent WO9639505.
A58691
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Griffiths,R. and Tiwari,B.
ATTAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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A58696
ISIS INNOVATION (GB)
                Patent: WO 9639505-A 10 12-DEC-1996;
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/db_xref="taxon:32644"
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AR058275 Sequence 2 from pa
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AR063890 Rattus norvegicus
S80542 related adhesion foc
D45854 Rattus norvegicus mR
L149207 Homo sapiens (clone
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COMMENT

Other

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JOURNAL
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Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked
Gene 197 (1-2), 225-229 (1997)
97473516
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                                                                                                                                                                                                                                                                                                       Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University, Glasgow G12 8QQ, UK
                                                                                                                                                                                                                                                                                                                                            Direct Submission
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Griffiths,R. and Korn,R.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             publication AU 5906996 961224.
Location/Qualifiers
/protein_id="AAC60282.1"
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/db_xref="taxon:9031"
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                                                                                                                                                                                /gene="CHD-Z"
?28. .5654
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alignment_block:
US-08-973-363-8 x AF004397
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LOCUS A58684
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                                                                                                                                                                                                                                                             153 bp
Sequence 3 from Patent W09639505
A58684
1 (bases 1 to 153)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                                                                                                unidentified unidentified
                                                                                              unclassified
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RLAAAGNSKRKTRNKKNKKASKIKEEIKSDSSPQPSEKSDEDEEEDNKDEIYSYK
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ESEELHQKTFSVCKERMRPVKAALKQLDRPEKGLSEREQLEHTRQCLIKIGDHITECL
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SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKMKGWSHIHNTWETEET
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SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
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MIRTHEWMHPQTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGVDEAHRLKNDDSLLY
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CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
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1223 c 1520 g 1683
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BASE COUNT ORIGIN

REFERENCE AUTHORS TITLE

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SOURCE
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US-08-973-363-8 x A58685
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US-08-973-363-8 x A58684
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LOCUS A58685
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ACCESSION
                                                                                                                                                 Quality: 34.00
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                                                                   Align seg 1/1 to: A58685 from: 1 to: 153
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41 la 41
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AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                           unclassified.
1 (bases 1 to 153)
Griffiths, R. and Ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified
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Sequence 4 from Patent WO9639505.
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                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 9639505-A 4 12-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified.
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/db_xref="taxon:32644"
a 36 c 31 g 30
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US-08-973-363-8 x A58686
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Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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Mouse DNA-binding protein (CHD-1) mRNA, complete cds.
L10410 x66028
2 (bases 1 to 5349)
Perry, R.P.
                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5349)
1 (bases 1 to 5349)
1 (bases 1, to 5349)
2 (bases 1, to 5349)
2 (bases 1, to 5349)
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DNA binding protein.
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Griffiths, R. and Tiwari, B.
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                                                                                                          Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
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/db_xref="taxon:32644"
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alignment_scores:
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LOCUS AF006513
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                                                                                   seq_name: gb_pr:AF006513
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ELEPERNSKNWEEIIPEEQRRRLEEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRS
RSRRYSGSDSDSISEEKRPXKKGRPRTIPRENIKGFSDAEIRREIKSYKKFGGPLERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSTSGFLNIMMELKKCCNHCYLIKPPDNNEFYNKQEALOHLIRSSGKLILLDKLLIRL
REGGRAVLIFSQMVRMLDILAEYLKYROFPFQRLDS
GFLKSTRAGGLGINLASADTVIFOSDWNPQNDLQAQARAHRIGOKKQVDNIYRLVKG
CFLLSTRAGGLGINLASADTVIFOSDWNPQNDLQAQARAHRIGOKKQVNIYRLVKG
SVEEDILERAKKKMYLDHLVIQRMDTTGKTVLHTGSAPSSSTPFNKEELSAILKFGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NMIRTHEWMHPOTKRLKFNILLTTYEILLKDKAFLGGLNWAFIGVDEAHRLKNDDSLL
YKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYA
SLHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYKWILTRNYKALSKGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDSESEEERDKSSCDGTESDYEPKNKVRSRKPQNRSKSKNGKKILGQKKRQIDSSEDE
DDEDYDNDKRSSRRQATVNVSYKEDEEMKTDSDDLLEVCGEDVPQPEDEEFETIERVM
DCRVGRKGATGATTTIYAVEADGDPNAGFERNKEPGDIQYLIKWKGWSHIHNTWETEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRAASSGPRSPLDQRSPYGSRSPFEHSAEHRSTPEHTWSSRKT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRSKKSVVSDAPVHITASGEPVPIAEESEELDQKTFSICKERMRPVKAALKQLDRPEK
GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLH
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GKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDINSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRSREHRPSLEGGLKDRCHSDHRSHSDHRMHSDHRSSSEHTHHKSSRDYRYLSDWQLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VQVNAKLVIAHEDELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATARDAELVDKSETDLRRLGELVHNGCVKALKDSSSGTERAGGRLGKVKGPTFRISG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt RKQPQQAQQQRPASSNSGSEEDSSSSEDSDDSSSGAKRKKHNDEDWQMSGSGSPSQLG}
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/protein_id="AAB08486.1"
/db_xref="GI:455015"
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171. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
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1 (bases 1 to 5947)
Woodage, T., Basrai, M.A., Baxevanis, A.D., Hieter, P. and Collins, F.S. Characterization of the CHD family of proteins
Proc. Natl. Acad. Sci. U.S.A. 94 (21), 11472-11477 (1997)
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GLGKTIQTISTLNYLEHBHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDIN
GLGKTIQTISTLNYLEHBHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDIN
SRNMLRTHEWPHHQTKRLKFULLTTYEILLKOKAF-LGGLNWAFIGVDEAHRLKNDDS
LLYKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEBHGKGREYG
YASLHKELEPFLLRVKKCDVKSLPAKVGOILENEMSALOKQYYKWILTRNYKALSKG
SKGSTGFLNIMMELKKCCNHCYLIKPDDNUNEFYNKQBALOHLITSGKKLLDKLLI
RLRERCNRVLLTSQMVENLDILABYLKYGPFGRLDGSIKGELKKQALDHFNAEGSE
DFCFILLSTRAGGLGINLASADTVIFDSDWNPONDLQAQARAHRIGGKKQVNIYRLVT
KGSVEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSAPSSTFFNKEBLSAILKFG
AEELEKEPGEBGEGFQEMDIDEILKRAETHENEGGPLTVGDELLSQFKVANFSNMDED
DIELBPERGERGFQENDIDEILKRAETHENEGGPLTVGDELLSQFKVANFSNMDED
DIELBPERGESGFQENDIDEILKRAETHENEGGPLTVGDELLSQFKVANFSNMDED
DIELBPERGSDSDSISEKRPKKRGRPTIPRENIKGFSDAEIRRFIKSYKKFGGPLE
RLDALTADAELVDKSETDLRRLGELVHRGCIKALKDSSGOTETTGGRLGKVKGPTGRI
SGVQVNAKLVISHEBELIPLHKSIPSDPEERKOYTIPCHYKAAHFDINGKEDDSNLL
SGVQVNAKLVISHEBELIPLHKSIPSDPEERKOYTIPCHYKAAHFDINGKEDDSNLL
SGVQVNAKLVISHEBELIPLHKSIPSDPEERKOYTIPCHYKAAHFDINGKEDDSNLL
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EETLKQQNVRGMKKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVG
RIIAHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALISKKFQACIDEYFSRNQSKTTP
                             RASSSGPRSPLDQRSYGSRSPFEHSVEHKSTPEHTWSSRKT"
                                                                                                                                                                          GLSEREQLEHTROCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKFTEFDARKLH
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                                                                                                                                             KLYKHAIKKRQESQQNSDQNSNLNPHVIRNPDVERLKENTNHDDSSRDSYSSDRHLTQ
                                                                                                                                                                                                               ERSKKSSVSDAPVHITASGEPVPISEESEELDQKTFSICKERMRPVKAALKQLDRPEK
                                                                                                                                                                                                                                               EALSGAGSSKRRKARAKKNKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLSESKSDGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAB87381.1"
/db_xref="GI:2645429"
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/product="CHD1"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                            IGIYEYGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MNGHSDEESVRNSSGESSQSDDDSGSASGSGSGSSSSGSSSDGSS/
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US-08-973-363-8 x AF006513

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                                                                                                                                                                Align seg 1/1 to reverse of: AC092372 from: 1 to: 101220
                                                                                                                                                                                                                  US-08-973-363-8 x AC092372/rev
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                                                        26932 ATTCTTCCAGATGATCCCGATAAAAACCACAAGCAAAACAGTTGCAGAC 26883
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17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                    1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with ACO12624.
The number of bases overlapped is 90404.
Location/Qualifiers
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-UJL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Joint Genome Institute.
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/db_xref="taxon:9606"
/chromosome="5"
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18862 c 17827 g
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LOCUS AC021449
                                                                                                                                                                               seq_name: gb_htg:AC021449
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US-08-973-363-8 x AC012624
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LOCUS AC012624
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SOURCE
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                                                                                                                                                                                                                                                                                                                                           1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
                                                                                            AC021449 DNA linear HT HOMO Sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Malnut Creek, CA 94598, USA On Jul 21, 2001 this sequence version replaced gi:14277267.
Location/Qualifiers
1. .134365
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              AC021449
AC021449.3 GI:10047806
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-70N-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases I to 134565)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 13455)
DOE Joint Genome Institute and Stanford Human Genome Center.
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1 (bases 1 to 134365)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2082117"
a 24497 c 25503 g 43951
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DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreita,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
MacPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Sancos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirrell,A., Vassillev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Direct Schmidt, A., and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choenel Y. Collargelo M. Colling S. Collamore B. College
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L.,
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                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Insert size: 142179; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 134743 bases at least Q30 Consensus quality: 139272 bases at least Q30 Consensus quality: 140814 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: 58_M_1
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                                                                      46906 47005:
47006 5183
51831 51930:
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                                                    51931
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40512 432
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62719: gap of 100 bp 75408: contig of 12689
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                                             505: gap of 100 bp 100 continuous of 4825 bp in length 330: gap of 100 bp 100 bp 100 length 52619: continuous of 10689 bp in length
                                                                                                                                         p of 100 bp contig of 3526 bp in length
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US-08-973-363-8 x AC021449
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                                                                                                                                                                                                                                                                                                                                        gb_htg:AC008531
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                           Homo sapiens chromosome 5 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                 Homo sapiens
                                                                                                                                            HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                                                                  7 ordered pieces.
                                                                                                                        numan
                                                                                                                                                                        AC008531.3 GI:12830078
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92617 106409: contig of 13793 bp in length
106410 106509: gap of 100 bp
106510 143079: contig of 36570 bp in length.
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75509 9251
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51931. .62619
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40512, 43270
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clone_end:T7
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106510. .143079
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75509. .92516
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_lib="RPCI-11 Human Male
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92516: contig of 17008 bp
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REFERENCE
AUTHORS
TITLE
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US-08-973-363-8 x AC008531
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ORIGIN
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                                                                                                                                                              Align seg 1/1 to: AC008531 from: 1 to: 145659
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                                                    17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q20
Consensus quality: 142744 bases at least Q20
Consensus quality: 142744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 148059; sum-of-contigs estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs caps between the contigs

* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.

* This sequence will be replaced
* by the finished serious as soon as it is smallbloadd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 56174 contig of 56174 bp in length

56175 56274 gap of unknown length

56175 100974 gap of unknown length

100975 100974 gap of unknown length

100975 131372 contig of 12153 bp in length

113128 113277 gap of unknown length

113128 113277 gap of unknown length

113128 113290 contig of 4963 bp in length

113129 113690 gap of unknown length

118191 119694 contig of 1404 bp in length

119695 119794 gap of unknown length

119795 123297 contig of 3503 bp in length

1132398 123399 gap of unknown length

1132398 123399 gap of unknown length

1132398 123399; contig of 2262 bp in length.
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summary Statistics
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                      26.00
1.000
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/clone_lib="CalTech human BAC library C"
26309 c. 27580 g 48609 t 600 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                    Length: 26
Gaps: 0
Percent Identity: 100.000
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AUTHORS
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JOURNAL
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SOURCE
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LOCUS AC091946
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Consensus quality: 180259 bases at least Q20
Consensus quality: 184175 bases at least Q20
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; sum-of-contigs estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 5 clone RP11-36012, PROGRESS ***, 33 unordered pieces. AC091946
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1 (bases 1 to 19346)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
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Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will be preserved.
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Joint Genome Institute.
                                                                                12461
12561
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16382
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1458: gap of unknown length
2667: contig of 1209 bp in length
2767: gap of unknown length
3823: contig of 1056 bp in length
3923: gap of unknown length
5920: contig of 1056 bp in length
6020: gap of unknown length
6020: gap of unknown length
7494: contig of 1474 bp in length
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of 2051 bp in
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alignment_block:
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    Quality:
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 seq_name:
                                                                                                                                                                         Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                   Align seg 1/1 to: AC091946
                                                                                                                                         US-08-973-363-8 x AC091946
                                                                   87708
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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35252 c 37061
                                                                                                                                                                                                                                                                                   /clone="RP11-36012"
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169109: contig of
169209: gap of u
193446: contig o
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123738: contig of 1
123838: gap of 1
130583: contig of 1
130683: gap of 1
141544: contig of 1
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LOCUS AC022121
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US-08-973-363-8 x AC026778/rev
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WI-13675 G23101
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Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jun 1, 2001 this sequence version replaced gi:13677045. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-MAR-2000) Production Sequencing Facility, DOE Joi Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, 2004 (Dases 1 to 195433)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                 HTG
                                                                AC022121
                                                                                 Homo sapiens chromosome 5
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Finishing Completed at Stanford Human Genome Center
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DOE Joint Genome Institute.
Direct Submission
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AC026778
AC026778.4 GI:14277282
Homo sapiens
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates;
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Catarrhini; Hominidae
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                     17 rArgAlaAspTyrLeuIleLysLeuLeu 26
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4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (25-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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WI-13675 G23101
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Finishing Completed at Stanford Human Genome Center
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WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP=60.000 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60.000
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Database sequences: 1736436
Database length: 858457221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search information block:
Query: US-08-973-363-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9639505-A1
    17 rArgAlaAspTyrLeuIleLysLeuLeuAsnLysAspLeuAlaArgLysG
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAC41054 + /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT:AAT1338 + /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:AAS93365 + /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:AAS93666 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001.DAT:AAC9208 + /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAC9208 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAC9366 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAC9156 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAS11356 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb
                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-973-363-8 x AAT42754
                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 41.00
Ratio: 1.00
Percent Similarity: 100.000
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                                                                                                                                                                                                              Align seg 1/1 to: AAT42754 from: 1 to: 1316
The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate femala development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 8; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-043127/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT42754 standard; cDNA; 1316 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 41
Gaps: 0
Percent Identity: 100.000
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alignment_block:
US-08-973-363-8 x AAT42751
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                                                                                                                         Quality: 41.00
Ratio: 1.000
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  4080
                                                                                                                                                                                                                                    The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chicken CHD-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Griffiths
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT42751 standard;
                                                                                                                                                                                                               Sequence 6608 BP; 2289 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1996
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luAlaGlnArgLeuAlaGlyAla 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCACAGAGACTTGCTGGTGCA 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                        chromodomain-helicase-DNA binding genes determine sex — used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex determination; chromodomain-Helicase-DNA binding 1 Avian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gs
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                                                        AAT42751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                             76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 228..5390 /*tag= a
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                                                        from: 1
                                                                                                                         Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                               1207 C;
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to:
                                                                                                                                                                                                              1459 G; 1653 T; 0 other;
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alignment_scores:
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ID AAT42757 standard;
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                                                                         Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42755) genes determine sex in birds and can be used to identify the sex of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
                                                                                                                                                                             Claim
                                                                                                                                                                                                      birds
                                                                                                                                                                                                                                                                                Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHD-1A; CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bird; sex determination; chromodomain-Helicase-DNA binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT42757;
                                     Sequence 153 BP;
                                                             embryo,
                                                                                                                                                                                                                                             P-PSDB; AAW08147
                                                                                                                                                                                                                                                                                                        (ISIS-) ISIS INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17
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                                                                                                                                                                             8; Fig 3; 76pp; English.
                                                                                                                                                                                                     chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny % \left( 1\right) =\left\{ 1\right\} 
                                                              foetus
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                                                              etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
                                     58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                     A;
                                                             and to manipulate the sex of progeny
                                     40 C;
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                                     24 T; 0 other;
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amino
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alignment_block: US-08-973-363-8 x AAT42757

Percent Similarity:

Quality:

Ratio:

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Percent

Identity:

34 0 100.000

Align seg 1/1

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AAT42757

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Quality: 34.00
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AAT42758 standard; DNA; 153
                                                                                                                                                           Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 153 BP;
                                                                                                                                                                                                                                                                                                                                                        Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                   birds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key Location/Qualifiers misc_difference 52.81 /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird; sex determination; chromodomain-Helicase-DNA binding CHD-IA; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chick CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                            chromodomain-helicase-DNA binding genes determine sex in used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tiwari B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-GB01341
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                                                                                                                              56 A; 36 C; 31 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
Length: 34
Gaps: 0
Percent Identity: 100.000
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seq_documentation_block:
ID AAT42759 standard; DN
XX AAT42759;
XX AAT42759;
XX AAT42759;
XX I2-MAR-1997 (first e
XX Great tit CHD-W gene
XX Bird; sex determinati
XW CHD-1A; CHD-W; W Chrc
XX Parus major.
XX CHD-1A; CHD-W; W Chrc
XX PARUS MAJOS A1.
XX I2-DEC-1996.
Y*tag
FT Misc_difference 52.8
FT /*note
FT 
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US-08-973-363-8 x AAT42758
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                                                        Bases 3855-3977 (AAR142756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAR142757), Chicken CHD-W (W refers to the W chromosome) gene (AAR142758) and and the great tit CHD-W gene (AAR142759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAR142751) and CHD-W (see also AAR142754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152
                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 3; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 la 41
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                                                                                                                                                                                                                                                                                                                                                                                        chromodomain-helicase-DNA binding genes determine sex - used for sex determn, and to control sex of progeny % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             determination; chromodomain-Helicase-DNA binding
HD-W; W chromosome; ss.
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       60 A;
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"bases 52-81 are a repeat of bases
and are ignored in the translated
acid sequence given in Fig 3"
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          29 T;
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          0 other;
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alignment_scores:

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ID AAV59280 standard;
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                          The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangelctasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expressing A-TRF also have an increased life span in vitro, e.g.
                                                                                                                                                                                                             Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, us to inhibit shortening of telomerases caused by ageing or disease, also used to extend life of cells in culture
                                                                                                                                                                                                                                                                                                                                     Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                 Claim 14; Page 110-111; 163pp; English.
                                                                                                                                                                                                                                                                                           p-PSDB;
                                                                                                                                                                                                                                                                                                         WPI; 1998-480769/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        telomere; ageing; ataxia telangeictasia; Down's syndrome; tumour; viral.
               for expression of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
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Ratio: 1.000
Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sLeuLeuAsnLysAspLeuAlaArgLysGlu 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy
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97US-0800264
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1..1311
recombinant proteins or where testing, eliminating the need
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Gaps: 0
Identity: 100.000
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               intended for subsequent
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alignment_scores:
Quality:
       ID AAT42756 standard;
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US-08-973-363-8 x AAV59280
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Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAM08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of
                                                                                                                                          Avian
birds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bird; sex determination; chromodomain-Helicase-DNA binding CHD-1; CHD-W; W chromosome; ss.
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                                                                                                               Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                Griffiths R,
                                                                                                                                                                                                                                                                06-JUN-1995;
                                                                                                                                                                                                                                                                                         05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGTGCAGACTACCTCATCAAACTA 1311
                                                                                                                                                                            1997-043127/04.
DB; AAW08146.
                                                                                                                                      chromodomain-helicase-DNA binding genes determine - used for sex determn. and to control sex of prog
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                                                                                                                                                                                                                 Tiwari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 3855-977).
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L.000
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seq_documentation_block:
ID ABL06443 standard;
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Ratio: 1.000
Percent Similarity: 100.000
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                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01810-ABL10175) and the encoded proteins (ABL01810-ABL10175) and the encoded proteins
           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                    Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
P-PSDB; ABB62340.
                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US09231.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL06443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 ACTACTT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 153 BP; 61 A; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               progeny.
                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                   (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL06443 standard; cDNA; 6240 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 sLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                    Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                    Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 19
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                    Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 T; 0 other;
                             WIPO
                                                                                                                                                         is
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alignment_scores:

is

Quality:

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seq_documentation_block:
ID ABL06442 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-973-363-8 x ABL06443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQ
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4205 AAGCCCCAGGCCAAGCAGCTGCAGACGCGTGCC 4237
                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG105 ABLIG105) expressed DNA sequences (ABLIG106 ABLIG175) and the encoded proteins (ABB70713 - ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from was the content of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other;
Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL06442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter JC, Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB62339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 11
Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                    The invention
                                                                                           WIPO
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alignment_block: us-08-973-363-8
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11-JUL-2000
11-JUL-2000
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26-JUL-2000
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14-AUG
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04-FEB-2000;

24-FEB-2000;

02-MAR-2000;

16-MAR-2000;

17-MAR-2000;

18-APR-2000;

19-MAY-2000;

07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            documentation_block: AAK888882 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; digestive system antigen; gene therapy; cancer; ulcerative colitis; infection; Hirschsprung's disease; digestive system disorder; Meckel's diverticulum; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              digestive system antigen
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2000US-0186350
2000US-0186350
2000US-0186350
2000US-0189874
2000US-0198123
2000US-029515
2000US-02914886
2000US-0216880
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2000US-0225681
2000US-0225681
2000US-0225681
2000US-02258924
2000US-02258924
2000US-02259343
2000US-02259343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0179065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      appendicitis; chronic colitis;
 01-SEP-2000
05-SEP-2000
05-SEP-2000
06-SEP-2000
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08-SEP-2000
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S-0249210.
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S-0249211.
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S-0249213.
                                                                                           s-0246613.
s-0249207.
                                                                                                                                            3-0241808

3-0241826

3-0244617

3-0246476

3-0246476

3-0246477

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3-0246523
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5-0235834

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5-0235836

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5-0236399

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5-0237038

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S-0232398.
S-0232400.
S-0232401.
S-0233063.
S-0233064.
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S-0229509.
S-0229513.
                                                                                                                     3-0246610.
3-0246611.
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seq_documentation_block:
ID AA157603 standard; cDNA; 421 BP.
XX
AC AA157603;
XX
DT 19-OCT-2001 (first entry)
XX
DE Human colorectal cancer antiqen cD
                                                                                                                                                                                                                                                                                                                                                                             alignment_scores: 10.00
Quality: 10.00
Ratio: 1.000
Percent Similarity: 100.000
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US-08-973-363-8 x AAK88882
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                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAK88882 from: 1 to:
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17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
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17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
06-DEC-2000
08-DEC-2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a cDNA encoding a digestive system antigen of the invention.
    Human colorectal cancer antigen cDNA SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases \cdot
                                                                                                                                                                                                             146 AAGCAGCTACAGACCCGAGCGGATTACTTG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 421 BP; 148 A; 78 C; 127 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1198; 986pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                 13 LysGlnLeuGlnThrArgAlaAspTyrLeu 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-502630/55.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0249215
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2000US-0249297
2000US-0251980
2000US-0251980
2000US-0251980
2000US-0251866
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Gaps: 0
t Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 T; 7 other;
                                                                                                                                                                                                                                                                                        421
    67
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11 - JUL - 2000

11 - JUL - 2000

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26 - JUL - 2000

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15 - AUG - 2000

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24-FEB-2000;
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2000US-0225214
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29-SEP-2000;
02-OCT-2000;
03-NOV-2000;
08-NOV-2000;
08-NO
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25-SEP-2000;
26-SEP-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                             2000US-0235836.
2000US-0235836.
2000US-0236369.
2000US-0236369.
2000US-0236369.
2000US-0236802.
2000US-0237037.
2000US-0237039.
2000US-0237039.
2000US-0241786.
2000US-0241786.
2000US-0241786.
2000US-0241808.
2000US-0241808.
2000US-0246476.
2000US-0246476.
2000US-0246477.
2000US-0246610.
2000US-0246611.
2000US-0246611.
2000US-0249211.
2000US-0249213.
2000US-0249214.
2000US-0249215.
2000US-0249214.
2000US-0249214.
2000US-0249214.
2000US-0249216.
  2000US-0250160

2000US-0250391

2000US-0251030

2000US-0251988

2000US-0251479

2000US-0251479

2000US-0251868

2000US-0251868

2000US-0251869

2000US-0251990

2000US-0251990

2000US-0251990
           seq_documentation_block:
ID AAV33521 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-973-363-8 x AAI57603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 10.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-457727/49
P-PSDB; AAM38625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen
        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 421 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                 Au-Young J,
                                                                                                                                      07-AUG-1996;
                                                                                                                                                                                 07-AUG-1996;
                                                                                                                                                                                                                            06-OCT-1998
                                                                                                                                                                                                                                                                    US5817479-A
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-DEC-1998
                                                                                       (INCY-) INCYTE PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 LysGlnLeuGlnThrArgAlaAspTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCAGCTACAGACCCGAGCGGATTACTTG
        1998-556387/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23789 cDNA fragment encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                   Bandman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI57603
                                                                                                                                                                                 96US-0700575
                                                                                                                                         96US-0700575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA;
                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from:
                                                     Hawkins PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ç;
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The present invention provides the protein and coding seque number of colorectal cancer antigens. These are shown in AAI57547-AAI57619 and AAM38569-AAM38641. These can be used diagnosis, prevention and treatment of cancer of the colon The present sequence is a colorectal cancer antigen coding the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the colon and rectum including colorectal cancers and also for testing and detection e.g. diagnosis –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-2001; 2001US-0259678.
Protein kinase; cell signalling; inflammation; carcinoma; diabetes; human x-linked agammaglobulinaemia; nonspherocytic haemolytic anaemia; artherosclerosis; glioma; restenosis; cholera-based septic shock; CHKFRNK chiken tyr kinase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did no specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                            /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:AAV33521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO: 67; 522pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
Percent Identity:
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                                                                                  a human protein kinase
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100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          part of the printed directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences
                                                                                    homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
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Wilde

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seq_documentation_block:
ID ABA61903 standard; DNA; 544 BP
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                                                                                                                                                                                   04-FBB-2000; 2000US-0180312
26-MAY-2000); 2000US-0207456
30-JUN-2000); 2000US-0608408
03-AUG-2000); 2000US-0632366
21-SEP-2000; 2000US-0234687
27-SEP-2000); 2000US-0236359
    Penn SG, Hanzel DK,
                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human foetal liver single exon nucleic acid probe #10208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 252 BP; 63 A; 70 C; 72 G; 47 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Columns 29-30; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human kinase poly:nucleotide(s) and recombinant products - useful for identification of modulators of the enzyme, and treatment of diseases associated with abnormal kinase expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AAACTGCTCAACAAAGACCTGGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 LysLeuLeuAsnLysAspLeuAla 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                        2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.000
Chen W,
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    Rank DR;
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Single exon nucleic acid probes for analyzing gene expression in

human

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PTT
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ID AAK10214 standard.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-973-363-8 x ABA61903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAK10214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: ABA61903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity: 100.000
                                                                                                                                                                26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. For this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver \boldsymbol{\cdot}
                              WPI; 2001-483446/52.
                                                           Penn SG,
                                                                                                                                                                                                             04-FEB-2000;
                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                     epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human brain expressed single exon probe SEQ ID NO: 10205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK10214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 TACCTGATAAAGTTATTAAATAAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 544 BP; 144 A; 128 C; 88 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 10208; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483447/52.
                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                       04-OCT-2000;
                                                                                                                                                     21-SEP-2000;
                                                                                                                                                                                                                                              30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                           WO200157275-A2
                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK10214 standard; DNA; 544 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 TyrLeuIleLysLeuLeuAsnLys 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                         Hanzel DK,
                                                                                                                                 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                       2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.000
                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
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                                                           Rank DR;
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brains

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seq_documentation_block:
ID AAK36112 standard; DNA; 544 BP.
XX
AC AAK36112;
XX
DT 06-NOV-2001 (first entry)
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed exon
KW Human; bone marrow expressed exon
KW Human; bone marrow expressed exon
KW Human; bone marrow expressed exon
KW Homo sapiens.
XX
DF 09-AUG-2001; 2001W0-US00668.
XX
DF 09-AUG-2001; 2001W0-US00668.
XX
DF 30-JAN-2001; 2000US-0180312.
PR 26-MAY-2000; 2000US-0608408.
PR 30-JUN-2000; 2000US-0632566.
PR 30-JUN-2000; 2000US-0632566.
PR 30-JUN-2000; 2000US-0636359.
PR 21-SEP-2000; 2000US-0236359.
PR 21-SEP-2000; 2000US-0608408.
PR 30-JUN-2000; 2000US-0608408.
PR
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TXXXCCCCCCXXXX
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US-08-973-363-8 x AAK10214
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure generation in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4;
      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the humbone marrow. They can be used to measure gene expression in bone man
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bone marrow expressed single exon probe SEQ ID NO: 10669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                        Example 4; SEQ ID NO: 10669; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                          genome-derived single exon nucleic acid probes useful
zing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone marrow expressed exon; gene expression analysis; probe;
rray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO: 10205; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                     Rank
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      in the human
in bone marrow
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alignment_block:
US-08-973-363-8 x AAK36112
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                                                                                                                                                                                           alignment_scores:
                                                                                                                                    Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                             Align seg 1/1
                                                                                                                                                                                                                                                                   samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
243 TACCTGATAAAGTTATTAAATAAG 266
                                                                                                                                                                                                                                         Sequence 544 BP; 144 A; 128 C;
                               21
                TyrLeuIleLysLeuLeuAsnLys 28
                                                              to:
                                                              AAK36112
                                                              from: 1
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Gaps: 0
Percent Identity: 100.000
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gb_est2:BI035224
gb_est1:AW961278
gb_est2:BG757172
gb_est1:AW364689
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gb_est1:RF881342
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Query leng
Database:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database sequences: 13736207
Database length: -1841457050
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Query: US-08-973-363-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: Aug 3, 2002 5:46 AM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est1
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       out_format : pfs
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.0e-23
.6e-19
.7e-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | AL659353 AL659353 XGC-neurula | AL659353 AL659353 XGC-neurula | AL644594 AL644594 XGC-egg Silux | AL644594 AL644594 XGC-egg Silux | AL604254 DKFXp313J01040_F1 313 | AL601246 DKFXp313J01040_F1 313 | AL601246 DKFXp313J01040_F1 315 | BB461055 BB461055 RIKEN full-le | BB461055 BB461055 RIKEN full-le | BB461055 BB46105 RIKEN full-le | AL0125712 AU125712 AU125712 AU125712 AU125713 GO13606F1 NIH_MGC_71 | AW99778 QV3-EN0047-230200-102-1 | BB303730 BB303730 RIKEN full-le | BB239967 601905170F1 NIH_MGC_54 | AW99705 QV3-EN0047-150400-152-1 | AL1268261 Tetracodon nigroviridis | BF881342 PMO-ET0208-031200-001-1 | AL1087785 Qa26905.S1 Soares_Nhhh C84397 C84397 Osteolast Subtration | AW168274 X962801.X1 NCL_GGAP_Ut | BM362956 BS320051000D4 Subtration | AW168274 X962801.X1 NCL_GGAP_Ut | BM362956 BS320051300D4 SUBtration | AW168274 X962801.X1 NCL_GGAP_UT | AW168274 X962801.X1 NCL_GGAP_UT | AW168274 X962801.X1 NCL_GGAP_UT | AW16
                                                                                                                                               | Maj60956 | Maj2005100004 | Subtract | Maj703 | W73e03:sl Soares fetal | AA305759 | SST176834 | Colon carcinal | AA305759 | SST176834 | Colon carcinal | AA305759 | SST176834 | Colon carcinal | Maj0450 | W146f05.xl | NCI_CGAP_Ut | H61077 | W150f12.sl | Soares fetal | AI915135 | W150e08 | xl | NCI_CGAP_CC | BM365726 | BS32001700E12 | Subtract | BM365128 | BS32002300003 | Subtract | BM365128 | BS32002300013 | Subtract | BM365156 | BS32001700017 | Subtract | BM364534 | BS32001300019 | Subtract | BM364534 | BS32002300019 | Subtract | BM366454 | BS32002300019 | S
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H53564 yq86h11.s1 Soares fetal
BI035224 QVZ-NN2003-230401-631-
AW961278 EST373350 MAGE reseque
BG757172 602710541F1 NIH MGC_48
AW364689 PM3-DT0037-231299-001-
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gb_est1:B42780677
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AUTHORS
TITLE
seq_documentation_block:
LOCUS AL644594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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alignment_block:
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LOCUS AL659353
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AL659353 from: 1 to:
                                                                                                                                                                               1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Silurana tropicalis
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia, Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hinxton, Cambridgeshire, CB10 1SA, UK Email: tropésanger.ac.uk Sanger Xenopus tropicalis EST project 2001 TROPICALIS_ESQUENCE_ID: TNeu045e20.sp6 Sequencing primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL659353 XGC-neurula Silurana tropicalis cDNA clone TNeu045e20 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Huckle E
Sanger Centre
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/Clone_Lib="XGC-neurula"
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//Ab_host="Escherichia coli DH10B"
//Ab_host="Scherichia coli DH10B"
//Ab_host="Scheric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Silurana tropicalis"
/db_xref="taxon:8364"
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| H38315 yp70c06.r1 Soares adu
| AW354153 32640 MARC 2PIG Sus
| AA427958 zw50a01.r1 Soares_t
| BH228000 1006143E10.x1 1006
| AA477885 zu34e05.r1 Soares o
| BF901677 PM4-MT0201-091200-0
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US-08-973-363-8 x AL644594
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AL644594
AL644594.1
                                                                                                                                                                                                                                                                                  DKFZp313J1040_r1 313 (synonym: hlcc2) Homo DKFZp313J1040 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 430)
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Sanger Centre
Bloecker, H., Boecher, M., S.
                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                             AL601246.1 GI:15164752
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
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/clone="Libida"
/clone=1b="XGC"
/clone=1b=XGC"
/clone=1b="XGC"
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/clone=1b="XGC"
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/db_xref="taxon:8364"
/clone="L1E1d12"
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US-08-973-363-8 x AL601246
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Percent Similarity: 100.000
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                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 CCGTGCAGACTACCTCATCAAATTACTT 295
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                                                                                                                                                                                                                                                                                                                                                                          wm95f11.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2443725 3' similar to SW:CHD1_HUMAN 014646 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1;, mRNA sequence.

A1890775
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This clone (DKFZp313J1040) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the
                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Bloecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST (Bloecker, H.,
Wiemann, S.)
                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                    Unpublished (1997)
                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 547)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                                                                                                                                              human.
CDNA Library Preparation: Life Technologies, CDNA Library Arrayed by: Greg Lennon, Ph.D.
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/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="DKFZp313J1040"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
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/db_xref="taxon:9606"
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US-08-973-363-8 x AI890775/rev
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LOCUS BB155356
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 619)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y., Muramatsu, M. and Hayashizaki, Y., Muramatsu, M. and Hayashizaki, Y., Takada, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y., Et al. 2001)

On Jun 29, 2000 this sequence version replaced gi:8811286.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sclences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Mus musculus
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Seq primer: -40UP from Gibco
High quality sequence stop: 418.
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Insert Length: 1924 Std Error: 0.00
                                                                                                                                                                   Contact: Yoshihide Hayashizaki
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/clone_lib="NCI_CGAP_UTC"
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adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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alignment_block: US-08-973-363-8 x BB155356

Align seg 1/1 to: BB155356

from: 1 to: 619

Quality: 26.00 Ratio: 1.000 Percent Similarity: 100.000

Percent Identity: 100.000

Length:

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alignment_scores:
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare monuse itspues
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.;
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                194 a
                                                                                                                                                                                   prepared and sequenced in Mouse Genome Encyclopedian Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="thymus"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Contact: Yoshihide Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Koud
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasak
,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagama,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
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                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Arakawa,T., Carninci,P., Fukuda,S.,
                                                                             Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Email: genome-res@g
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                        fuman Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                 library was prepared and sequenced in Mouse Genome
                         Location/Qualifiers
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481 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
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                                          1532-3 Yana, Kisarazu,
Tel: 81-438-52-3951
                                                                                                                                  Unpublished (2000)
Contact: Takao Iso
                                                                                                                                                                             HRI human cDNA project (Ota,T., Saito,K., Yamamoto,J., Nakamura,Y., Sugano,S., Isogai,T.)
                                                                                                                                                                                                                                                                                                 Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S.,
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU125712 NT2RM4 Homo sapiens cDNA clone
                       Fax: 81-438-52-3952
                                                                                     Helix Research Institute
                                                                                                          Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU125712.1 GI:10950428
Email: genomics@hri.co.jp
                                                                                                                                                                                                                                                                       Nakamura,Y., Nishikawa,T.,
                                                                                                                                                                                                                                                                                                                  (bases 1 to 866)
                                                                                                                                    Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I." a 130 c 168 g 151 t
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/db_xref="taxon:10090"
/clone="D130070B13"
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/dev_stage="12 days embryo"
/lab_host="DH10B"
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Percent Identity:
                                                                  Chiba
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Nakamura,Y., Nishikawa
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                                                                292-0812, Japan
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Nishikawa, T., Nagai
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100.000
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NT2RM4002061 5', mRNA
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US-08-973-363-8 x AU125712
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Ratio: 1.000
Percent Similarity: 100.000
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1 (bases 1 to 1028)

NHH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BE895133.1 GI:10358221
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                                                                                                                                                                                                                                     Plate: LLAM9753 row: h column: 16 High quality sequence stop: 488.
                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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/cell_line="NT2"
/note="terator: pME18SFL3; mRNA from uninduced NT2 neuronal
/note="tector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="imAgg:3921087"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_hosf="DHIOB (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
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/clone_lib="NT2RM4"
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/db_xref="taxon:9606"
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1. .1028
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Gaps: 0
Percent Identity: 100.000
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US-08-973-363-8 x BE895133
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LOCUS AW996787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Ratio:
                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=QV3-BN0047-230
200-102-d03xt3-2000-02-3x4z=1)
Seq primer: puc 18 forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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                                                                                                                                                                                                                                                                       High quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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a 205 c 2
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
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                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0047"
                                                                                                              /dev_stage="Adult"
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US-08-973-363-8 x AW996787/rev
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Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii
Hayatsu, N., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.,
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.,
2001)
                                                                                                                             Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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Contact: Yoshihide Hayashizaki
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sug
                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Iakimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Ishii, Hayatsu, N., Hiraamoto, K., Hiraacka, T., Hirozanae, T., Imotani, K., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ookazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Saito, R., Sahiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al., Rike
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                                                                                                                                 1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
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Contact: Yoshihide Hayashizaki
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1 (bases 1 to 446)
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/db_xref="taxon:10090"
/clone="G930013K04"
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Normalization and subtraction of cap-trapper-selected coNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for e mouse tissues.
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                                                                                                                            Homon Sapiens
Homo Sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 821)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                            BF239967.1 GI:11153890
                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       601905170F1 NIH_MGC_54
CDNA Library Preparation: CLONETECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone="G930033721"
/clone="G930033721"
/clone="G930033721"
/clone="fysical-tength enriched, mammary gland RCB-0527 Jyg-MC(B) cDNA"
/tissue_type="mammary gland"
/cell_ine="RCB-0527 Jyg-MC(B)"
/cell_ine="RCB-0527 Jyg-MC(B)"
g c 108 g 100 t
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Gaps: 0
Percent Identity: 100.000
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Homo sapiens
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                                                    MEDLINE
COMMENT
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SOURCE
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VERSION
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BASE COUNT ORIGIN

FEATURES

source

JOURNAL COMMENT REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION

KEYWORDS

DEFINITION

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alignment_block:
US-08-973-363-8 x BF239967
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Quality: 21.00
Ratio: 1.000
Percent Similarity: 100.000
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)
Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,P.F.,
Nagai,M.A., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
"M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 073-BN0047-150400-152-c03 BN0047 Homo AW997058
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Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
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EST.
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//db_xref="taxon:9666"
//clone=_lib="NIMACE_4133129"
//clone=_lib="NIH_MGC_54"
//tissue_type="from chronic myelogenous leukemia"
//tissue_type="from chronic myelogenous le
                                                                                                                                                             Natl.
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Gaps: 0
Percent Identity: 100.000
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sapiens cDNA,
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                                                                                                                 TITLE
                                                                                                                                                                                  AUTHORS
                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 AAACCACAAGCAAAACAGTTGCAGACCCGTGCAGACTACCTCATCAAATT 55
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Ratio:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                    GSS; genome survey sequence. Tetraodon nigroviridis.
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AL286261.1 GI:8024707
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Fax: +55-11-2707001
                                                                                                                                 Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS04DVG
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                                                                                       Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                         Roest-Crollius, H.,
                                                                   Unpublished
                                                                                                                                                                                                    (bases 1 to 856)
                                              (bases 1 to 856)
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154 c 126 g 241 t
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Fizames,C., Wincker,
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  Wincker, P.,
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Gaps: 0
Identity: 100.000
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                  Dasilva,C.,
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ilva,C., Bouneau,L., Fisher,C.
Brottier,P., Quetier,F.,
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nce T7 ′
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                                                                                                                                                           Bernot, A.
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end of clone
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SOURCE

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US-08-973-363-8 x CNS04DVG/rev
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LOCUS BF881342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Madhmaria, Walling Law, Date Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W.Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOllveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rnis sequence is a single read and was generated as part of a l scale clone-end sequencing project of the Tetraodon nigroviridi genome. For more information, please take a look at http://www.genome.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF881342.1 GI:12271468 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Email: asimpson@ludwig.org.br
This sequence was derived from the
                                                                                                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shotgun sequencing of the human transcriptome with ORF expressed
                                                                            Fax: +55-11-2707001
                                                                                                               Tel: +55-11-2704922
                                                                                                                                                                                            Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                                                                                                                                                                                                               sequence tags
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Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=pM0&t2=pM0-ET0208-031200-001-fi2&t3=2001-12-03&t4=1)

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1.129
Location/Qualifiers
1.129
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Database sequences: 1797656
Database length: 1873337701
Search time (sec): 4908.870000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_pr:AC012624
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                                                                                                                                                                                                                                                                                                    1316 | AS8896 Sequence 15 from Patent 1608 | A58891 Sequence 10 from Patent 6608 | A58891 Sequence 10 from Patent 6872 | AF004397 Gallus gallus chromo-153 | A58684 Sequence 3 from Patent N 153 | A58685 Sequence 4 from Patent N 153 | A58685 Sequence 4 from Patent N 153 | A58685 Sequence 3 from Patent N 101220 | AC02137 Homo sapiens Chromo-143079 | AC021624 Homo sapiens Chromo-143079 | AC021449 Homo sapiens Chromo-143079 | AC021449 Homo sapiens Chromo-143079 | AC02131 Homo sapiens Chromo-193446 | AC02131 Homo sapiens Chromo-193436 | AC025131 Homo sapiens Chromo-193436 | AC025121 Homo sapiens Chromo-193436 | AF060702 Struthio camelus clone-193436 | AC019185 Drosophila melanogaster 14530 | AC019185 Drosophila melanogaster 14530 | AC019187 Drosoph
69893 | ACO87641 Homo Sapiens Chromos
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2754 | AF181827 Aymphicus hollandicus
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153 | A58686 Seque
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9b_pat:HSU33284
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9b_ro:D45854
                                                                                                                              REFERENCE
AUTHORS
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ACCESSION
VERSION
KEYWORDS
SOURCE
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Ratio: 1.000
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/db_xref="taxon:32644"
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Sequence 15 from Patent WO9639505. A58696
Patent: WO 9639505-A 15 12-DEC-1996; ISIS INNOVATION (GB)
                                                             1 (bases 1 to 1316)
Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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! AR05575 Sequence 2 from pa
! AR05875 Sequence 2 from pa
! AY05875 Seguence 2 from pa
! U33284 Human protein tyrosi
! AF063890 Rattus norvegicus
! S80542 related adhesion foc
! D45854 Rattus norvegicus mR
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Griffiths, R. and Tiwari, B.
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/db_xref="taxon:32644"
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Griffiths,R. and Korn,R.M.
A CHD1 gene is z chromosome linked
Gene 197 (1-2), 225-229 (1997)
97475516
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Griffiths,R. and Kor
Direct Submission
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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HIRTHEMMHPQTYRFLKENILLTTYEILLKDKS FIGGLKWAFIGVDEAHRLKNIDSSLLY
RTLIDFKSNHRLLITGTPFLONSLKELMSLHFINPEKFSSWEIGFDEEBHGKGREYGYAS
IHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALOKOYYKWILTRNYKALSKGSKG
STSGFLNIMMELKKCCNHCYLIKPDDWEFYNNQEALOHLIRSSGKLIILDEKLLIRLR
ERGNRVLIFSOMVEMLDILABYLKYROFPFORLDGSINGELKROALDHFNAEGSEDFC
FLLSTRAGGLGINLASADTVVIFDSDWNPQNDLOAQARAHRIGOKKQVNIYRLVTKGS
WEEDILERAKKKNYLDHLYIGRADTTOKTVLHTGSTPSSSTPFNEELSAILKGAEB
LFKEPBGEEGOEPOEMDIDEILKRAFTRENEPGPLTVGDELLSOFKVAHFSNMDEDDIE
LEPERNSRNWEEIIPESORRRIEEEEFQKELEEIYMLPRMRNCAKQISFNGSBGRRSR
                                             SRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLERLD
AVARDAELVDKSETDLRRLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPTFRISGV
QVNAKLVISHBEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSNLLVGI
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CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
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LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERII
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DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
DDDEDYDKRGSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTEEDEFETIEKFMD
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                         YEYGYGSWEMIKMDPDLSLTQKILPDDPDKKPQAKQLQTRADYLIKLLNKDLARKEAQ
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/note="CHD protein with hydrophilic domain
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/db_xref="GI:2501846"
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/db_xref="taxon:9031"
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(CHD-Z) mRNA, compl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
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BASE COUNT ORIGIN

2446 a

misc_feature

alignment_scores:

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alignment_block:
US-08-973-363-9 x AF004397
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                Quality: 27.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                             Align seg 1/1 to: A58684 from: 1 to: 153
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A58684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 153)
Griffiths, R. and Ti
                                                                                                                                                                                                                                                                                                                                                                               ISIS INNOVATION (GB)
Other publication AU 5906996 961224
                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: WO 9639505-A 3 12-DEC-1996;
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                                                                                                                                                                                                                                                                                           /organism="unidentified"
/db_xref="taxon:32644"
a 40 c 31 g 24
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THVIRNPOVERLKETTWHDDSSROSYSSDRHLSQYEDHHKDRHGGDAYKKSDSRKREY
SAFSNGKDHRDWDHYKQDSRYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
SDHRIHSDHRSTSEYSHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
HRSPFEHSSDHKSTPBHTWSSRKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="short insert found in longer variant mRNA of CHD-2"
1223 c 1520 g 1683 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tiwari, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 34
Gaps: 0
Percent Identity: 100.000
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: 100.000
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                                                                                                                                                              REFERENCE
AUTHORS
TITLE
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SOURCE
ORGANISM
                                                                         JOURNAL
MEDLINE
REFERENCE
AUTHORS
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AUTHORS
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LOCUS A58685
DEFINITION Sequence 4 fi
ACCESSION A58685
                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_ro:MUSCHD1x
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US-08-973-363-9 x A58685
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ACCESSION
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Ratio: 1.000
Percent Similarity: 100.000
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                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 SLeuLeuAsnLysAspLeuAlaArgLysGlu 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 5349)

Delmas, V., Stokes, D.G. and Perry, R.P.

A mammalian DNA-binding protein that contains a chromodomain and a SNF2/SWI2-like halicase domain

Proc. Natl. Acad. Sci. U.S.A. 90 (6), 2414-2418 (1993)
                                                                                                                                                                                                                                                                                       Mouse DNA-binding protein
L10410 x66028
L10410.1 GI:455014
DNA binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other publication AU 5906996 961224.
Submitted (08-APR-1993) Robert Perry, The Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA On Feb 16, 1994 this sequence version replaced g1:293322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: WO 9639505-A 4 12-DEC-1996;
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Griffiths, R. and Ti
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                                                          Direct Submission
                                                                                                                                                                                                                                                                         house mouse.
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AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION IN
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                                                                                           (bases 1 to 5349)
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/db_xref="taxon:32644"
36 c 31 g 30
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1. .153
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Percent Identity: 100.000
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in (CHD-1) mRNA, complete cds
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DEFINITION ACCESSION VERSION

KEYWORDS

ORGANISM

unidentified.

unclassified

REFERENCE

COMMENT

JOURNAL TITLE

FEATURES

source

BASE COUNT

82

seq_documentation_block:

seq_name: gb_pat:A58684

4180 AA 4181

34 lu 34

us-08-973-363-9 x A58684

alignment_scores: Quality: Ratio:

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alignment_block:
US-08-973-363-9 x MUSCHD1X
VERSION
KEYWORDS
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                                                                                                                                                                                             seq_name:
                                                          ACCESSION
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                                                                                                                                                                                                                                                        CCGTGCAGACTACCTCATCAAACTACTT 4103
                                                                                                                                                                                          gb_pr:AF006513
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Ratio:
                                                    Homo sapiens CHD1 mRNA, AF006513
                             AF006513.1 GI:2645428
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CFLLSTRAGGLGINLASADTVVIFDSDWNPQNDLQAQARAHRIGQKKQVNIYRLVTKG
SVEEDILERAKKKMVLDHLVIQRWDTTGKTVLHTGSAPSSSTPFNKEELSAILKFGAE
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YKTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYA
SLHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYKWILTRNYKALSKGSK
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IAHSNQKSAAGLEDYYCKWQGLEYSECSWEDGALISKKRQTCIDEYFSRNQSKTTEPK
DCKVLKQPRFRYALKKOPSYIGGHEGLELDYDLNGLAHSWCKGNSCILADEWG
GKTIQTISFLNYLFHEHQLYGPFLLVVPLSTLTSWQREIQTWASQMNAVVYLGDINSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \label{eq:constraint} QYHDHHKDRHQCDSYKKSDSRKRPYSSFSNGKDHREWDHYRQDSRYYSDREKHRKLDD HRSREHRPSLEGGLKDRCHSDHRSHSDHRMHSDHRSSSEHTHHKSSRDYRYLSDWQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRSKKSVVSDAPVHITASGEPVPIAEESEELDQKTFSICKERMRPVKAALKQLDRPEK
GLSEREQLEHTRQCLIKIGDHITECLKEYSNPEQIKQWRKNLWIFVSKFTEFDARKLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IYEYGYGSWEMIKMDPDLSLTHKILPDDPDKKPQAKQLQTRADYLIKLLSRDLAKREA
QRLCGAGGSKRRKTRAKKSKAMKSIKVKEEIKSDSSPLPSEKSDEDDDKLNDSKPESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSRRYSGSDSDSISERKRPKKRGRPRTIPRENIKGFSDAEIRREIKSYKKFGGPLERL
DAIARDAELVDKSETDLRRLGELVHNGCVKALKDSSGTERAGGRLGKVKGPTFRISG
VQVNAKLVIAHEDELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLLIG
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ELEPERNSKNWEEIIPEEQRRRLEEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRS
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1.000
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/protein_id="AAB08486.1"
/db_xref="GI:455015"
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171. .5306
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/db_xref="taxon:10090"
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                                                                              complete cds.
                                                                                                         5947 bp
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Gaps:
                                                                                                         mRNA
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0
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alignment_block: US-08-973-363-9 x AF006513

Percent Similarity:

Align seg 1/1 to: AF006513

from: 1

to: 5947

alignment_scores:

Quality:

Ratio:

26.00 1.000 100.000

Gaps: Percent Identity:

Length:

26 0 100.000

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REFERENCE
AUTHORS
TITLE
BASE COUNT
ORIGIN
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TITLE
JOURNAL
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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RLRERGNRVLIFSQMVRNLDILAEYLKYRQFPFQRLDGSIKGELKRQALDHFNNEGSE
DFCFLLSTRAGGLGINLASADTYVIFDSDWNPQNDLQAARAHRIGOKKQVNIYRLYF
KGSVEEDILERAKKKMVLDHLVIQRMDYTGKTVLHTGSAPSSSTPFNKEELSAILKFG
AEELFKEPEGEEQEPQEMDIDEILKRAETHENEPGPLTVGDELLSQFKVANFSNMDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKDCKYLKQRPRFYALKKQPSYIGGHEGLELRDYQLNGLNWLAHSWCKGNSCILADEM
GLGKTIQTISELNYLFHBHQLYGPFLLVVPLSTLTSWQRBIQTWASQMNAVYXLGDIN
SRNMIRTHEWTHHQTKRLKFNILLTTYBILLKDKAFLGGLIWAFIGVDEAHRLKNDS
LLYKTLLDFKSHRRLLTIGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEBHGKGREYG
YASLHKELEPFLLRRVKKDVEKSLPAKVEQILRMEMSALQKQYYKWILTRNYKALSKG
                                                                                                                                                                                                                                     SGVQVNAKLVISHEEELIPLHKSIPSDPEERKQYTIPCHTKAAHFDIDWGKEDDSNLL
IGIYEEYGYGSWEMIKMDPDLSLTHKILDDDPDKEPOAKOLQTRADYLIKLLSEDKSDEK
EALSGAGSSKERKRARAKKKMKMSIVVKEEIKSDSSPLPSEKSDEDDDKLSESKSDEDDKE
ERSKKSSVSDAPVHITASGEPVPISEESEELDQKTFSICKERMRPVKAALKQLDRPEK
                                                                                                                                                                                                                                                                                                                                                                                                              DIELEPERNSKNWEEIIPEDQRRRLEEEEERQKELEEIYMLPRMRNCAKQISFNGSEGR
RSRSRRYSGSDSDSISEGKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EETLKQQNVRGMKKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVG
RIIAHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALISKKFQACIDEYFSRNQSKTTP
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KKQQQQQQQQQHQASSNSGSEEDSSSSSEDSDDSSSEVKRKKHKDEDWQMSGSGSPSQS
                                                                    RASSSGPRSPLDQRSYGSRSPFEHSVEHKSTPEHTWSSRKT
                                                                                                                                                                                                     GLSEREQLEHTRQCLIKIGDHITECLKEYTNPEQIKQWRKNLWIFVSKFTEFDARKLH
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                                                                                                    RSRDHRSNLEGSLKDRSHSDHRSHSDHRLHSDHRSSSEYTHHKSSRDYRYHSDWQMDH
                                                                                                                                        YHDHHKDRHQGDSYKKSDSRKRPYSSFSNGKDHRDWDHYKQDSRYYSDREKHRKLDDH
                                                                                                                                                                     KLYKHAIKKRQESQQNSDQNSNLNPHVIRNPDVERLKENTNHDDSSRDSYSSDRHLTQ
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164. .5293
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/db_xref="taxon:9606"
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seq_name: gb_pr:AC012624
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US-08-973-363-9 x AC092372/rev
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                                        26882 CCGTGCAGACTACCTCATCAAATTACTT 26855
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Ratio:
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Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
Location/Qualifiers
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
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Homo sapiens chromosome 5 clone RP11-58M12, complete sequence
AC092372
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101220)
DE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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/db_xref="taxon:9806"
/db_cref="toxon:9806"
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/ 18862 c 17827 g 30409 t
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alignment_block:
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LOCUS AC021449
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Submitted (21-7UI-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jul 21, 2001 this sequence version replaced gi:14277267.
Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143079)
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Submitted (01-7UN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone CTD-2082117, complete sequence.
AC012624
                                                                               Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT
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DOE Joint Genome Institute.
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
DDE Joint Genome Institute and Stanford Human Genome Center.
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JOURNAL
REFERENCE
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TITLE
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J., Talamas, J., Talamas, J., Tesfaye, S., Theodore, J., Stojanovic, N., Sastlev, H., Vel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Talamas, J., Tesfaye, S., Theodore, J., Stojanovic, N., Sastlev, H., Vel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Theodore, J., Stojanovic, N., Sastlev, H., Vel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Theodore, J., Walley, R., Welley, H., Vel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Theodore, J., Stojanovic, M., Sastlev, H., Vel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Theodore, J., Theodor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-58M12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 143079)
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Insert size: 142179; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Tonsensus quality: 140814 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project Information Center project name: L5154 Center clone name: 58_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                          51831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40412 40511: gap of 100 bp
40512 43279: contig of 2768 bp in length
43280 43379: gap of 100 bp
43380 46905: contig of 3526 bp in length
46906 47005: gap of 100 bp
47006 51830: contig of 4825 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38821 38920: gap of 100 bp
38921 40411: contig of 1491 bp in
40412 40511: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                  62719:
                                                                 92616:
                                                                                                                                                                                             75508:
                                                                                                        1930: gap of 100 bp in 16 62619: contig of 10689 bp in 16 12719: gap of 100 bp in 16 75408: contig of 12689 bp in 16 75508: gap of 100 bp 100 
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KEYWORDS
SOURCE
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US-08-973-363-9 x AC021449
                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AC008531
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                REFERENCE
                                                                         REFERENCE
                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                 seq_name: gb_htg:AC008531
                                                                                                                                                              VERSION
                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 100.000
                                            AUTHORS
TITLE
                                                                                                                                                                                                                                                                                             116197 CCGTGCAGACTACCTCATCAAATTACTT 116224
                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                     ORGANISM
 AUTHORS
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                                                                                                                                                                                                                                                                                                                         17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                            1 (bases 1 to 145659)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
2 (bases 1 to 145659)
DOE Joint Genome Institute.
                                                                                                                                           AC008531.3 GI:12830078
HTG: HTGS_PHASE2; HTGS_DRAFT.
                                                                                                                                                                             AC00853
                                                                                                                                                                                                       AC008531 145659 bp
Homo sapiens chromosome 5 clone
                           Unpublished
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                     Homo sapiens
                                                                                                                                    numan
                                                                                                                                                                                           7 ordered pieces.
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106510 143079: contig of 36570 bp in length.
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75509 92516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
47006. .51830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
106510. .143079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-58M12"
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26246 c 26678 g 45278 t
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CTC-480B11,
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                                                                                                                                                                                                          linear
, WORKING
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DRAFT SEQUENCE,
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TITLE

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alignment_block:
US-08-973-363-9 x AC008531
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seq_name: gb_htg:AC091946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 26.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                       46820 CCGTGCAGACTACCTCATCAAATTACTT 46847
                                                                                                                                                                                                                     46770 ATTCTTCCAGATGATCCCGATAAAAAACCACAAGCAAAACAGTTGCAGAC 46819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                            17 rArgAlaAspTyrLeuIleLysLeuLeu 26
                                                                                                                                                                                                                                                       1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh 17
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Consensus quality: 139128 bases at least Q40

Consensus quality: 142556 bases at least Q30

Consensus quality: 142556 bases at least Q30

Consensus quality: 143744 bases at least Q30

Consensus quality: 143744 bases at least Q30

Consensus quality: 143745 bases at least Q30

Estimated insert size: 148000; pulse field gel estimation

Quality coverage: 6.7 in Q20 bases; pulse field gel estimation

Quality coverage: 6.4 in Q20 bases; pulse field gel estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 15674; contig of 61674 bp in length

* 56275 100874; contig of 44600 bp in length

* 110875 100974; gap of unknown length

* 111328 111327; contig of 12153 bp in length

* 111328 111327; gap of unknown length

* 111328 11190; contig of 1404 bp in length

* 111995 112974; gap of unknown length

* 111995 112979; contig of 3503 bp in length

* 111995 112397; contig of 3503 bp in length

* 112328 12397; contig of southown length

* 11328 13297; contig of southown length

* 11328 13297; contig of southown length

* 11328 13297; contig of southown length

* 11329 12397; contig of southown length
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Direct Submission
Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Feb 14, 2001 this sequence version replaced 91:7528342.
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Center Project Name: 369535
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/clone_lib="CalTech human BAC library C"
_ 26309 c 27580 g 48609 t 600 others
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/db_xref="taxon:9606"
/chromosome="5"
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145659: contig of 22262 bp in length.
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LOCUS AC091946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q20
Consensus quality: 18075 bases at least Q20
Consensus quality: 18075 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; agarose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1358. Contig of 1358 bb is least
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ------Genome Center Center: Joint Genome Institute
Center Code: JGI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193446)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
Direct Submission
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12561
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A 1358: contig of 1358 bp in length
1458: gap of unknown length
2667: contig of 1209 bp in length
3823: contig of 1056 bp in length
3923: gap of unknown length
5920: contig of 1957 bp in length
6020: gap of unknown length
7494: contig of 1474 bp in length
7596: contig of 1502 bp in length
7996: contig of 1502 bp in length
10260: contig of 1502 bp in length
10260: contig of 1604 bp in length
10260: contig of 1064 bp in length
10260: contig of 1064 bp in length
10260: contig of 1064 bp in length
10460: contig of 2070 bp in length
10460: contig of 2070 bp in length
10461: contig of 2070 bp in length
10461: contig of 1670 bp in length
10461: contig of 2366 bp in length
10434: contig of 2366 bp in length
20534: gap of unknown length
20534: gap of unknown length
23655: gap of unknown length
23655: contig of 2368 bp in length
23655: contig of 3948 bp in length
23655: contig of 3948 bp in length
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DEFINITION ACCESSION
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US-08-973-363-9 x AC091946
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                                                   seq_name: gb_pr:AC026778
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Ratio: 1.000
Percent Similarity: 100.000
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Homo sapiens chromosome 5 clone CTC-428I11, AC026778
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/db_xref="taxon:9606"
/chromosome="5"
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/clone_lib="RPCI human BAC library 11"
35252 c 37061 g 60360 t 3202 others
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110866: contig of 7972 bp in length
110966: gap of unknown length
117571: contig of 6605 bp in length
117571: contig of 6605 bp in length
117671: gap of unknown length
123738: contig of 6067 bp in length
123838: gap of unknown length
130583: contig of 6745 bp in length
130683: gap of unknown length
130683: gap of unknown length
141544: contig of 10861 bp in length
141544: gap of unknown length
141644: gap of unknown length
169109: contig of 27465 bp in length
169209: gap of unknown length
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Gaps: 0
Percent Identity: 100.000
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Submitted (24-MAR-2000) Production Sequencing Facility,
Submitted (24-MAR-2000) Production Sequencing Facility,
                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 219258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu Quality: Phrap Quality >=40 99.9% of Sequence; Estimated Total Number of Errors is 0.2.
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Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:13677045.
Draft Sequence Produced by DOE Joint Genome Institute
Www.jgi.doe.gov
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DOE Joint Genome Institute and Stanford Human Genome Center.
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WI-13675 G23101
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3 (bases 1 to 195433)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Joint Genome Institute and
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Stanford Human Genome Center.
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AL Submitted (210-201) DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission

AL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 21 3 (bases 1 to 219258)

RS DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission

AL Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submission

AL Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

DOE Joint Genome Institute and Stanford Human Genome Center. Direct Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

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STS Content: WI-5811 G04974 WI-15875 G23101 SHGC-5844 G38487 SHGC-103595 G57841.
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/db_xref="taxon:9806"
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Query: US-08-973-363-9
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                                                                                                                                                                                                                                                                    OMALITY: 34.00
Ratio: 1.000
Percent Simularity: 100.000
                                                          Align seg 1/1 to: AAT42759
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from: 1

to: 153

Length: 34
Gaps: 0
Percent Identity: 100.000

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seq_documentation_block:
ID AAT42759 standard; DNA; 153 BP.
XX
AC AAT42759;
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AC AAT42759;
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AC AAT42759;
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AC AAT42759;
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AC AAT42759;
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AC AAT42759;
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AC AAT42759;
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Bird; sex determination; chromodowne; ss.
XX

Bird; sex determination; chromodowne; ss.
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Parus major.

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FT | Location/Pub/F | Security | Securit
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                Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                           Bases 3855-3977 (AAR142756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1a (A = Avian) gene (AAR142757), chicken CHD-W (W refers to the W chromosome) gene (AAR142758) and and the great tit CHD-W gene (AAR142759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAR142751) and CHD-W (see also AAR142754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          key Location/Qualifiers misc_difference 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bird; sex determination; chromodomain-Helicase-DNA binding CHD-lA; CHD-W; W chromosome; ss.
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alignment_scores:
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ID AAT42754 standard; cDNA; 1316 BP
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                                                                        alignment_block:
US-08-973-363-9 x AAT42754
                                                                                                              Quality: 34.00
Ratio: 1.000
Percent Similarity: 100.000
                                             Align seg 1/1 to: AAT42754
                                                                                                                                                                                                                                               The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a Wchromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102
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                                                                                                                                                                                                                                                                                                                                                                                                                           Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
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                                                                                                                                                                                                         Sequence 1316 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-043127/04.
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1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAAACCACAGGCAAAGCAGTTGCAGACCCGTGCAGATTACCTCATTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex determination; chromodomain-Helicase-DNA binding 1; chromodomain-Helicase-DNA binding on the W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-GB01341
                                                                                                                                                                                                         492 A;
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alignment_block:
US-08-973-363-9 x AAT42751
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ID AAT42751 standard;
                                                                                                                                                                                                  alignment_scores:
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                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                  The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-1A was deduced from 3 clones isolated from a stage 10-12 chicken embryo cDNA library using a great tit CHD-W sequence (see also AAT42755) as probe. The CHD-1A (A = Avian) gene shows close identity to the mouse CHD-1 gene (see also AAT42756-57). It is located on an autosome or Z chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-1A nucleic acids can also be used to control the sex of the progeny of a bird.
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                                                                                                                                                                                                                                                                                               Sequence 6608 BP; 2289 A; 1207 C; 1459 G; 1653 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 5; 76pp; English.
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TCGTGCAGATTACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGG
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                                                                                                                                                                Quality:
                                                                                                                                  Ratio:
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AAT42751

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seq_documentation_block:
ID AAT42757 standard; DNA; 153 BP.
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                 Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAM08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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P-PSDB; AAW08147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chick CHD-1A gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT42757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995; 95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9639505-A1
                                                                                                                                                                  Sequence 153 BP; 58 A; 40 C; 31 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 lu 34
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                          Quality:
Ratio:
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                                                     27.00
Percent Identity: 100.000
                                                     Length:
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alignment_block:
US-08-973-363-9 x AAT42757
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ID AAT42758 standard; DNA; 153 BP
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                        Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A - Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                               Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                  WPI; 1997-043127/04.
                                                                                                                                                                                                                                                                                                                  Griffiths R, Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers misc_difference 52.81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHD-1A; CHD-W; W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chick CHD-W gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT42758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 ATTACTGAATAAAGACCTTGCAAGAAAGGAA 132
Sequence 153 BP; 56 A; 36 C; 31 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                    P-PSDB; AAW08148
                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 AAGAAACCCCAGGCAAAGCAGCTACAGACCCGTGCAGACTACCTCATTAA 101
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                                                                                                                                                                                                                                                                                                                                                                                    95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-GB01341
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and are ignored in the translated amino
acid sequence given in Fig 3"
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alignment_scores:

Quality: 27.00 Ratio: 1.000 Percent Similarity: 100.000

Length: 27
Gaps: 0
Percent Identity: 100.000

alignment_block: US-08-973-363-9 x AAT42758

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seq_documentation_block:
ID AAV59280 standard;
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                     The altered vertebrate telomere repeat binding protein (A-TRF) has a telomere repeat binding factor (TRF) dimerisation domain, and forms a hetero-dimer with TRF, preventing it from binding to the specified repeat sequence. A-TRF, optionally expressed by gene therapy, is used to inhibit shortening of telomeres associated with ageing (for cosmetic purposes) and disease, e.g. ataxia telangeictasia, Down's syndrome, atrophy of the skin, age-related macular degeneration, atherosclerosis, tumours and viral (including human immune deficiency virus) infection. Cells expression of recombinant proteins or where intended for subsequent transplant or for testing, eliminating the need for transformation.
                                                                                                                                                                                                       Claim 14; Page 110-111; 163pp;
                                                                                                                                                                                                                                                                                                                                                        Bianchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-1998;
13-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; human; telomere repeat binding factor; A-TRF; dimerisation domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102
Sequence 1311 BP;
                                                                                                                                                                                                                                        also
                                                                                                                                                                                                                                                                  Nucleic acid encoding altered telomere repeat binding protein and related vectors - transformants, hetero-dimers and antibodies, us
                                                                                                                                                                                                                                                                                                              P-PSDB; AAW59280.
                                                                                                                                                                                                                                                                                                                              WPI; 1998-480769/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                      (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     telomere; ageing; ataxia telangeictasia; Down's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 sLeuLeuAsnLysAspLeuAlaArgLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52
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                                                                                                                                                                                                                                      inhibit shortening of telomerases so used to extend life of cells in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysLysProGlnAlaLysGlnLeuGlnThrArgAlaAspTyrLeuIleLy
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                                                                                                                                                                                                                                                                                                                                                         De Lange T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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97US-0800264
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1..1311
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/product= "A-TRF"
441 A; 257 C; 316 G;
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                                                                                                                                                                                                                                      caused by ageing culture
297 T; 0 other;
                                                                                                                                                                                                                                                    or disease,
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alignment_block:
US-08-973-363-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1237 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
                                            Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (see also and AAT42757), chicken CHD-W (W refers to the W chromosome) gene (see also AAT42758) and the great tit CHD-W gene (see also AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify
                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_difference
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                                  the sex of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse CHD-1 gene (bases 3855-977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IleLeuProAspAspProAspLysLysProGlnAlaLysGlnLeuGlnTh
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                                                                                                                                                                                                                     1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42756
                                                                                                                                             8; Fig 3; 76pp; English.
                                                                                                                                                                     chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHD-W;
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                                   an embryo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 153 BP
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                                  foetus etc. and to manipulate the sex of
                                                                                                                                                                                                                                                                                                                                                                                          "bases 52-81 are a repeat of bases and are ignored in the translated acid sequence given in Fig 3"
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Sequence 153

BP;

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alignment_block:
US-08-973-363-9 x AAT42756
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG105-ABL30511), expressed DNA sequences (ABLIG1675) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 13811.
                                                                                                                                                                                                                                Claim 1; SEQ ID NO 13811; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL06443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 ACTACTT 108
                                         (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                     Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical; gene;
Sequence 6240 BP; 1675 A; 1682 C; 1760 G; 1123 T; 0 other.
                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABB62340
                                                                                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
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alignment_scores:

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alignment_block:
US-08-973-363-9 x ABL06443
alignment_block:
US-08-973-363-9 x ABL06442
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ID ABL06442 standard; cDNA; 9933 BP.
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                                                     Percent Similarity: 100.000
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                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABLIG10511), expressed DNA sequences (ABLIG1840-ABLIG175) and the encoded proteins (ABLO1840-ABLIG175) and the encoded proteins The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                               Sequence 9933 BP; 2711 A; 2468 C; 2538 G; 2216 T; 0 other;
                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 13808; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY.
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11-JUL-2000; 2000US-0614150.
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; digestive system antigen; gene therapy; cancer; appendicitis; ulcerative colitis; infection; Hirschsprung's disease; chronic colitis; digestive system disorder; Meckel's diverticulum; ss.
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2000US-0234274
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ID AAI57603 standard; cDNA; 421 BF
XX
AC AAI57603;
XY
DT 19-CCT-2001 (first entry)
XX
DE Human colorectal cancer antigen
XX
OS Homo sapiens.
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US-08-973-363-9 x AAK88882
                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAI57603
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynuclectides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
                                                                                                                       Human colorectal cancer antigen cDNA SEQ ID NO: 67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1198; 986pp; English.
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P-PSDB; AAM93109.
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                                                             Human; colorectal cancer; colorectal cancer antigen; gene therapy; ss.
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2000US-0259390.
2000US-0259391.
2000US-0251988.
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Gaps: 0
Percent Identity: 100.000
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2000US-0205515.
2000US-0209467.
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preventing and/ or prognosing rectum including colorectal cale.g. diagnosis -

colorectal cancers

sequences

of

in the and/or rectum.

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17-NOV-2000
17-NOV-2000
01-DEC-2000
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                   GENOME SCI INC
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ID AAV33521 standard;
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US-08-973-363-9 x AAI57603
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Human kinase poly:nucleotide(s) and recombinant products - useful for identification of modulators of the enzyme, and treatment of diseases associated with abnormal kinase expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            number of colorectal cancer antigens. These are shown in AAI57647-AAI57619 and AAM38669-AAI38641. These can be used in the diagnosis, prevention and treatment of cancer of the colon and/or recturate present sequence is a colorectal cancer antigen coding sequence of the present sequence is a colorectal cancer antigen coding sequence of the invention.
                                                                                                                                                                                                                                                                                  Protein kinase; cell signalling; inflammation; carcinoma; diabetes; human X-linked agammaglobulinaemia; nonspherocytic haemolytic anaem artherosclerosis; glioma; restenosis; cholera-based septic shock; CHKFRNK chiken tyr kinase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide disorders related to and also for testing
                                                                                                                                                                     07-AUG-1996;
                                                                                                                                                                                                                             US5817479-A
                                                                                                                                                                                                                                                                                                                                                       Clone 23789 cDNA fragment encoding a human protein kinase homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 AAGCAGCTACAGACCCGAGCGGATTACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-457727/49.
P-PSDB; AAM38625.
                                                                                                               (INCY-) INCYTE PHARM INC.
                                                                                                                                            07-AUG-1996;
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                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                     Bandman O,
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and
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colon and
detection
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Percent Identity:
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to:

421

Length:

100. .00 61 T; 7 other;

175 22

anaemia;

Wilde င္ပ

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seq_documentation_block:
ID ABA61903 standard; DN
XX ABA61903;
XX Human foetal liver;
XX Human; foetal liver;
XX Human; foetal liver;
XX Human; foetal liver;
XX WO200157277-A2.
XX WO20015727-A2.
XX WO200157270-A2.
XX ABA61903;
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US-08-973-363-9 x AAV33521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA61903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention provides polynucleotides which encode novel protein kinase homologs expressed in various human cells and tissues. The present sequence represents the clone 23789 cDNA fragment derived cfrom a human inflammed adenoid cDNA library. The cDNA encodes a protein kinase which shows homology to the CHKFRNK chiken tyr kinase. Vectors and host cells can be used for recombinant production of the protein kinase homolog. The recombinant production of the polynucleotide sequences, i.e. probes and antisense constructs, the peptides and antibodies are claimed to be useful as tools for the polynucleotide sequences, i.e. probes and antisense constructs, the peptides and antibodies are claimed to be useful as tools for studying signalling cascades in cells and proteins, and for identifying inhibitors (drugs) to treat diseases and inflammatory conditions associated with abnormal kinase expression. Diseases that are claimed to be treatable include human x-linked agammaglobulinaemia, onespecytic haemolytic anaemia, artherosclerosis, carcinomas, diabetes, gliomas, restenosis, cholera-based septic shock, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity: 100.000
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          Human genome-derived single exon nucleic acid probes useful for
                                                                                                        WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human foetal liver single exon nucleic acid probe #10208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABA61903 standard; DNA; 544 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AAACTGCTCAACAAAGACCTGGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 252 BP; 63 A; 70 C; 72 G; 47 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Columns 29-30; 30pp; English.
                                                                                                                                                                                               Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
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); 2000US-0207456.

); 2000US-0608408.

); 2000US-0632366.

); 2000US-0234689.

); 2000US-0236539.

); 2000US-0236539.
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                                                                                                                                                                                               Chen W,
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                                                                                                                                                                                                     Rank DR;
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seq_documentation_block:
ID AAK10214 standard; DNA; 544 BP
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US-08-973-363-9 x ABA61903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 100.000
                                                                                                                                                                                          04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-0508408; 30-JUN-2000; 2000US-0508408; 03-AUG-2000; 2000US-0532366; 21-SEP-2000; 2000US-0234687; 27-SEP-2000; 2000US-0234589; 04-OCT-2000; 2000GB-0024263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                  Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single exon probe SEQ ID NO: 10205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAK10214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 TACCTGATAAAGTTATTAAATAAG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 544 BP; 144 A; 128 C; 88 G; 184 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 10208; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing gene expression in human fetal liver -
                                                                                             WPI; 2001-483446/52.
                                                                                                                              Penn SG,
                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                 WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epilepsy; cancer;
                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 TyrLeuIleLysLeuLeuAsnLys 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.000
                                                                                                                              Chen W, Rank DR;
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Gaps: 0
Percent Identity: 100.000
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Example 4; SEQ ID NO: 10205; 650pp + Sequence Listing; English

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seq_documentation_block:
ID AAK36112 standard; DN
XX
AC AAK36112;
XX
O6-NOV-2001 (first e
DT 06-NOV-2001 (first e
XX
VX
Human bone marrow ex
XX
Human; bone marrow ex
XX
W Human; bone marrow ex
XX
W Homo sapiens.
XX
O9-AUG-2001; 2001W0-1
XX
O9-AUG-2001; 2000US-1
PN 04-FEB-2000; 2000US-1
PR 26-MAY-2000; 2000US-1
PR 26-MAY-2000; 2000US-1
PR 21-SEP-2000; 2000US-1
PR 21-SEP
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US-08-973-363-9 x AAK10214
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon;
microarray; cancer; leukaemia; lymp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243
                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed single exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCTGATAAAGTTATTAAATAAG
                                                                                                                                                                                                                                                                                                                genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                   SEQ ID NO: 10669; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0180312
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
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                                                                                                                                                                                                                                                                                            expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA; 544 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leukaemia; lymphoma; myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 C;
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Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                            human
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Rank DR;
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                                                                                                                                                                                                                                                                                              bone
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alignment_block:
US-08-973-363-9 x AAK36112
                                                                                                                alignment_scores
                                                                                                                                             SO
                                     Align seg 1/1 to:
                                                                                    Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                             Sequence 544 BP;
243 TACCTGATAAAGTTATTAAATAAG
           21 TyrLeuIleLysLeuLeuAsnLys
                                       AAK36112
                                                                                                                                             144 A;
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9b_est1:BB461065
9b_est2:BB95133
9b_est1:BB95133
9b_est1:BB95133
9b_est1:BB95737
9b_est1:BB930730
9b_est1:BB930930
9b_est1:BB930958
9b_est2:BB930958
9b_est2:BB930958
9b_est2:BB930958
9b_est2:BB930958
9b_est2:BB36295
9b_est1:AW168274
9b_est1:AW168274
9b_est2:BM366210
9b_est2:BM3665102
9b_est2:BM366624
9b_est2:BM366624
9b_est2:BM366629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database sequences: 13736207
Database length: -1841457050
Search time (sec): 4311.510000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
Query: US-08-973-363-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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-DB-EST -QFMT-fastap -SUFFIX-011p2n.rst -GAPOP-4.500
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-THR_MIN-1 -ALIGN-15 -MODE-LOCAL -OUTEMT-pfs -NORM-ext
-HBAPSIZE-500 -MINLEN-0 -MAXLEX-20000000
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47 i AL899775 wm95fl1 xl NCI_CGAP_Ut

19 i BB15356 BBL65365 RIKEN full-le

50 i BB461065 BB461065 RIKEN full-le

19 i BB25712 AU125712 NT2RW4 Homo

50 i BB25713 A0125712 NT2RW4 Homo

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50 i BB29730 BB20730 RIKEN full-le

60 i BB29730 BB20730 RIKEN full-le

61 i BB23967 601905170F1 NIH_WGC_54

62 i BB23967 601905170F1 NIH_WGC_54

63 i AW997058 QV3-BN0047-130400-152-1

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65 i AL286261 Tetraodon nigroviridia

99 i BF881342 PMn-ET0208-031200-0011-1

60 i AL286261 Tetraodon nigroviridia

90 i BF881342 PMn-ET0208-031200-0011-1

61 i AL286261 Tetraodon nigroviridia

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62 i AU397768 QV3-BN0047-15040-150-1001-1

63 i AU36776 G2397 Osteoclast Subtra
AW162274 x952001.X1 NC1_CCAP_UT
BW162976 BS320051000p4 Subtract
IN49703 yy23e03.S1 Soares fetal
AN305759 EST176834 COLOR CARCUT
ALBOM50 W146f05.X1 NC1_CCAP_UT
H61027 yr50f12.S1 Soares fetal
AN305756 BS320017000E12 Subtract
BW165102 BS320017000E12 Subtract
BW165102 BS320017000E7 Subtract
BW165102 BS320017000E7 Subtract
BW165108 BS32002300E3 Subtract
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gb_gss:AQ794671
gb_est1:AA177423
gb_est2:H38315
gb_est1:AA477858
gb_est1:AA477856
gb_est2:BF901677
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ORIGIN
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LOCUS AL659353
            seq_documentation_block:
LOCUS AL644594
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US-08-973-363-9 x AL659353/rev
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                                                                                                            seq_name: gb_est1:AL644594
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_ESQUENCE_ID: TNeu045e20.sp6
Sequencing primer: SP6
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
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//bb_xref="taxon:8364"
//bb_xref="taxon:8364"
//clone=_lib="xGC-neurula"
//dev_stage="neurula"
//dev_stage="neurula"
//lab_host="tescherichia coli DH10B"
//note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from neurula.
EcoRI at the 5', end and NotI at the 3', end."

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                mRNA
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linear

EST 07-NOV-2001

DEFINITION

AL644594 XGC-egg

Silurana tropicalis cDNA clone L1E1d12 5', mRNA

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ACCESSION
VERSION
KEYWORDS
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US-08-973-363-9 x AL644594
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ORIGIN
                       REFERENCE
                                                                                 SOURCE
                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                     seq_name: gb_est1:AL601246
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                                                                                                                         KEYWORDS
                                                                                                                                               VERSION
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Ratio: 1.000
Percent Similarity: 100.000
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.

1 (bases 1 to 645)
1 (bases 1 to 645)
                                                                                                                                                                DKFZp313J1040_r1 313 (synonym: hlcc2) Homo DKFZp313J1040_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project
TROPICALIS_SEQUENCE_ID: L1E1d12.plc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J Sanger Xenopus tropicalis EST project 2001 (10_2001)
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae. 1 (bases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing primer: PlC This sequence is from a Xenopus Gene Collection constructed by Aaron M. Zorn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                               Homo sapiens
                                                                                                                         EST
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  Bloecker,H.,
                                                                                                      human.
                                                                                                                                            AL601246.1 GI:15164752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="XGC-egg"
/dev_stage="egg"
/lab_host="sscherichia coli XL1-blue"
/lab_host="sscherichia coli XL1-blue"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cD /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cD was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
a 125 c 156 g 141 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Silurana tropicalis"
/db_xref="taxon:8364"
/clone="L1E1d12"
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Boecher, M.,
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Brandt, P.,
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Gaps:
Mewes, W.,
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                                        Hominidae;
                                                                                                                                                                                                      sapiens cDNA clone
Weil,B.
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                                                           Euteleostomi;
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and Wiemann
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ACCESSION
VERSION
KEYWORDS
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LOCUS AI890775
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US-08-973-363-9 x AL601246
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                                                                                                                                                         AUTHORS
TITLE
                                                                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                  wm95f11.x1 NCI_CGAP_Ut2 Homo say
similar to SW:CHD1_HUMAN 014646
PROTEIN 1 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd.,
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 547)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone (DKFZp313J1040) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                               Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                   EST
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This is the 5' sequence of the clone insert
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                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                       Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No si sequence available.
cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pTriplEx2; Site_1:
cDNA-collection"
a 81 c 86 g 100 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="DKFZp313J1040"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
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1.000
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/db_xref="taxon:9606"
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Percent Identity:
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alignment_block:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 619)

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Insert Length: 1924 Std Error: 0.00
Seq primer: -40Up from Gibco
Seq primer: -40Up from Gibco
High quality sequence stop: 418.
Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Unpublished (2001)
On Jun 29, 2000 this sequence version replaced gi:8811286.
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                                                                                                                                                                                                                                                                                                              , Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinayawa, A., Shiraki, T., Soyabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
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/clone_lib="NCI_CGAP_Ut2"
/tissue_type="moderately-differentiated endometrial adenocarcinoma, 3 pooled tumors"
/lab_host="DH10B"
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Wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., wathiki, M., Yoneda, Y., Ishkawa, T., Ozawa, K., Tanaka, T., Matsuura S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara Y., Carninci, P., Sugahara T., Carninci, P., Sugahara
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
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URL:http://genome.gsc.riken.go.jp/
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                                                                                                                                                                                                                                                                                                                                                                                               194 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="thymus"
/dev_stage="16 days neonate"
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/lab_host="pH10B"
/nore="Site_1: Sal1; Site_2: BamHI; cDNA library was
/nore="Site_1: Sal1; Site_2: BamHI; cDNA library was
/norea" on d sequenced in Mouse Genome Encyclopedia
/project of Genome Exploration Research Group in Riken
/roject of Genome Exploration Research from in Riken
/roject of Genome Sciences Center and Genome Science Laboratory in
/rikethouse RIKEN. Division of Experimental Animal Research in Riken
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                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.p., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Large Control of Cap-trapper-selected CDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Large Charles (10), 1617-1630 (2000)
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Kara,A. and
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RIKEN Mouse ESTS (Arakawa,T., et al.
Unpublished (2001)
On Jul 21, 2000 this sequence versior
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                     Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                              prepare mouse tissues
                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome
                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                             Location/Qualifiers
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US-08-973-363-9 x BB461065
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                                                                                                                                                                                                                                                                                                                  TITLE
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481 ATTCTTCCAGATGATCCTGATAAAAAACCACAAGCAAAACAGTTACAGAC
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1532-3 Yana, Kisarazu, Tel: 81-438-52-3951 Fax: 81-438-52-3952
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 866)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU125712 MT2RM4 Homo sapiens cDNA clone NT2RM4002061
                                                                                                         Unpublished (2000)
Contact: Takao Isogai
                                                                                                                                                Saito, K., Yamamoto, J., Naki, Y., Sugano, S., Isogai, T.)
                                                                                                                                                                                            Isogai, T.
HRI human cDNA project (Ota, T.,
                                                                                                                                                                                                                                   Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuh
                                                                                                                                                                                                                                                                                                                                                                                                            AU125712.1 GI:10950428
                                                               Helix Research Institute
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m c} 168\ {
m g} 151\ {
m t}
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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spinal ganglion"
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/db_xref="taxon:10090"
/clone="D130070B13"
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/dev_stage="12 days embryo"
/lab_host="DH10B"
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l 5', mRNA
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US-08-973-363-9 x AU125712
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Ratio: 1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. CONSOrtium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9753 row: h column: 16
High quality sequence stop: 488.
Location/Qualiflers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1078)
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/cell_type="NT2"
/cell_type="NT2"
/cell_type="NT2"
/cell_type="NT2"
/cell_type="teratocarcinoma"
/cell_
/clone="IMAGE:3921087"
/clone_lib="NIH_MGC_72"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/tab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
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/db_xref="taxon:9606"
/clone="NT2RM4002061"
/clone_lib="NT2RM4"
                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-08-973-363-9 x BE895133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 337)

Dias NetO,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bad,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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QV3-BN0047-230200-102-d03 BN0047 Homo sapiens cDNA,
AW996787
                                                                                                                                                                                                                                                                                                                          This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=QV3-BN0047-230200-102-d03st3=2000-02-23st4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
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Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Average insert size 2 kb. Library co
Technologies."
a 205 c 238 g 198 t
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
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/db_xref="taxon:9606"
/clone_lib="BN0047"
/dev_stage="Adult"
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BB830730
                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Contact: Yoshihide Hayashizaki
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Eukaryota; M
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                   RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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LOCUS BB834922
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                                                                                                                                                                                                                                                                                                                                Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
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BB834922
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Computer-based methods for the mouse full-length cDNA
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction o
nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                 Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(SSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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m Jyg\text{-}MC(B)} CDNA Mus musculus cDNA clone G930033J21 3', mRNA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                         Fax: 81-45-503-9216
                                                                                                                                                                                                                                                     Unpublished (2001)
                                                                                                                                                                                                                                                                                                         RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
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                                                                                   -22 Suehiro-cho,
: 81-45-503-9222
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/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
1 96 c 108 g 96 t
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/db_xref="taxon:10090"
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                                                                                                             Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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REFERENCE
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LOCUS BF239967
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
                                                                                                                 Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 821)

NIH-MGC http://mgc.nci.nih.gov/.
mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone_lib="RIKEN [full-length enriched, mammary gland
RCB-0527 Jyg-MC(B) cDNA"
/tissue_type="mammary gland"
/cell_line="RCB-0527 Jyg-MC(B)"
g 9 c 108 g 100 t
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/db_xref="taxon:10090"
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LOCUS AW997058
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 686)
Dias Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Nagai,M.A., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneal,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
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                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/clone="INAGE:4133129"
/clone="INAGE:4133129"
/clone="INTH_MCC_54"
/tissue_type="from chronic myelogenous leukemia"
/tissue_type="from chronic myelogenous leukemia"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="NIH.0B (Tl phage-resistant)"
/note="Organ: bone marrow, Vector: pDNR-LIB (Clontech);
Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
Site_1: Sfil (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
daptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAAAGGCCGAGGCGCCGACATG-dT(3))BN-3'
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                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS04DVG 856 bp DNA linear GSS 21-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 103KOB of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                             AL286261.1 GI:8024707
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2-QV3-BN0047-150
400-152-c03&t3=2000-04-15&t4=1)
Seq_primer: puc 18 forward
                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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High quality sequence stop: 678.
Location/Qualifiers
  Roest-Crollius, H., Jai
Bernot, A., Fizames, C.,
                                                                        Unpublished
                                                                                               Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fis
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A.
                                                                                                                                                                                                                     Tetraodontidae; Teti
1 (bases 1 to 856)
                                                                                                                                                      Weissenbach,J.
                                                    (bases 1 to 856)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Dasilva,C., Bouneau,L., Fisher,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of scale clone-end sequencing project of the Tetraodon nigrovigenome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saurin,W. and Weissenbach,J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF881342 129 bp mRNA linear PMO-ET0208-031200-001-f12 ET0208 Homo sapiens cDNA,
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Unpublished
Email: asimpson@ludwig.org.br
This sequence was derived from the
                                         Fax: +55-11-2707001
                                                              Tel: +55-11-2704922
                                                                                                                                                                  Contact: Simpson A.J.G.
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High quality sequence start: 22
High quality sequence stor: 128.
Location/Qualifiers
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: gb_ba:*
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0 0	ATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGC 	94	B 63
94	YTCTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAGAACAG Y	8 8	D Qy
2880 2880	1 GATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTGATTCTGACTGGAATC [82	P Q
2820 2820	1 ATCATTTCAATGCAGAAGGATCAGAGGATTTCTGTTTTTTACTGTCTACAAGAGCTGGAG 	276 276	Db Qy
2760 2760	1 AGTTTCCCTTCCAGAGACTTGATGGATCAATAAAAGGGGAATTGAGGAAGCAAGC	270 270	라 ઇ
2700 2700	1 TGATTTTCTCTCAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCGCC	264 264	dq VQ
2640 2640	1 GGAAACTAATCCTTCTTGACAAGCTACTGATTCGTCTGCGAGAACGTGGCAACAGAGTTC 	258 258	ρ γο
2580 2580	1 CAGATGATAATGAATTCTATAATAACAGGAGGCCTTACAGCATTTGATACGTAGCAGCG	252 252	g dq
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2460 2460	GGATTTTAACAAGGAATTATAAAGCCCTCAGTAAAGGTTCAAAAGGCAGTACCTCAGGCT 	240 240	g dq VQ
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TCATCCCATGCCACACCAAGGCTGC
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TTTAAAGGACAATTCATCTGGACAA
TAAATCTGAGACAGACCTTAGACG
AGAAATTTGGTGGCCCTCTGGAAAGG
CTCGAGAAAATATTAAAGGATTTAGT CTCGAGAAAATATTAAAGGATTTAGT
ATAGTGACTCCATCACAGAAAGAAAA
GATCAGCTTTAATGGGAGTGAAGGA {
RAAGACAAAAAGAACTTGAAGAAATA
AATTCAAGAAATTGGGAAGAAATCATC
TTCAAGGTGGCGAACTTTTCCAATATG

5400	1 CAGATCACAAAAGTACACCTGAACATACATGGAGTACCCGGAAGACATAACAAAGACTGA 	ω ω	Db Qy
ũ ũ	AGAGGTCTCCTTATGGTTCAAGATCTCCCCTAGGACACAGATCTCCATTTGAACACTG	. mo a	Db dg
28	TCAGACTGGCAAATGGACCACAGAGCTTCTGCTAGTGGCCCGAGGTCACCACTAGI	, n n	B 54
5220 5220	CAGATCACCGTTCCACTTCAGAATA	16	gb dy
5160 5160	ACTTAAAAGACAGCCGGGGTCATTCAGATCACCGCTCCCATTCAGACCACAGGATAC 	10	P 64
	NTAGAAAGTTAGATGACCACAGGAGCAGAGACCACAGGTCAAACCTGGAAG 	504:	р 8
5040 5040	L ATGGAAAAGATCACAGAGACTGGGATCACTACAAACAGGACAGCAGATACTACAGTGATA	4981 4981	dq Qy
4980 4980	ATCAGGGAGATGCTTACAAGAAAAGTGACTCCAGGAAAAGGCCATATTCAGCCTTCAGTA 	4921 4921	Ωу
4920 4920	GGGACAGTTATTCTTCTGATAGACATTTATCACAATACCATGATCATCACAAAGACAGGC 	4861 4861	ОУ
4860 4860	TAATCAGAAATCCAGATGTGGAAAGACTGAAGGAGACTACAAACCATGATAGTAGCA 	4801	р 9
4800 4800	AGCGCCAAGAGTCTCAGCAACACAATGACCAAAACATTAGCAGCAATGTGAATACACATG	474: 474:	pb Qq
4740 4740	CCAAGTTTACAGAATTTGATGCCAGAAAGCTGCACAAACTCTACAAACATGCAATCAAAA	4681 4681	р
4680 4680	L AGGAGTACACAAATCCCGAGCAAATAAAACAGTGGAGGAAAAATTTGTGGATTTTTGTGT 		D 04
4620 4620	L AGCTGGAACATACTAGGCAGTGTCTAATCAAAATTGGGGATCACATTACAGAATGCCTGA 		рь
4560 4560	CTGTCAAAGCAGCACTGAAACAGCTGGATAGACCAGAGAAGGGCCTTTCTGAAAGGGAGC 	450: 450:	рβ
4500 4500	L CAGAAGAATCTGAAGAACTCCATCAGAAGAACATTTAGTGTGTGCAAAGAAGAAGAATGAGGC 	4441	DP 6A
4440 4440	AAATTCCATTGCTGGATACTCCAGTTCATATTACTGGAACCAGTGAACCAGTTCCTATCT 		Ф
4380 4380	L ATGAGGAGGAGATAACAAGGTAAATGAAATGAAATCTGAAAATAAAGAAAATCTAAAA 	432 432	Ωу
4320	L TAAAAGAAGAATAAAGAGTGATTCTTCACCACAACCCTCAGAAAAATCTGATGAAGATG	426	В

Qy Db	Qy Db	Qу	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qу Дъ	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Qy Db	Оу
6421 6421	6361 6361	6301	6241 6241	6181	6121 6121	6061	6001	5941 5941	5881 5881	5821 5821	5761 5761	5701 5701	5641 5641	5581 5581	5521 5521	5461 5461	5401 5401
GCCAAGATTCATTGTAAATCCATTTGTTTTCCCTCTTTAACATGGGCAATAATGTCAAAT 	AGGTGCATTGGTTTAAAAGAAGGAAGTGTTCTATAGGTGAACACTTCAAAACCCAGATCA 	TGATTGTTGTAATGAACAGTGAGAATATCCCACTCTAAACTGTGCCCTGGAAAGCTTTTC 	TACATACCTGTTTTTGGTTGTTTTATTTTATTTTTTTTTT	GTAAAAATGGGGAAGGAATATTTATTCCATTTAGTGCTCCTTTTTATTGGATACTTT 6	TCTTTTCACAAAGTCAGTATACTTACATGTTTTAATAAATA	AAATGAGCTTTTTTCCGTCAGGCTTTTTTTTGGCTGTTCCTTTCCCCAACAACTCAGGCCT 6	CAATTAAAAAAAAAACACAACAAAACCAACAAATGGCTGTAAATTATTGTAAATTAATT	TTTCTCCTGTTTGTGATCAGTTATAATGCCTTTTTATGAAACAAAC	GCTTTTCATCACAAGCTTGAATATTTAAATTCTGTACCTACAGTTGTAAAATAGCCAGGA 5	AAGGACTTTGTTCACATTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCC 5	CTTATGTTTCAGGAAAGAATGGGGGATTTATTTTGTTTTATTTCTTGGTAGAGAACTCTC 5	TTCTAGGCTGAACACAGATTAAATTATGTTTGTAAATGAACACTTAAACACTGACCTGTG 5	GACCTCAACACTGCCCCTTTCAGACTGGATCTTACTATAAACTCTTCATGTCAAAGTGG 5	TGTGCTGCAAATGTTGTGGCACTTTTTTTTAAGAAATGGAAGATGTTTACTTTTACAGG 5 	TGCAAGGTCTATTATCCCAACAGAAGAAAAATATTTTTGTATTTAAAGTTTATGCTGCAC 5 	GACTIGAAAGATAIGGACTGGATAITCTAICAGTAGCAGTAITGITACTICTITCCAGGA 5	CATTTTCTGGACCTTCTTTTTAGCCATATACAGTAAACTAACACAGTAATTGCCTTACAT 5
6480 6480	6420 6420	6360 6360	300	240	180	120	060	000	940	880	820	760	700-	640	580	520	460

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Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked in the chicken Gallus domesticus Gene 197 (1-2), 225-229 (1997)
97473516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University,
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Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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CKVLKORPRFVALKKOPSYIGGHESLELRDYOLNGLNWLAHSWCKGNSCILADEMGLG
KTIOTISFLNYLFHEHOLYGPFLLRVPLSTLTSWOREIOTWAPOMNAVVYLGDITSRN
                                                                                    FLLSTRAGGLGINLASADTVVIFDSDMNPQNDLQAQARAHRIGQKKQVNIYRLVTKGS
VEEDILERAKKKMVLDHLVIQRMDTTGKTVLHTGSTPSSSTPFNKEELSAILKFGAEE
                                                                                                                                                         MIRTHEMMHPQTKRLKFNILLTTYEILLKDKSFLGGLNWAFIGVDEAHRLKNDDSLLY
RTLLDFKSNHRLLTGTPLONSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYAS
LHKELEPFLLRYKKDVEKSLPAKVEGILRHEMSALDKOYYKHLTRNYKALSKGSKG
STSGFLNIMMELKKCCNHCYLIKPPDDNEFYNKQEALOHLIRSSGKLILLDKLLIRLR
                                                                                                                                                                                                                                                                                                                                              DDDEDYDKRGSRRQATVNVSYKEÅEETKTDSDDLLEVCGEDVPQTEEDEFETIEKFMD
SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC60282.1"
/db_xref="G1:2501846"
/db_xref="G1:2501846"
/translation="MNGHSDEESVRNSSGESSRSDDDSGSASGSGSSSSSSSSSSSSSS
SQSGSSDSESGSSGSESESDTSREKKQVQAKPPKADGSEFWKSSPSILAVQRSAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="CHD-Z"
228. .5654
                         SRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGPLERLL
                                                                  LFKEPEGEEQEPQEMDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSNMDEDDIE
                                                                                                                                       ERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGSEDFC
                                                                                                                                                                                                                                                                                                                            <u>LKQQNVKGMNKLDNYKKKDQETKRWLKNASPEDVEYYNCQQELTDDLHKQYQIVERII</u>
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DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="chromo-helicase-DNA-binding on the Z chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
AVARDAELVDKSETDLRRLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPTFRISGV
                                             <u>LEPERNSRNWEETIPESQRRRIEEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRSR</u>
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                                                 CGGAAGATGGGGGATAAAAGCAGTTGTGAAGAAAGTGAATCTGACTATGAGCCAAAAAAACA
                                                                                                                                                 AAGACTGGCAAATGTCAGGGTCAGGGTCAGTATCAGGAACTGGTTCTGATTCTGAATCGG
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CGGAAGATGGGGATAAAAGCAGTTGTGAAGAAAGTGAATCTGACTATGAGCCAAAAAAACA
                                                                                                  AAGACTGGCAAATGTCAGGGTCAGGGTCAGTATCAGGAACTGGTTCTGATTCTGAATCGG
                                                                                                                                                                                                  GTAGTGAAGATTCTGCCGATGATTCGTCCAGTGAAACTAAGAAGAAAAAAGCATAAAGATG
                                                                                                                                                                                                                                                 GTAGTGAAGATTCTGCCGATGATTCGTCCAGTGAAACTAAGAAGAAAAAAGCATAAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                     CTGAGTTTTGGAAGTCCAGTCCAAGCATACTTGCTGTACAGAGATCAGCAGTGCTCAAGA
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1860 1860	1801 AACTGTATGGCCCTTTTCTTCTGCGCGTGCCACTTTCTACCTTGACATCTTGGCAAAGAG	Qy
1800	1741 TGGGTCTGGGTAAAACAATACAAACAATTTCTTTTCTGAACTACCTGTTTCATGAACATC 	Qу Дъ
1740 1740	1681 GATTGAATTGGCTCGCTCATTCATGGTGCAAAGGAAATAGTTGTATTCTTGCAGATGAAA 	p Q
1680 1680	1621 AGCAACCATCTTACATTGGAGGACATGAAAGTCTGGAGTTAAGAGATTATCAGTTAAATG 	₽ 8
1620 1620	1561 CTACTCCCTTTAAGGACTGCAAGGTTCTAAAACAGAGACCAAGATTTGCTTGC	д 9
1560 1560	501 TCATTGCCAL	P 64
1500 1500	441 ACTACTATTGCAAATGGCAGGGTCTGCCTTACTCAC	99 97
1440 1440	1381 ATCAAATAGTGGAAAGAATAATTGCTCATTCAAATCAAA	Qy Db
1380 1380	1321 CAGAAGATGTGGAATATTATAAACTGCCAGCAGGAGCTTACAGATGATCTGCACAAACAA	B 64
1320 1320	1261 AACTGGACAACTACAAGAAAAAGGATCAGGAGACAAAAACGCTGGCTG	40 VQ
1260 1260	1201 TCCATAACACTTGGGAAACTGAAGAAACGCTGAAGCAACAAAATGTTAAAGGAATGAACA 	g Qy
1200 1200	41 AAAAGTCAAAAGGAGCTGGGAGAAATACAGTAT 	D Qy
1140 1140	.081 CTGGTGCCTCAACCACCATCTATGCCGTTGAGGCAGATGGTGACCCAAATGCTGGGT 	д Q
1080	1021 AAGATGAATTTGAAACTATAGAGAAGTTTATGGACAGTCGAATTGGCCGAAAAGGAGCCA 	P Q
1020 1020	961 CCAAGACAGATTCTGATGATTTGCTGGAAGTTTTGTGGAGAGAGTGTCCCACAGACTGAAG	рь Оу
960	901 ATAAGAGAGGATCTCGTCGCCAGGCAACAGTGAATGTTAGTTA	В 6
900	841 GACAGAAGAAGAGGCAACTTGATTCATCAGAGGAGGAGGAGGAGGATGATGAAGATTATG 	Дb
840 840	81 AAGTCAAAAGCCGT <i>t</i> 	Qу

3000	ATATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGA	2941	Qy
2940	CACAGAATGATCTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAAAAACAGGTTA	2881	рb
2940	ACAGAATGATCTGCAGGCACAGGCGAGAGCTCATAGAATTGGACAGAAGAAACAGGTT	2881	Qy
2880	GATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTTGATTCTGACTGGAATC	2821	Db
2880	ATTAGGTATTAACTTGGCATCTGCTGACACTGTAGTTATTTTTGATTCTGACTGGAAT	2821	Qy
2820 2820	ATCATTTCAATGCAGAAGGATCAGAGGATTTCTGTTTTTTACTGTCTACAAGAGCTGGAG	2761 2761	Фр
76	TTTCCCTTCCAGAGACTTGATGGATCAATAAAAGGGGAATTGAGGAAGCAAGC	70	Db
76	AGTTTCCCTTCCAGAGACTTGATGGATCAATAAAAGGGGAATTGAGGAAGCAAGC	70	Qy
2700	AGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCG	2641	Дb
2700	GATTTTCTCTCAGATGGTGAGGATGCTGGACATCCTAGCAGAATATCTGAAGTATCGC	2641	Qy
2640	GGAAACTAATCCTTCTTGACAAGCTACTGATTCGTCTGCGAGAACGTGGCAACAGAGTTC	5	Дb
2640	GAAACTAATCCTTCTTGACAAGCTACTGATTCGTCTGCGAGAACGTGGCAACAGAGTT	2581	Qy
2580	CAGATGATAATGAATTCTATAATAAACAGGAGGCCTTACAGCATTTGATACGTAGCAGCG	2521	Db
2580	AGATGATAATGAATTCTATAATAAACAGGAGGCCTTACAGCATTTGATACGTAGCAGC	2521	Qy
5	TTCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCATTGCTACCTCATTAAGCCAC		Db
2520	TCTGAACATTATGATGGAACTTAAGAAGTGTTGTAACCATTGCTACCTCATTAAGCCAC	4	Qy
2460	GGATTTTAACAAGGAATTATAAAAGCCCTCAGTAAAGGTTCAAAAGGCAGTACCTCAGGCT	2401	Db
2460	GATTTTAACAAGGAATTATAAAGCCCTCAGTAAAGGTTCAAAAGGCAGTACCTCAGGCT	2401	Qy
4		34	Db
2400	TAAGGTTGAACAAATTCTGAGGATGGAAATGAGTGCATTGCAGAAGCAATATTACAAGT	2341	Qy
2340	AAGAGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAAGTGTAGAAAAGTCTTTACCTG	2281	Db
2340	AGCTTGAACCATTTTTACTAAGAAGAGTTAAAAAAGATGTAGAAAAGTCTTTACCTG		Qy
2280			Db
2280	GGAAGATTTTGAAGAGGAGCATGGCAAAGGAAGAGAGTATGGTTATGCAAGTCTTCACA	N	Qy
2220	ATTCCCTCAAAGAGCTGTGGTCTTTGTTGCATTTCATCATGCCAGAAAAATTTTCCTCCT	2161	Db
2220	TTCCCTCAAAGAGCTGTGGTCTTTGTTGCATTTCATCATGCCAGAAAAATTTTCCTCCT	2161	Qy
ï		10	Db
2160	GACTTTAATAGACTTTAAGTCCAACCATCGACTTCTGATTACTGGAACCCCACTGCAAA	2101	Ωy
2100	GGGCATTCATAGGAGTTGATGAAGCTCATCGTTTAAAAAATGATGACTCTTCTGTACA	2041	Db
2100	GGCATTCATAGGAGTTGATGAAGCTCATCGTTTAAAAAATGATGACTCTCTTCTGTACA	2041	Qy
2040	TACTTCTGACGACATATGAAATTTTACTGAAGGATAAGTCATTCCTTGGTGGTCTCAATT	1981	Db
2040	ACTTCTGACGACATATGAAATTTTACTGAAGGATAAGTCATTCCTTGGTGGTCTCAATT		Qy
1980	GAAATATGATAAGGACTCATGAATGGATGCATCCACAGACTAAACGATTAAAGTTTAACA	1921	Db
1980	AAATATGATAAGGACTCATGAATGGATGCATCCACAGACTAAACGATTAAAGTTTAAC	ف	Qy
N		œ	Db
1920	attcaaacttgggctcctcagatgaatgctgtagtttacttaggagatataactagt	1861	Qy

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                                                                            ACTTCGATATAGATTGGGGTAAAGAAGATGATTCCAATCTGTTAGTAGGCATCTATGAAT 4020
                                                                                                       ACTTCGATATAGATTGGGGTAAAGAAGATGATTCCAATCTGTTAGTAGGCATCTATGAAT 4020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Funahashi, J., Sekido, R., Murai, K., Kamachi, Y. and Kondoh, H. Delta-orystallin enhancer binding protein delta EF1 is a zinc finger-homeodomain protein implicated in postgastrulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (29-JAN-1993) Jun-ichi Funahashi, Inst. Devel., Aging Cancer, Tohoku Univ.; 4-1 Seiryo-machi, Aoba-ku, Sendai 980-77, Japan (Tel:022-272-9499, Fax:022-272-3982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Funahashi,J.
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/dev_stage="13 day embryo"
257, 1939
GRRSRSRRYSGSDSDSITERKRPKKRGRPRTIPRENIKGFSDAEIRRFIKSYKKFGGP
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CAGAATCCCAACGGAGAAGGATAGAGGAGGAGGAAAGACAAAAAGAACTTGAAGAAATAT
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RISGVQVNAKLVISHEEELAPLHKSIESDPEEKRRYVIPCHTKAAHFDLDWGKEDDSN
LLVGIYEXAYGSWQCKVNGSRSQLNTEILPDDPDRTPRQNSYRPVQTTSLNY"
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                               1 (bases 1 to 345)
Griffiths,R., Double,M.C., Orr,K. an ADNA test to sex most birds
Mol. Ecol. 7 (8), 1071-1075 (1998)
98377745
2 (bases 1 to 345)
Griffiths,R., Double,M., Kate,O. and Direct Submission
Submitted (02-JUN-1997) Zoology, Mol Glasgow G12 800, UK
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Gallus gall
Eukaryota;
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Gallus gallus (
AF006659
AF006659.1 GI:
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               Location/Qualifiers
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Best Local Similarity
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ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
1. 111
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1 (bases 1 to 111)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
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Sequence 32 from Patent W09639505.
A58713
A58713.1 GI:3714255
   AF181828
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/db_xref="taxon:32644"
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<1. .>345
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/gene="CHD-Z"
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Nymphicus hollandicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele

Eukaryota; Aves; Neognathae; Psittaciformes; Cacatuidae;
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binding protein 1 (CHDIZ) mRNA, partial cds.
AF181828.1 GI:5917752
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Fridolfsson,A.K. and Ellegren,H.
Molecular evolution of the avian CHD1
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//trans_lat_ion="ELIDDLHKOYO]TVERITAHSNOKSTPEFKOKVLJKORPHYLLKKOPLYIGGHESLE
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LSTITSWOREIGTWASGNAVYVLGDITSRNMIRTHEWMHPQTKRLKEVILLTTYEIL
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FPORLDGSIKGELRSGKLULDHRNAEGSEDFCFLSTPAGGIG INLASADTVIFDD
NEFYNGGEALGHLIRSSGKLILLDKLLITLYWKGSVEEDILERAKKWLDHLVIGNMTTG
KTYLHTGSTPSSSTPPKKELSAILKFGAELFKEPEGEEDEPQEMDIDGILKRAETT
RENEPGPLTVGDELLSGFKANGSMEDDIELEFKEPEGEDEPQEMDIDGILKRAETT
GEENBAKGTSTSSSTPNKEGSTALKFGAELFKEPEGEDEPQEMDIDGILKRAETT
PRENIKGTSDAEIRRETKSYKKFGGPLERLDAVARABELTURKSEEDLAPLHKSITSDPEE
KRYVLTGSDAEIRRETKSYKKFGGPLERLDAVARABELTURKSEELAPLHKSITSDPEE
RKRYVIPCHTKAAHFDIDWGKEDDSNILLIGITEYGYGSWEMIKMDPDLSLTQKILFPDD
RKRYOLFTTAAHFDIDWGKEDDSNILLIGITEYGYGSWEMIKMDPDLSLTQKILFPDD
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<1..>2754
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/codon_start=1
/product="chromodomain helicase DNA binding protein 1"
/protein_id="AAD56025.1"
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/strain="Lutino cockatiel"
/db_xref="taxon:13180"
/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103;
                                                                                                                                                                                                                                       Submitted (30-AUG-1999) Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University, Norbyvagen
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; c
Archosauria; Aves; Neognathae;
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Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                                                                                                                                                                                                                                          Fridolfsson, A.-K. and Ellegren, H. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                    Fridolfsson, A.K. and Ellegren, H. Molecular evolution of the avian CHD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aegolius funereus
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Aegolius funereus chromosome W chromodomain helicase
Protein 1 (CHD1W) mRNA, partial cds.
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A58684
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                                                                                                                             /chromosome="W"
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/codon_start=1
                                                                                                           /gene=
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                                                                                                                                                                          organism="Aegolius funereus"
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translation="ELTDDLLKQYQIVERIIAHSNQKSAAGYPDYYCKWQGLPYSECs"
                                                                                            ne="CHD1W"
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Neognathae; Strigiformes; Strigidae; Aegolius.
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Pred. No. 3.3e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                   Submitted (03-JUN-1997) Laboratory of Gene Transfer, National Human Genome Research Institute, National Institutes of Health, 49 Convent Drive, Bethesda, MD 20892-4442, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens CHD1 mRNA, AF006513
                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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LSTLTEWQREIQTWAFQMNSVYYLGDIISRNNIRTHEWMHPOTKERENILLTTYEIL
LKDKSFLGGLNWVFIGVDEAHRLKNDSLLYKTLIDEWMHPOTKRIKENILLTTYEIL
LKDKSFLGGLNWVFIGVDEAHRLKNDSSLLYKTLIDERFLLRRYKKOVEKSLW
SLLHFIMPEKFSSWEDFEEEHGKGREBGYASLHKELEPFLLRRVKKOVEKSLPAKVEQ
LLRMEMSALQKOYYKWILTRNYKALSKGSKGSTSGFLNIMMELKKCCNHCYLIKPPD
REFYNKQEALQHLIRSGKLILLDKLLIRLRERGNRVLIFSQMVRMLDILASDTVVIFDSDW
REFYNKQEALQHLIRSGKLILLDKLLIRLRERGNRVLIFSQMVRMLDILASDTVVIFDSDW
NPONDLQAARAHRIGQKKQVNIYRLJTKGSVEEDLILERAKKKMVLDHLVIGRMDTTG
KTVLHTGSTPSSSTPFNKEELSAILKFGAEELFKEPEGEEEEPQEMDIDEILKRAETR
ENEPGFLTVGGELISQIKVAMFSNMDEDDIELEPEQAFKKWEEIIPEVQRRRREEEEER
PRENIKGFSDAEIRRFIKSYKKFGGPLERLDAIARDAELVDKSETDLRRLGELVHNGC
IKALKDNSFGQERAGGRLGKVKGPTFRISGVQVNAKLVISHEEELAPLHKSIPSDPED
RKRYVIPCHTKAAHFDIDWGKEDDSNLLIGIYEYGYGSWEMIKMDPDLSLTQKILPDD
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                                                                                                                       codon_start=1
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164. .5293
                                                                                                                                                                                              /map="5q15-21; near WI-5811"
L. .5947
                                                                                                                                                                                                                                 /chromosome="5"
                                                                                                                                                                                                                                            /organism="Homo sapiens"
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       Direct Submission
Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                           Direct Submission
Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101220 bp DNA linear PRI 07-DEC
Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
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DOE Joint Genome Institute.
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DOB Joint Genome Institute and Stanford Human Genome Center.
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www-shgc.stanford.edu
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LLYKTLIDFKSMHRLITOTPLONSLEDENGLHFIN MEEKSSELOKQY YKWILTRNYKALSKG
YASLHKELEPFLLRRVKKDVEKSLPAKVEQILLMEMSALQKQY YKWILTRNYKALSKG
SKGSTSGFLNIMMELKKCCNHCYLLK PEDNINEFY NKQEALQHLITASGGKLILLDKLLI
RLERGRINKLIF GOMYMALDILASLTLK RAEPFEPORLDGSIKGELRKOALDHENABGS
DFECFLLSTRAGGLG NLASADTVVIFDSDMINDONLOAQARAHRIGOKKOVNIY RLYT
KGSVEEDILERAKKWVLDHLY IQRMDTTGKTVLHTGSABSSSTPFNKEELSAILKEG
AEELFK BEGEGEDEPGMDLDEILKRAETHENEDGPLTVCDELLSQFKVANTSNMDE
DIELEPERNSKMWEEII PEDQRRRLEEBEROKELBEIYMLFRNICAKQISFNGSEGE
RSKRKYGSOSDSIS ISEGKREKKRORFRTIPBRENIKGFSDAEIRFIKSYKKEGGELE
RLDAIARDAELVDKSETDLRRLGELVHNGCIKALKDSSGTERTIGGRLGKVKGPTFRI
SGYOVNAKLVISHEEBLIPHKSIFSDEPERNOKTPORTSCHORTSKEDDSKUL
IGITEYGYGSNEMIKADPDLSTIMKILPDDVEKKOLOTRADYLIKLLSENDLAKK
EALLGGASGSKRKAKARAKKNAMKSIKVKEETKSDESPLOKTPSEKSDEDDDKLESEKSDENGKE
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GLSERGOLEHTRQCLLKIGHTTECLKETTNEDQIKOMENDHYSOSROSYSSDRHLTQ
YHDHKORHQGOSYKKSDSKROSSSHELHSDHRSHSDHRLHSDHRSSSETTHRAEDDH
RSBDHRSNLEGSLKDBSHDHRSHSDHRLHSDHRSSSETYHKSSRONYSDROMDH
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FMDCRIGRKGATGATTIIXAVEADGDPNAGFEKNKEPGEIQYLIKWKGWSHIHNTWET
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BASE COUNT ORIGIN

Matches

RESULT 10 AC092372/c LOCUS

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REFERENCE AUTHORS

JOURNAL AUTHORS

COMMENT

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Conservative

1.2%; Score 82; DB 9; Length 134365; 100.0%; Pred. No. 7.7e-30; Ltive 0; Mismatches 0; Indels 0;

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REFERENCE AUTHORS

SOURCE VERSION DEFINITION **(EYWORDS**

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Qy 5836 TTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAG 5895
Db 12061 TTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAG 12002
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DOE Joint Genome Institute and Stanford Human Genome Center.
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AC012624.6 GI:14993679
                                                                                                                                                     Submitted (21-7UI-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 21, 2001 this sequence version replaced gi:14277267.
                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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                                                                                                                                                                                                                                                                                   DOE Joint Genome Institute and Stanford Human Genome Center.
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           40414 a
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_romesome="5"
/clone="CTD-2082117"
24497 c 25503 g 43951 t
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18862 c 17827 g 30409 t
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/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boquslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrin, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stanga-Thomann, N.
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* NOTE: This is a 'working draft' sequence. It currently * consists of 10 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-58M12
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Sep 10, 2000 this sequence version replaced gi:7407963 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zimmer, A. and Zod
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Vassillev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
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HTG; HTGS_PHASE1;
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                                                                                                                                                                               Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 134743 bases at least Q40
Consensus quality: 139227 bases at least Q30
Consensus quality: 139227 bases at least Q30
Consensus quality: 140814 bases at least Q20
Insert size: 14400; agarose-fp
Insert size: 142179; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Contact: project Information
                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L5154
Center clone name: 58_M_12
                                                                                                                         Quality coverage: 4.6 in Q20 bases;
Quality coverage: 4.7.in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Zody, M.
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                       100% of reads
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               CTTGAATATTTAAATTCTGTAC 5917
CTTGAATATTTAAATTCTGTAC 131100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                       43971
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62720 75408: contig of 12689 bp in length
75409 75508: gap of 100 bp
75509 92516: contig of 17008 bp in length
92517 92616: gap of 100 bp
92617 106409: contig of 13793 bp in length
                                                                                                                  Conservative
                                                                                                                                                                                                                    clone_end:T7
vector_side:
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/note="assembly_fragment"
106510. .143079
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/db_xref="taxon:9606"
/clone="RP11-58M12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector_side:left"
                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
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1. .38820
                                                                                                                                                                                                    ector_side:right"
26246 c 26678 g
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20: gap of 100 bp
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Pred. No.
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                                                                                                                  Mismatches
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                                                                                                                 . 7.7e-30; ches 0;
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                                                                                                                                            Length 143079;
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Best Local (
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                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q20
Consensus quality: 142744 bases at least Q20
Consensus quality: 142744 bases at least Q20
Estimated insert size: 148080; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; sum-of-contigs estimation.
*NOTE: This is a 'working draft' sequence. It currently
*consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* but first factors.
                                                                                                                                                                                                                                                                                                                                              * This sequence will be replaced

* this sequence will be preserved.

* the accession number will be preserved.

* 56174 contig of 56174 bp in length

* 56274 gap of unknown length

* 100875 100974 gap of unknown length

* 100875 100974 gap of unknown length

* 113128 113227 gap of unknown length

* 113128 113227 gap of unknown length

* 113128 113227 gap of unknown length

* 11328 118190 contig of 4963 bp in length

* 118291 118290 gap of unknown length

* 118291 119694 contig of 4040 bp in length

* 119695 113974 gap of unknown length

* 113298 113397 gap of unknown length

* 123298 123397 gap of unknown length
ch 1.2%; Score 82; DB 2; Le
1 Similarity 100.0%; Pred. No. 7.7e-30;
82; Conservative 0; Mismatches 0;
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 14565)
DOE Joint Genome Institute.
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Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE.
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                                                                                                                                              /organism="Homo sapiens"
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/clone="CTC-480B11"
/clone="CTC-480B10"
/clone=1b="Calrech human B.
a 26309 c 27580 g 48609 t
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t 600 others
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Best Local Similarity 100.0%; Pred. No. 7.4e-30;
Matches 82; Conservative 0; Mismatches 0; Indels
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                                                                                                 5836 TTTCAAAGCTACTTGTTTACATTGTACACTGCGCACCACCTGCGCGCTTTTCATCACAAG 5895
74518 CTTGAATATTTAAATTCTGTAC 74497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (26-0AM-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US; 3 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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1 (bases 1 to 21958)
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AC022121.6 GI:15375145
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WI-13675 G23101
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DOE Joint Genome Institute.
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/chromosome="5"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Psittaciformes; Cacatuidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF181827 2754 bp mRNA linear VRT 07-AI Wymphicus hollandicus chromosome W chromodomain helicase DNA binding protein 1 (CHDIW) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (30-AUG-1999) Department of Evolutionary Biology, Evolutionary Biology Centre, Uppsala University, Norbyvagen 18D,
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LKDKSFLGGLNAVFIGVDEAHRLKNDDSLLYKFLIDFKSNHRLLTTGTPLQNSIREILW
SLLHFIMPEKFKSSWEDFEEBHGKGREBGYASLHKELEPFLLLRRVKKDVEKSLDAKVED
SLLHFIMPEKFKSSWEDFEEBHGKGREBGYASLHKELEPFLLLRRVKKDVEKSLDAKVED
LRMEMSALQKQYKWILTRNYKALSKGSKGSTSGFLNIMMELKKCCNHCYLIKPDD
NEFYNKOEALQKIJIRSGKLILLDKLLIRLREGNRVLIFSQRVTMILDILASRDTVNIFDSW
PPFQRLDGSIKGELRKOALDHFNAGESEDFCFLSTTAGGLGINLASADTVVIFDSW
RPONDLQAQARAHRIGOKKQVNIYRLVTKGSVEEDILERAKKKMVLDHLVIQRMDTTG
KTVLHTGSTPSSSTPFNKEELSAILKFGAEELFKEPEGEEEEPGMDIDEILKAEATR
ENEDGPITVGEELLSGOFKVANFSMNDEDDIELLFEPGONLRNWEEIIPFVORRRIEEEER
ENEDGPITVGEELLSGOFKVANFSMNDEDDIELFEPGONLRNWEEIIPFVORRRIEEER
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LRDYQLNGLNWLAWGNSCILADEMGLGKTIQTISFMNYLFHEHQLYGPFLLVVP
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/chromosome="W"
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IKALNDNSFVQERAAGRLGKVKGPTFRISGVQVNAKLVISHEEELAPLHKSIPSDPEE
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ALIGNMENTS

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WPI; 1997-043127/04.
        Griffiths R, Tiwari B;
                                                                              Gallus sp.
                (ISIS-) ISIS INNOVATION LTD
                          06-JUN-1995;
                                  05-JUN-1996;
                                                   WO9639505-A1.
                                           12-DEC-1996.
                          95GB-0011439
                                   96WO-GB01341.
                                                               Location/Qualifiers
228..5390
                                                            /*tag=
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Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian; CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.

Chicken CHD-1A gene.

12-MAR-1997 (first entry)

AAT42751;

AAT42751 standard; cDNA; 6608 BP.

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                                                    GTAGTGAAGATTCTGCCGATGATTCGTCCAGTGAAACTAAGAAGAAAAAGCATAAAGATG
                                                                                                                          ctgagttttggaagtccagtccaagcatacttgctgtacagagatcagcagtgctcaaga
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                   TGGGTCTGGGTAAAACAATACAAACAATTTCTTTTCTGAACTACCTGTTTCATGAACATC
                                                  gattgaattggctcgctcattcatggtgcaaaggaaatagttgtattcttgcagatgaaa
                                                                                            agcaaccatcttacattggaggacatgaaagtctggagttaagagattatcagttaaatg
                                                                                                      AGCAACCATCTTACATTGGAGGACATGAAAGTCTGGAGTTAAAGAGAGATTATCAGTTAAATG
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Qy	4021	TGGCTATGGCAGCTGGGAAATGATAAAAATGGATCCAGATCTCAGCTTAACACAGAAGA 4	1080
ф	4021	gcagctgggaaatgataaaaatggatccagatctcagcttaacacagaaga 4	1080
ρ _ν	4081 4081	AGGCAAAGCAGCTACAGACCCGTGCAGACT 4 	4140 4140
γ		CCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAAGCACAAAAGGCTTGCTGGTG 4	Ñ
ф	4141	.cctcattaaattactgaataaagaccttgcaagaaggaag	1200
pb Qy	4201 4201	GACAAGAAATAAGAAGAATAAGATGAAGGCTTCAAAAA 4 	4260 4260
} &	4261	AAGAGTGATTCTTCACCACAACCCTCAGAAAAATCTGATGAAGATG 4	1320
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B 8		AAATGAAATGAAATCTGAAAATAAAGAAAAAATCTAAAA 4 	1380
ν, ο	4381	AGTTCATATTACTGCAACCAGTGAACCAGTTCCTATCT 4	1440
Qy	4.4	AAGAATCTGAAGAACTCCATCAGAAGACATTTAGTGTGCAAAGAAAG	150
0		agaagaatctgaagaactccatcagaagacatttagtgtgtgcaaagaaag	5
р оу	4501	GCACTGAAACAGCTGGATAGACCAGAGAAGGGCCTTTCTGAAAGGGAGC 4 	1560 1560
유 성	4561 4561	ICAAAATTGGGATCACATTACAGAATGCCTGA 4 	1620 .
p 64	4621 4621	AATAAAACAGTGGAGGAAAAATTTGTGGATTTTTGTGT 4 	0891 0891
ν	4681	AAGTTTACAGAATTTGATGCCAGAAAGCTGCACAAACTCTACAAACATGCAATCAAAA 4	7
₽	4681	caagtttacagaatttgatgccagaaagctgcacaaactctacaaacatgcaatcaaaa 4	1740
β Q	4741 4741	GCCAAGAGTCTCAGCAACACAATGACCAAAACATTAGCAGCAATGTGAATACACATG 4 	6 6
요 성	4801 4801	2AGATGTGGAAAGACTGAAGGAGACTACAAACCATGATGATAGTAGCA 4 	1860
Qy		TGATAGACATTATCACAATACCATGATCATCACAAAGACAGGC 4	1920
ᄝ	4861	ggacagttattcttctgatagacatttatcacaataccatgatcatcacaaagacaggc 4	9
B 64	4921 4921	ATCAGGGAGATGCTTACAAGAAAAGTGACTCCAGGAAAAGGCCATATTCAGCCTTCAGTA 4	0861
P Q	4981	ACAAACAGGACAGCAGATACTACAGTGATA 5	5040
γ	5041	GGTCAAACCTGGAAGGAA 5	Ĺ
8	2	taaacatagaaagttagatgaccacaggagcagagaccacaggtcaaacctggaaggaa	

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Claim 8; Fig 3; 76pp; English
                                                                         Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and are ignored in the translated amino acid sequence given in Fig 3"
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                                                                           The chicken CHD-W gene (AAT42754) acting alone or in conjunction with the closely related CHD-1A gene (AAT42751) is suggested to initiate female development in birds. The sequence of CDH-W was deduced from 2 clones isolated from a 10-day chick embryo library using a fragment of the CHD-1A gene as a probe. The CHD-W gene is located on the W chromosome. Probes based on CHD-W and CHD-1A give a W chromosome-specific signal on hybridisation to genomic DNA of a non-rarite bird and can be used for sex determin. of a bird. CHD-W nucleic acids can also be used to control the sex of progeny of a constraint of the control the sex of progeny of a constraint of the control the sex of progeny of a constraint of the control the sex of progeny of a constraint of the control the sex of progeny of a constraint of the control the sex of progeny of a constraint of the control the sex of progeny of a constraint of the control the sex of progeny of a constraint of the control the sex of progeny of a constraint of the control the con
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                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 8; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicken CHD-W gene (partial sequence).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-043127/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromodomain-Helicase-DNA binding on the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 103; DB 18; Length 153; Pred. No. 1.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Sequence 1316 BP; 492 A; 208 C; 306 G; 304 T; 6 other

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δÃ

Score 49;

DB 23;

Length 4222;

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The invention relates to isolated polynucleotide (I) and CC polymeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CPR polynucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or guantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC composible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC and to produce other types of beat and products dependent or DNA and CC and to produce data for this patent did not appear in the printed CC and the products of the print of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 21771; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2943 ATTTATCGGCTAGTCACAAAAGGATCAGTAGAAGAAGATATTCTTGAAAGAGCCAAGAA 3001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB;
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AAS85967 standard; cDNA; 4222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #21771.
Sequence 4222 BP; 1040 A; 1041 C; 883 G; 1258 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \vdash
                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG21780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9%;
ilarity 100.0%;
Conservative
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mapping; gene mapping; gene therapy; forensic
medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 59;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18; I
6.3e-16;
hes 0;
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                                                             Matches
                                                                            Query Match
Best Local
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Best Local
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              4140 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAAGGAAAGGAACCACA 4186
                                                                                                                                                                   Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42758) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW08146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Avian chromodomain-helicase-DNA binding genes determine sex
birds - used for sex determn. and to control sex of progenu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chick CHD-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT42758;
                                                                                                                                        Sequence 153
                                                                                                                                                                                                                                                                                                              Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9639505-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHD-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bird; sex determination; chromodomain-Helicase-DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT42758 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1996
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 91
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DB; AAW08148.
tacctcattaaattactgaataaagaccttgcaagaaaggaagcaca
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                                                                                                                                                                                                                                                                                                                                             used
                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                             for sex determn. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INNOVATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Tiwari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-GB01341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                         56 A; 36 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                            0.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "bases 52-81 are a repeat of bases and are ignored in the translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid sequence given in Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ø
                                                             0;
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                                                                            Score 47;
Pred. No.
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                                                                                                                                        31 G; 30 T;
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                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                             to control sex of progeny
                                                                             No.
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                                                                            DB 18;
1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.7e-11
                                                                                                                                         0 other;
                                                                                         Length 153;
                                                             Indels
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amino
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                                                             Gaps
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SXCCCCCCCXXXXDDXXPXXPXXPXTTTTTTXXXXXXDXXAX
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                                                                                                                                              RESULT
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Best Local S
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                                                                                                                                                                                                    4140 TACCTCATTAAATTACTGAATAAAGACCTTGCAAGAAA 4177
                                                                                                                                                                                                                                                                                                                                      Bases 3855-3977 (AAT42756) of the mouse CHD-1 gene show homology to portions of the chicken CHD-1A (A = Avian) gene (AAT42757), chicken CHD-W (W refers to the W chromosome) gene (AAT42759) and and the great tit CHD-W gene (AAT42759). Translated amino acid sequences of this region are provided in AAW8146-49. The CHD-1A (see also AAT42751) and CHD-W (see also AAT42754-55) genes determine sex in birds and can be used to identify the sex of an embryo, foetus etc. and to manipulate the sex of progeny.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_difference 52..81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn, and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Great tit CHD-W genè fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT42759;
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                            Human secreted protein 5' EST, SEQ ID NO: 10365.
                                                        06-OCT-2000
                                                                                                                 AAC06290 standard; cDNA; 212 BP
                                                                                                                                                                                                                                                                                                                Sequence 153 BP; 60 A; 33 C; 31 G; 29 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS INNOVATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHD-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bird; sex determination; chromodomain-Helicase-DNA binding 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1997 (first entry)
                                                                                                                                                                                   91 tacctcattaaattactgaataaagaccttgcaagaaa 128
                                                                                                                                                                                                                                                         Local
                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997-043127/04.
                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW08149
                                                                                                                                                                                                                                          0.6%; Score 38; DB ilarity 100.0%; Pred. No. 1.5 Conservative 0; Mismatches
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tiwari B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95GB-0011439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-GB01341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "bases 52-81 are a repeat of bases 22-51 and are ignored in the translated amino acid sequence given in Fig 3"
                                                                                                                                                                                                                                                       Score 38; DB 18;
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                     Length 153;
                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                            Gaps
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WO200200928-A2

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RESULT 8
ABL32358/c
ID ABL323
В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNAs because they are often obtained from oligo-dT prined cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs with intact 5' ends and can therefore be used to obtain upstream regulatory sequences and to design expression and secretic vectors.
                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytosiatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6463 TGGGCAATAATGTCAAATGTGCTATGCAGC 6492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                             gene; as.
                                                                                                                                                                                                                                                                                                          26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                ABL32358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 212 BP; 72 A; 41 C; 32 G; 67 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 10365; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; chromosome mapping;
                                    Homo sapiens.
                                                                                                                                                                                                                                                                Human immune system associated gene SEQ ID NO: 331.
                                                                                                                                                                                                                                                                                                                                                                                       ABL32358 standard; DNA; 6237 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%; Pred. No. 0.1 nes 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 tgggcaataatgtcaaatgtgctatgcagc 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 30; DB 21; Length 212; 100.0%; Pred. No. 0.0056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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RESULT 9
ABL33370/c
ID ABL333
XX ABL333
AC ABL333
XX Human;
AC Human;
KW Human;
KW antiar
KW antiir
KW antiir
KW acute
KW neurog
KW gene;
XX Gene;
XX Homo &
XX Gene;
YX G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated associated as which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                          antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; a acute myeloid leukaemla; Alzheimer's disease; AlDS; epilep neurofibromatosis; rheumatoid arthritis; psoriasis; bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5979 AAACAAACAAACAAACAAAAAAAAAAATTAAA 6008
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                                                                        30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL33370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL33370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2001;
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                          (EPIG-)
                                                                                                                                                    02-JUL-2001;
                                                                                                                                                                                                     03-JAN-2002
                                                                                                                                                                                                                                                       WO200200928-A2
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                                                                                                                                                                                                                                                                                                      sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 331; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000DE-1032529
2000DE-1043826
                                                                        2000DE-1032529
2000DE-1043826
                                                                                                                                                    2001WO-EP07537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1614 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antianaemic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                               bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                              anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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RESULT 1
ABL33795/
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Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associat genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                Nucleic acid comprising frag
for diagnosis and treatment
cytosine methylation -
                                                                                                                                                                                                                                                                                                                                        antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; a
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek
                                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                        02-JUL-2001;
                                                                                                                                                                                                                                   03-JAN-2002
                                                                                                                                                                                                                                                            WO200200928-A2
                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                           neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL33795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL33795
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                                                                                                                                           (EPIG-)
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                                                                                                                                                                                                                                                                                      sapiens.
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29; Conser
                                                                                                                                           EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1343; 32pp + Sequence Listing;
                                                                                                               Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA; 5474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.4%;
nilarity 100.0%;
Conservative 0
                                                                                                                                                                   2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                         2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                  system associated gene SEQ ID NO:
                                                                                                                                         AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                              fragment of chement of diseases
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                                                                                                                 Berlin
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                             of chemically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24;
0.014;
                                               nically modified associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 6191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                            bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                          antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene, use
abnormal
                                                 abnormal
                                                            gene, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 system associated
                                                                                                                                                                                                                                                                                                                                                     anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Sequence

Listing;

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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5979 AAACAAACAAACAAACAAAAAAAACAATT 6005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AAZ12532 to AAZ1779. The polynucleotides can be used as a source of primers and probes, which can
                                                                                                                                                                                                                                                                                                         Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
Escobedo J, Garcia PD, Garcia V, Gisee K, Innis
Jones WL, Kassam A, Kennedy GC, Kita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reini
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2887 AAACAAACAAACAAACAAAAAAAAAATT 2861
                                                                                                                                                                          Claim 1; Page 849; 2479pp; English.
                                                                                                                                                                                                            Novel human genes and their expression products which are differentially expressed in different cell types
                                                                                                                                                                                                                                                                        WPI; 1999-494092/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-1998;
31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human gene expression product cDNA sequence SEQ ID NO:815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ13346 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5474 BP; 1286 A; 201 C; 1404 G; 2583 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.4%;
1 Similarity 100.0%;
27; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA; 300 BP
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                              Innis MA;
                                                                                                                                                                                                                                                                                                                             Reinhard C;
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RESULT AAK75594 AK75594 AK75594 AK75594 AK XX AC AAK XX Hum XX Hu
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Best Local S
Matches 26
31-JAN-2000; 2000US-0179055.
04-FEB-2000; 2000US-0184664.
24-FEB-2000; 2000US-0184664.
02-MAR-2000; 2000US-0189550.
16-MAR-2000; 2000US-0199076.
17-MAR-2000; 2000US-0199076.
18-APR-2000; 2000US-0219513.
19-MAY-2000; 2000US-021967.
28-JUN-2000; 2000US-021967.
28-JUN-2000; 2000US-0219680.
17-JUL-2000; 2000US-021680.
17-JUL-2000; 2000US-021680.
11-JUL-2000; 2000US-021990.
11-JUL-2000; 2000US-021990.
11-JUL-2000; 2000US-021990.
14-JUL-2000; 2000US-021990.
14-JUL-2000; 2000US-021990.
14-JUL-2000; 2000US-021991.
14-AUG-2000; 2000US-022991.
14-AUG-2000; 2000US-0225213.
14-AUG-2000; 2000US-0225213.
14-AUG-2000; 2000US-0225213.
14-AUG-2000; 2000US-0225266.
14-JUL-2000; 2000US-0225270.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK75594 standard; DNA; 2785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 300 BP; 113 A; 66 C; 59 G; 62 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30 aaacaaacaaacaaacaaaaacaat 55
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26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune; haematopoietic; immune/haematopoietic antigen; cancer;
itic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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REFERENCE OF COLOCOLO COLOCA C
                                                                                                                                            CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic actived cells. AAK64703 CC cancers and cancer metastases of haematopoietic antigen genomic concerns and produce the expresent invention. AAK54942 to AAK84950 and AAM82169 CC represent sequences used in the exemplification of the present invention.
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
17-NOV-2000
01-DEC-2000
01-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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useful f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metastasis
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                                                                                                         2785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preventing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ
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2000US-0246613
2000US-0246613
2000US-0249207
2000US-0249210
2000US-0249211
2000US-0249211
2000US-0249213
2000US-0249214
2000US-0249214
2000US-0249216
2000US-0249216
2000US-0249216
2000US-0249217
2000US-0249217
2000US-0249244
2000US-0249244
2000US-0249245
2000US-0249245
2000US-0249245
2000US-0249264
2000US-0249264
2000US-0251030
2000US-0251030
2000US-02511030
                                                                                                         BP;
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                                                                                                         840
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          0.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human immune/hematopoietic antigen diagnosing and/or treating cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben
                                                                                                         572
                                                                                                      C;
          Score ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3071pp +
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                                                                                                         594
26;
No.
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                                                                                                         779
          DB 22;
0.32;
                                                                                                         T;
                                                                                                         0 other;
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                                Length 2785;
                                                                                                                                                         present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides, and
                                                                                                                                                                                                                                                                                                     the
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14-AUG-2000
14-AUG-2000
11-AUG-2000
11-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
20-SEP-2000
20-SEP-2000
20-SEP-2000
20-SEP-2000
20-SEP-2000
20-SEP-2000
20-SEP-2000
20-SEP-2000
20-SEP-2000
21-SEP-2000
21-SEP

2000US-0225447.
2000US-0225758.
2000US-0225758.
2000US-0225759.
2000US-02256868.
2000US-0226681.
2000US-0226686.
2000US-022668.
2000US-0226868.
2000US-0225983.
2000US-0229344.
2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-02231143.
2000US-0231143.
2000US-0231143.
2000US-0231143.
2000US-0231244.
2000US-023124.
2000US-023124.
2000US-023124.
2000US-023124.
2000US-0231268.
2000US-0231298.
2000US-023298.
2000US-023298.
2000US-0233063.
2000US-0234997.
2000US-0236370.
2000US-0246677.
2000US-0246677.
2000US-0246677.
2000US-0246677.
2000US-0246677.
2000US-0246623.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246523.

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RESULT 13
AAS46349/c
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                                                                                                             The invention relates to a nucleic acid comprising a sequence of 18 cb bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a pertide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for CC arrows and theorem of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC differences serving as basis for diagnosis and/or prognosis events which CC are disadvantageous to patients. The present sequence is one of the CC concernes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5977 TGAAACAAACAAACAAAAAAAAAAA 6002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2000; 2000DE-1013847.
06-ARR-2000; 2000DE-1019058.
07-ARR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS46349 standard; DNA; 5919 BP
Sequence 5919 BP; 1421 A; 69 C; 1641 G; 2788 T; 0 other;
                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 71; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-602752/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-MAR-2001; 2001WO-EP02955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200168912-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour suppressor gene derived chemically modified sequence #71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 tgaaacaaacaaacaaacaaaaaca 217
                                 ftp.wipo.int/pub/published_pct_sequences.
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RESULT 14
ABL32732/c
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Best Local S
Matches 26
                                Matches
                                                               Query Match
                                                                                                                                                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid_arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; notropic; neuroprotective; anti-HV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; oancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5979 AAACAAACAAACAAACAAAAAAAACAAT 6004
5979 AAACAAACAAACAAACAAAAAAACAAT 6004
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01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3118 AAACAAACAAACAAACAAAAAAAAAAA 3093
                                                                                                              Sequence 5919 BP; 1421 A; 69 C; 1641 G; 2788 T; 0 other;
                                                                                                                                           diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 705; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                             cytosine methylation
                                                                                                                                                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated gene SEQ ID NO: 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL32732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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                                               Local
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                              Conservative
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                                             0.4%; Score 26;
100.0%; Pred. No.
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100.0%; Pred. No.
tive 0; Mismatc
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. 0.31;
                                             DB 24;
0.31;
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                                0,
                                                             Length 5919;
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3118 AAACAAACAAACAAACAAAAAAACAAT

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RESULT 15
AAS6118/c
ID AAS611
XX PUMAN
DE Human;
KW cardia
XX Human;
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XX Human;
KW cardia
XX POOLOTE
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PR 07-APR
PR 01-SEP
XX D6-APR
PR 01-SEP
XX CEPIG-
XX D6-APR
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XX CEPIG-
XX D7-ED
XX CEPIG-
XX D7-ED
XX CEPIG-
XX D8-ED
XX CEPIG-
XX D1-ED
XX CEPIG-
XX CEP
                                                                                                                                                                                                                                             The invention relates to 224 nucleic acid sequences comprising at least CC 18 bases of a chemically pretreated gene associated with gene regulation converted from 43 known genes (or complementary sequences). The CC chemical pretreatment converts cytosine bases unmethylated at the CC 5-position to uracil or another base with hybridisation behaviour cd dissimilar to cytosine, to enable analysis of cytosine methylations. CC The DNA sequences, oligomers (or sets/arrays) and method are cuseful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by CC enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis cand therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, CC esthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, cardiac sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part cf. fr. with ventilehold at the compact.
Query Match
Best Local S
Matches 26
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; Inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preeclampsia; cardiac allograft vascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ
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th 0.4%; Score 26; Similarity 100.0%; Pred. No. 26; Conservative 0; Mismatci
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Mismatches

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ALIGNMENTS

	FEATURES Source	AUTHORS TITLE JOURNAL COMMENT	KEYWORDS SOURCE ORGANISM	RESULT 1 BM486590 LOCUS DEFINITION ACCESSION VERSION
/organism="Gallus gallus" /strain="Commercial broiler and Ottawa Res. Centre Strains 90 & 21" /db_xref="taxon:9031" /db_xref="taxon:9031" /clone="ipm2n.pk002.b16" /clone=lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)" /sex="Male and Female" /tissue_type="Breast muscle, leg muscle and epiphyseal growth plate"	Universit Townsend Tel: 302 Fax: 302 Email: co	Cogburn,L.A. and Monsonego-Ornan,E. ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome Project Unpublished (2002) Contact: Larry A. Cogburn	EST. Chicken. Chicken. Chicken. Chicken. Chicken. Chicken. Chicken. Chicken. Callus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 597)	BM486590 pgm2n.pk002.bl6 Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk002.bl6 5' similar to gblAc60282.1 (AF004397) chromo-helicase-DNA-binding on the Z chromosome protein (Gallus gallus), mRNA sequence. BM4865901 BM4865900 BM4865901 GR:118607520

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RESULT
BM491730
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VERSION
KEYWORDS
SOURCE
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ORIGIN
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                                                                                                                               BM491730 648 bp mRNA linear EST 07-FEB-2002 pgp2n.pk007.e18 Normalized Chicken Pituitary/Hypothalamus/Pineal Library (pgp2n) Gallus gallus cDNA clone pgp2n.pk007.e18 5' similar to gb|AAC60282.1 (AF004997) chromo-helicase-DNA-binding on the Z
            Gallus gallus
Eukaryota; Metazoa; Chordata; (
Eukaryota; Aves; Neognathae;
Archosauria; Aves; Neognathae;
Phasianinae; Gallus.
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/lab_host="E. coli EMDH10B"
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99.8%;
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Pred. No. 1.1e-173;
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                             TCTCAAT
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                                                            GTTTAACATACTTCTGACGACATATGAAATTTTACTGAAGGATAAGTCATTCCTTGGTGG
                                                                                                                         AACTAGTAGAAATATGATAAGGACTCATGAATGGATGCATCCACAGACTAAACGATTAAA
                                                                                                                                                                                       GCAAAGAGAGTTCAAACTTGGGCTCCTCAGATGAATGCTGTAGTTTACTTAGGAGATAT
                                                                                                                                                                                                                                                      TGAACATCAACTGTATGGGCCTTTTCTTCTGGTCGTGCCACTTTCTACCTTGACATCTTG
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ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Delaware
Townsend Hall, Newark, DE
Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library, USDA/IFAFS Animal Unpublished (2002) Contact: Larry A. Cogburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                             2039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cogburn@udel.edu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. coli EMDH10B"
/note="Vector: pCMVSPORT6; Library made from pools of total RNA isolated from each tissue ages. Single pass sequencing from 5'-end" a 116 c 127 g 190 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pituitary/Hypothalamus/Pineal Library (pgp2n)"
    /sex="Male and Female"
    /tissue_type="pituitary Gland/Hypothalamus/Pineal Gland"
    /dev_stage="Embryonic (d12,d14,d19); post-hatch (1,3,5,7, weeks)"
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/clone_lib="Normalized C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="Commercial broiler
/db_xref="taxon:9031"
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164616 BARC 5BOV Bos ta
BE479788
BE479788.1 GI:9599321
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USDA, ARS, Beltsville Agricultural Research Center
Bdlg, 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
                                                          AW075773.1 GI:6030771
EST.
                                                                                                        xa85c01.x1 NCI_CGAP_CML1 Homo mRNA sequence.
aw075773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emmail: tads@lpsi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
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Seq primer: ATTTAGGTGACACTATAG.
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1 (bases 1 to 476)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1.3%; SCOTE 87; DB 10; Length 476;
llarity 100.0%; Pred. No. 3.3e-25;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /not="Vector: PCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and disease states."

a 94 c 67 g 178 t
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1 (bases 1 to 234)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Elisabeth Paietta, Jonathan D. Licht, M.D.,

Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Lif
Technologies, Inc. CDNA Library Arrayed by: Christa Brange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA824571 254 bp moon clone IMAGE:1355877, oc78h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1355877,
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                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 252)
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AA824571
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Similarity 100.0%; Pred. No. 5.5e-23;
82; Conservative 0; Mismatches 0;
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

MASSINGTON University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
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/clone=lib="NCI_CGAP_MLI"
/clone_lib="NCI_CGAP_MLI"
/clone_lib="NCI_CGAP_MLI"
/clone_lib="NCI_CGAP_MLI"
/tissue_type="myeloid cells, 18 pooled CML cases, BCR/ABL rearrangement positive, includes both chronic phase and myeloid blast crisis"
myeloid blast crisis
/lab host="pHIJ0B"
/lab host="pHIJ0B"
/lab host="PHIJ0B"
/lab host="Organ: whole blood; Vector: pCMV-SPORT6; Site_1: 5all; Site_2: Not1; Cloned unidirectionally. Primer: 0ligo dT. Library constructed by Life Technologies."
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/db_xref="taxon:9606"
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through the I.M.A.G.E. Consortium/LLNL at:

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ne70d08.s1
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          cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 280 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 296)
                                                                                                                                                                                                                                                                                                     Homo sapiens
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Location/Qualifiers
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                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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/db_xref="taxon:9606"
/clone="IMAGE:1355877"
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sequence stop:
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Pred. No.
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Homo sapiens cDNA clone IMAGE:909615, mRNA
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yv78d12.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
IMAGE:248855 3', mRNA sequence.
                                                                                                                                                                                                                                                                       High quality sequence stops: 224
Source: IMAGE Consortium, LINL;
This clone is available royalty-free through LINL;
IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., F
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E.,
,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hillier, L., Clark, N., Dubuque, T., Elliston, K.,
                                                                                                                                                                                                               High quality sequence stop: 224.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="IMAGE:909615"
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/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
/tissue_type="melanocyte"
/tissue_type="melanocyte"
/lab_host="bettor: pTJ73D (pharmacia) with a modified
/note="vector: pTJ73D (pharmacia) with a modified
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                                                                               /clone_lib="Soares melanocyte
/sex="Male"
                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:248855"
                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:3866561"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lln1.gov/bbrp/image/hage.html
Seq primer: -41m13 fwd, ET from Amersham.
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/tissue_type="Ewing's sarcoma"
/lab_host="DH10B"
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5836 TTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAG 5895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5896 CTTGAATATTTAAATTCTGTAC 5917
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R., Williamson, A., Wohldman
The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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Seq primer: m13 -40 forward
High quality sequence stop: 400.
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                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:3872638"
/db_xref="taxon:9606"
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                                                                                                   Score 82; DB 10; ; Pred. No. 4.3e-23;
                                                                       Mismatches
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               CTTGAATATTTAAATTCTGTAC 5917
                                                                                     TTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAG 5895
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                                                                    TTTCCAAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAG 132
                                                                                                                                             82;
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High quality sequence stops: 360
Source: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Insert Length: 929 Std Error: 0.00
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The WashU-Merck EST Project
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
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Mammalia; Eutheria;
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314 286 1810
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                  double-stranded cDNA was size selected, ligated to Eco adapters (Pharmacia), digested with Not I and cloned in the Not I and cloned in the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino." a 61 c 73 g 126 t 1 others
                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:262972"
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/db_xref="GDB:3872614"
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Primates;
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4.3e-23;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                    TTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAG 214
                                                                                                                                                                                                                                                                                                     CTTGAATATTTAAATTCTGTAC 192
                                                                                                                                           2w55h08.rl Soares_total_fetus_Nb2HF8_9w IMAGE:774015 5', mRNA sequence. AA442118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further is see primer: -40UP from Gibco
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 419)
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Mammalia; Eutheria;
1 (bases 1 to 408)
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                                                            Homo sapiens
                                                                                 human
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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53 c 77 g 128 t
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/clone_lib="Soares_NFL_T_GBC_S1"
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/db_xref="taxon:9606"
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                                                                                                                      GI:2153996
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100.0%; Pred. No. 4.
tive 0; Mismatches
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Primates;
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TITLE JOURNAL COMMENT

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FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

21 (bases 1 to 434)
22 1 (bases 1 to 434)
33 Kizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marrin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Materston, R. and Wilson, R.

WashU-NCI human EST Project
WashU-NCI human EST Project
Washungton University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lencon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. Tan,F., Theising,B., White,Y., Wylie,Mashu-Merck EST project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                               AA609977
af09h02.sl Soares_testis_NHT
3', mRNA section co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 372.
Location/Qualifiers
                                                                                                                                                                                                                                                                        AA609977
AA609977.1 GI:2458405
EST.
                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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larity 100.0%;
Conservative
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/clone="IMAGE:774015"
/clone=1ih="Soares_total_fetus_Nb2HF8_9w"
/dev_stage="8-9 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .419
∕organism⊷"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 4.2e-23;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                            sapiens cDNA
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1 (Dases 1 to 453)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 871 Std Error: 0.00
Seq primer: -40ml3 fvd.EF from Amersham.
            High quality sequence stops: 311 Source: IMAGE Consortium, LINL rhis clone is available royalty-free through LINL; contact the TMAGE Consortium (info@image.lln1.gov) for further information. Seq primer: ml3 -40 forward High quality sequence stop: 311.
                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V20387 453 bp yx37f09.s1 Soares melanocyte 2NbHM IMAGE: 263945 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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/db_xref="taxon:9606"
/clone="IMAGE:1031187"
/clone_lib="Soares_testis_NHT"
/sex="male"
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o. 4.2e-23;
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Homo sapiens cDNA clone
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REFERENCE AUTHORS

COMMENT

KEYWORDS SOURCE ORGANISM

VERSION ACCESSION LOCUS DEFINITION

RESULT 13 AA609977/c

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Query Match Best Local (Matches

BASE COUNT ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                           456 bp mRNA linear EST 10-NOV-
ouθ7h05.s1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE: 1634841 3', mRNA sequence.
                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                   Tumor Gene Index
                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in
                                                                 /clone="IMAGE:1634841"
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/clone="IMAGE:263945"
/clone_lib="Soares melanocyte 2NbHM"
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                                                                                                           /db_xref="taxon:9606"
                                                                                                                      /organism="Homo sapiens"
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/db_xref="GDB:3873587"
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Pred. No.
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hes 0;
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a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1:
309384-310919, 33208-325895 Soares NbBF pool 1:
145032-147355, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares Nb2HF-9W pool 1:
758280-760553, 772104-774407 Soares NbHFA pool 1:
758280-760553, 772104-774407 Soares NbHFA pool 1:
3044776-30631, 320136-322823, 326280-32663 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
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                         5896 CTTGAATATTTAAATTCTGTAC 5917
                                                                             5836 TTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAG 5895
 197
                                                   257 TTTCCAAAGCTACTTGTTTACATTGTACACTGCGACCACCTTGCCGCTTTTCATCACAAG 198
CTTGAATATTTAAATTCTGTAC 176
                                                                                                      82;
                                                                                                      Conservative
                                                                                                                    1.2%;
100.0%;
                                                                                                        0;
                                                                                                                    Score 82; DB 9; L
Pred. No. 4.1e-23;
                                                                                                        Mismatches
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Search completed: August 2, 2002, 22:41:57 Job time: 30172 sec

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9b_htg:AC091946
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Query: US-08-973-363-11
Query length: 88
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Database length: 1873333701
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-Q-(cgn2_1//USPYO_spool/US08973363/runat_01082002_080123_19828/app_query.fasta_1.638
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-GAPOP-6.000 -GAPEXT-7.000 -YGAPOP-60.000 -YGAPEXT-60.000
-EAROP-6.000 -FGAPEXT-7.000 -YGAPOP-60.000 -YGAPEXT-60.000
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-USER-US08973363_eCGL1_1_451 -NCPU-6 -ICPU-3 -LONGLOG
-USCR-US0873363_eCGL1_1_451 -NCPU-6 -ICPU-3 -LONGLOG
-USCR-US0873363_eCGL1_1_451 -NCPU-6 -ICPU-3 -LONGLOG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
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        ESCOTE Len
6.9e-83 68
1.8e-70 26
0.0022 1
1.8e-70 26
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1.91 1.94
1.20 1
1.64 15.85
11.54
15.85
10.84 17.56
39.24 21.58
161.75 1.20
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51 | A.S.654 Sequence 12 from patent
71 | A.S.654 Sequence 13 from patent
71 | A.S.654 Sequence 13 from patent
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! AF004397 G
ACO96005 Rattus norvegicus dal132666 Human chromosome 14 ACO91435 Felis catus clone H ACO91435 Felis catus clone H ACO99734 Oryza sativa chromo ACI044/4 Oryza sativa chromo ACI044/4 Oryza sativa chromosome 14 ACO3961 Homo sapiens chromosome 14 ACO3961 Homo sapiens chromosome 15 Homosome 16 ACO79069 Homo sapiens chromosome 17 ACO79553 Homo sapiens chromosome 18 ACO87135 Mus musculus clone
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Gallus gallus
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A CHDI gene is Z chromosome linked
Gene 197 (1-2), 225-229 (1997)
97473516
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Griffiths, R. and Korn, R.M.
Direct Submission
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1 (bases 1 to 6872)
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0221 | AC102955 Rattus norvegicu
8216 | AC006875 Caenorhabditis e
3 | 256422 H.Sapiens CpG island
1 | AX186575 Sequence 2327 from
4 | AX187647 Sequence 3327 from
7 | AX184770 Sequence 465 from P
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REFERENCE
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                                                                                                                                                                                                                                         265 bp
Sequence 12 from Patent W09639505.
A58693
A58693.1 GI:3714251
                                                                                                                                              1 (bases 1 to 265)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                                                                                                                                                                          unidentified
                                                                                                                 Patent: WO 9639505-A 12 12-DEC-1996;
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Location/Qualifiers
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35 GluLysArgGluThrLysGluLysGluAsnLys
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                                                                                                                                                                                                                                                                                                                                      137 bp
Sequence 13 from Patent W09639505.
A58694
                                                                                                                                                                                                                        Patent: WO 9639505-A 13 12-DEC-1996; ISIS INNOVATION (GB)
                                                                                                                                                                                                                                                     1 (bases 1 to 137)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                                                                                                                                                                                                                                                               unidentified unidentified
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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1 (bases 1 to 164144)
Birren,B., Linton,L., )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 13664 bases at least 040
Consensus quality: 147222 bases at least 020
Consensus quality: 152549 bases at least 020
Consensus quality: 152549 bases at least 020
Insert size: 17300; agarose-fp
Insert size: 159344; sum-of-contigs
Quality coverage: 3.1 in 020 bases; sum-of-contigs
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                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
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1084: contig of 1084 bp in length
1085 1184: gap of 100 bp
1185 2467: contig of 1283 bp in length
2468 2567: gap of 100 bp
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nusbaum, C. and Lander, E.
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E, 47 unordered
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84179 84278:
84279 8936
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27825 27924:
           94501 94600: gap of 100 bp
94601 99471: contig of 4871 bp in length
99472 99571: gap of 100 bp
99572 104500: contig of 4870 bp
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89465 94500
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30150 31707: contig of 1558 bp in length
31708 31807: gap of 100 bp
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18337 198
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106: gap of ...
7051: ~...
571: gap of 100 bp
104300: contig of 4729 bp in length
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89364: contig of
                                                                                                                                                                                                                                                                                                                                                                                               240: gap of 100 bp
84178: contig of 3938 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp 100 to 100 bp 100 to 10
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76509: contig of 3899 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4182: contig of 1615 bp in length
2: gap of 100 bp
5706: contig of 1424 bp in length
                                                                                                                                                                                            gap of 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p of 100 bp
contig of 1754 bp in length
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of 1424 bp in length
                                                                                                                                                                                                                                                                                                                                                 100 bp
                                                                                                                                                                                                                                                                                                    5086 bp in length
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alignment_block:
US-08-973-363-11 x AC012577/rev
                                                                                                                                                              alignment_scores:
Quality:
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                                                                                                                                 Quality: 11.00
Ratio: 1.000
Percent Similarity: 100.000
                                                           Align seg 1/1 to reverse of: AC012577
misc_feature
                                                                                                                                                                                                                                                                     misc_feature
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121222 121321: gap of 100 bp

121322 127038: contig of 5717 bp

121322 127138: gap of 100 bp

127039 127138: gap of 6757 bp

137039 133995: gap of 100 bp

137039 133995: gap of 100 bp

13896 140279: contig of 6284 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11388 111487: gap of
111488 116244: contig
116245 116344: gap of
116345 121221: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140280 140379:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147005 147104:
                                                                                                                                                                                                         /note="assembly_fragment"
31808. 33988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
5807. .7051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
2568. .4182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 164144: contig of 17040 bp in length Location/Qualifiers
                                                                                                                                                                                                                                                                      /note="assembly_fragment"
27925. .30049
                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
26071. .27824
                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
19916. .21938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-1J4"
                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment"
                                                                                                                                                                                                                                                     'note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                             'note≖"assembly_fragment"
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100 b
147104: contig of 6625 b
147104: gap of 100 '
164144: conti
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1037°
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116244: contig of 4757 bp
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                                                                                                                           Length: 11
Gaps: 0
Percent Identity: 100.000
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6987 bp
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4877 bp in
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6625 bp in length
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R.,
McCarthy, M., McDan, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Venna, C., Talamas, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
                                  * NOTE: This is a 'working draft' sequence. It currently * consists of 5 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * arbitrary of N, but the exact sizes of the gaps are unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-MAR-2000) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 3, 2000 this sequence version replaced gi:7670170. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 177957)
Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC025298 177957 bp DNA linear H' Homo sapiens clone RP11-2N21, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                            Center project name: L2880

Center clone name: 2_N_21

Center clone name: 2_N_21

Center clone name: 2_N_21

Sequencing vector: M13; M7815; 100% of reads chemistry: Dye-terminator B19 Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 174723 bases at least Q40

Consensus quality: 174723 bases at least Q30

Consensus quality: 176598 bases at least Q20

Consensus quality: 177197 bases at least Q20

Insert size: 182000; agarose-fp

Ouality coverage: 6.7 in Q20 bases; agarose-fp

Ouality coverage: 6.8 in Q20 bases; sum-of-contigs
This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Troject Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                             sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG 03-JUN-2000
E, 5 unordered
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FEATURES

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alignment_block:
US-08-973-363-11 x AC025298
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LOCUS ACDOS
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 10120)

DE Joint Genome Institute and Stanford Human Genome Center.
                 Direct Submission
Submitted (03-UUL-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USI
3 (bases 1 to 101220)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC092372 101220 bp DNA linear PRI 07-DEC
Homo sapiens chromosome 5 clone RP11-58M12, complete sequence.
AC092372
Direct Submission
                                                                                                                                                                                                            2 (bases 1 to 101220)
DOE Joint Genome Institute.
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101525 177957: contig of 76433 bp in length.
Location/Qualifiers
1. .177957
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1829 1928: gap of 100 bp
1929 26417: contig of 24489 bp in length
26418 26517: gap of 100 bp
26518 35437: contig of 27920 bp in length
54438 54537: gap of 100 bp
54538 101424: contig of 46887 bp in length
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101525. 177957
| 101525 . 177957
| note="assembly_fragment"
| 34244 c 35114 g 54995 t
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54538. .101424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
26518. .54437
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1929. .26417
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clone_end:T7
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/db_xref="taxon:9606"
/clone="RP11-2N21"
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                                                                                                          USA
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AUTHORS
TITLE
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AUTHORS
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ACCESSION
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                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                               FEATURES
                                                                                                                                                                              COMMENT
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LOCUS AC012624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                  JOURNAL
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Ratio:
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BASE COUNT ORIGIN

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JOURNAL TITLE AUTHORS REFERENCE AUTHORS TITLE

REFERENCE

SOURCE ORGANISM

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alignment_block:
US-08-973-363-11 x AC092372/rev
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                                                                                                   Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 2, 2001 this sequence version replaced gi:14277267.
Location/Qualifiers
1. .134365
                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (31-CCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US;
3 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACU12624 134365 bp DNA linear PRI 21-JUL-
Homo sapiens chromosome 5 clone CTD-2082I17, complete sequence
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Estimated Total Number of Errors is 0.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 146.7kb). It is clipped at the overlap with AC012624.
The number of bases overlapped is 90404.
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                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                       4 (bases 1 to 134365)

DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
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AC012624.6 GI:14993679
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18862 c 17827 g 30409 t
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/db_xref="taxon:9606"
/chromosome="5"
                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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/chromosome="5"
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LOCUS AC021449
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Quality:
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meddrim, J., Meneus, L., McGurk, A., McKernan, J.,
McPheeters, R., Meddrim, J., Meneus, L., McGurk, A., Naylor, J.,
McPheeters, R., Meddrim, J., Meneus, L., McGurk, A., McKernan, K.,
Plarre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
Roy, A., Santos, R., Severy, P., Seponcer, B., Stanger-Thomann, N.,
Roy, A., Santos, R., Severy, P., Seponcer, B., Stanger-Thomann, N.,
Roy, A., Santos, R., Severy, P., Seponcer, B., Stanger-Thomann, N.,
Roy, A., Santos, R., Severy, P., Seponcer, B., Stanger-Thomann, N.,
Roy, A., Santos, R., Severy, P., Seponcer, B., Stanger, Rothman, D.,
Roy, A., Santos, R., Severy, P., Seponcer, R., Seponc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 10, 2000 this sequence version replaced gi:7407963. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theod Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC021449.3 GI:10047806
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Linton,L., Nusbaum,C.
Homo sapiens, clone RP11-58M12
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Homo sapiens clone RP11-58M12, V
                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 143079)
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   Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
                                                                                                                                                          Center clone name: 58_M_12
                                                                                                                                                                                           Center project name: L5154
                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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1 24497 c 25503 g 43951 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 134365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA linear HTG 10-SEP-2000 WORKING DRAFT SEQUENCE, 10 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Theodore, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ye,W.J.,
                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
Quality: 10.00
Ratio: 1.000
Percent Similarity: 100.000
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runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46906 47005: gap of 100 bp 107006 51830: contig of 4825 bp in length 51831 51930: gap of 100 bp 51931 62619: contig of 10689 bp in length 62620 62719: gap of 100 bp 62720 75408: contig of 12689 bp in length 75409 75508: gap of 100 bp 75509 92516: contig of 17008 bp in length 92517 92616: gap of 100 bp 1006409: contig of 13793 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 144000; agarose-fp
Insert size: 142179; sum-of-contigs
Quality coverage: 4.6 in Q20 bases;
Quality coverage: 4.7 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Consensus quality: 134743 bases at least Q40 Consensus quality: 139227 bases at least Q30 Consensus quality: 140814 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92617 106409: courty 100 bp
106410 106509: gap of contig of 36570 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38820: contig of 38820 bp in length

38821 38920: gap of 100 bp

38921 40411: contig of 1491 bp in length

40412 40511: gap of 100 bp

40512 43279: contig of 2768 bp in length

43280 43379: gap of 100 bp

43380 43379: gap of 100 bp

43380 43379: gap of 3526 bp in length
vector_side:right"
26246 c 26678 g
                                                                 /note="assembly_fragment"
106510...143079
/note="assembly_fragment"
                                                                                                                                              /note="assembly_fragment"
92617. .106409
                                                                                                                                                                                                                                             /note="assembly_fragment"
62720. .75408
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                                               clone_end:T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_end:SP6
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/clone="RP11-58M12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-11 Human Male
1. .38820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                              note="assembly_fragment"
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9
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  906 others
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Percent Identity:

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US-08-973-363-11 x AC021449
FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 LysGluLysArgGluAsnLysValLysGlu 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 139128 bases at least Q40
Consensus quality: 142556 bases at least Q20
Consensus quality: 143744 bases at least Q20
Consensus quality: 143744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 145059; sum-of-contigs estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* motic course.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Direct Submission Production Sequencing Facility, DOE Joint Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced 91:7528342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 14559)

DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
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Homo sapiens chromosome 5 clone CTC-480B11, WORKING DRAFT SEQUENCE,
7 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics
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Center Project Name: 369535
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Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.jgi.doe.gov
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE2; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence will be replaced by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                      the accession
                           56175
56275
100875
100975
113128
113228
11391
118191
118695
119795
119795
119795
1123298
             ssion number will be preserved.

56174: contig of 56174 bp in length
56274: gap of unknown length
100874: contig of 46600 bp in length
100874: contig of 44600 bp in length
100874: gap of unknown length
113127: contig of 12153 bp in length
113127: gap of unknown length
118190: contig of 4963 bp in length
118190: gap of unknown length
118290: gap of unknown length
119584: contig of 1404 bp in length
119794: gap of unknown length
112397: gap of unknown length
112397: gap of unknown length
113397: gap of unknown length
114569: contig of 2262 bp in length.
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VERSION
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US-08-973-363-11 x AC008531
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LOCUS AC091946
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Ratio: 1.000
Percent Similarity: 100.000
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                                            Consensus quality: 157767 bases at least Q40
Consensus quality: 180259 bases at least Q20
Consensus quality: 184175 bases at least Q20
Consensus quality: 184175 bases at least Q20
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.38 in Q20 bases; sugrose-fp estimation
Quality coverage: 5.79 in Q20 bases; sum-of-contigs estimation.
**NOTE: This is a 'working draft' sequence. It currently
**consists of 33 contigs. The true order of the pieces
**is not known and their order in this sequence record is
**arbitrary. Gaps between the contigs are represented as
**runs of N. but the exact sizes of the gaps are unknown.
**This record will be updated with the finished sequence
**as soon as it is available and the accession number will
** be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193446 bp DNA linear HTG 09-JUN Homo sapiens chromosome 5 clone RP11-36012, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.
AC091946
AC091946 I GI:14333882
HTG: HTGS PHACET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project Information
Center Project Name: 544799
Center clone name: RPCI-11_36012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 193446)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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DOE Joint Genome Institute.
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Gaps: 0
Percent Identity: 100.000
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BASE COUNT
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0 193446: contig of 24237
Location/Qualifiers
                                                                                                                                                                      123838: gap of unknown length
130583: contig of 6745 bp in len
130683: gap of unknown length
141544: contig of 10861 bp in len
141644: gap of unknown length
169109: contig of 27465 bp in length
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                 alignment_block:
US-08-973-363-11 x AC026778/rev
                                                                                                                                                       alignment_scores:
Quality:
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US-08-973-363-11 x AC091946
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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LysGluLysArgGluAsnLysValLysGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (24-MAR-2000) Production Sequencing
Genome Institute, 2800 Mitchell Drive, Walnut
3 (bases 1 to 195433)
DOE Joint Genome Institute and Stanford Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:13677045.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                         Estimated Total Number of Errors is 0.2. STS Content: WI-13675 G23101
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Finishing Completed at Stanford Human Genome C
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
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DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute.
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/db_xref="taxon:9606"
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US-08-973-363-11 x AC022121/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (11-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 219288)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Homo sapiens chromosome 5 clone CTD-2007H13, complete sequence.
ACO22121
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SHGC-103595 G57841.
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Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
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Center Code: JGI
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276181 bp DNA linear HTG 03-JUL-2001
Homo sapiens chromosome 5 clone RP11-75H1, WORKING DRAFT SEQUENCE,
47 unordered pieces.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 276181)
DOE Joint Genome Institute.
                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Submitted (03-JUL-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 2 (bases 1 to 276181)
DOE Joint Genome Institute. Sequencing of Human Chromosome 5

Consensus quality: 229677 bases at least 040
Consensus quality: 256163 bases at least 020
Consensus quality: 260799 bases at least 020
Estimated insert size: 174820; agarose-fp estimation
Estimated insert size: 271581; sum-of-contigs estimation
Ouality coverage: 8 62 in 020 bases; agarose-fp estimation
Ouality coverage: 8 55 in 020 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 47 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved. Project Information Center Project Name: 435334 Center clone name: RPCI-11_75H1 Web site: http://www.jgi.doe.gov

1061: contig of 1061 bp in length
1101: gap of unknown length
2827: contig of 1666 bp in length
2827: gap of unknown length
4227: gap of unknown length
4227: gap of unknown length
5618: contig of 1300 bp in length
5618: contig of 1291 bp in length
5718: gap of unknown length
6983: contig of 1265 bp in length
7083: gap of unknown length
8422: contig of 1339 bp in length 8: gap of unknown length
4: contig of 1116 bp 14:
4: gap of unknown length
5: contig of 1292 bp in length
6: gap of unknown length
6: gap of unknown length
7: contig of 1454 bp in length gap of contig gap of contig gap of contig gap of gap of contig gap of contig f unknown g of 1051 f unknown g of 1207 f unknown g of 1327 f unknown g of 1249 length bp in length bp in length bp in length length length bp in length Length bp in length length bp in length length

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BASE COUNT
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US-08-973-363-11 x CNS01BAC/rev
seq_documentation_block:
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Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
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                                                                                AGAGAGAAGAAGAGAAGATAAA 631
                                                                                                     ArgGluLysLysGluLysGluAspLys 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   720 bp mRNA linear PLN 02-1
Botrytis cinerea strain T4 cDNA library under conditions of
nitrogen deprivation.
ALI13980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 EVRY Cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes Helotiales; Sclerotiniaceae; Botryotinia.

1 (bases 1 to 720)

Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library; nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana
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2 (bases 1 to 720)
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                                                                                                                                                                                                                                                                                                                                                                                                        105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library was produced in an oriented direction,
                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Botryotinia fuckeliana"
/strain="T4"
/db_xref="taxon:40559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  /note="Genoscope sequence ID : W25F061"
192 c 128 g 295 t
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Gaps: 0
Percent Identity: 100.000
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t Identity:
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Botryotinia.
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JOURNAL REFERENCE
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AUTHORS
                                                                                                                                                         BASE COUNT
ORIGIN
alignment_block:
US-08-973-363-11 x AB009080
                                                                                                     alignment_scores:
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DEFINITION
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Ratio: 1.000
Percent Similarity: 100.000
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TITLE
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Submitted (21-NOV-1997) Junichi Saito, University of Tokyo,
Submitted (21-NOV-1997) Junichi Saito, University of Tokyo,
Department of Life Sciences, Graduate School of Arts & Sciences;
Department of Life Sciences, Graduate School of Arts & Sciences;
3-8-1, Komaba, Meguro-ku, Tokyo 153, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum (strain:AX2) DNA.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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J. Biol. Chem. (1998) In press
2 (bases 1 to 4875)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saito, J., Adachi, H. and Sutoh, K.
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                                                                                                                                                                                                                                                                                                                                                                                  /note="15 a nucleotides"
1 758 c 627 g 1327 t
                                                                                                                                                                                                                                                          SSSSSTNTGSSSTNSAKNERDRDRERERERERDREREREREREREKKQPTR
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PSIVKLAEEKRETVI VDKERS PTP I I TEK PDEK OVEK VTDKES SI VEKS VD KERKES P
SSSSSKE BIEKETEKEKE KEKEKEKEKE VEKEVEKE VEKETENDKEKEKE PER OVEENKS VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:44689"
join(354. .1352,1489. .1581,1669. .2485,2596. .4859)
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/gene="trfA"
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                                 Length: 9
Gaps: 0
Percent Identity: 100.000
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Align seg 1/1 to: AB009080 from: 1 to: 4875
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Date: Aug 3, 2002 7:18 AM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search information block:
Query: US-08-973-363-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                       Search time (sec): 521.050000
                                                                                                                                                                                                                                                                                                                                                                                                                  Database sequences: 1736436
Database length: 858457221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MODEL-frame+_p2n.model -DEV=x1h
-Q-/cgn2_1/USP70_spcol/US60973563/runat_01082002_080123_19849/app_query.fasta_1.638
-DB-M_Genseq_032802 -CFMT-fastap -SUFFIX=011p2n.rng
-GAPOP=4.500 -GAPEXT=0.050 -MIMMATCH=0.100 -LOOPEXT=0.000
-CAPEXT=0.000 -GAPEXT=0.050 -GAPEXT=7.050 -XGAPOP=60.000
-XGAPEXT=60.000 -FCAPOP=6.000 -GEAPEXT=7.000 -YGAPOP=60.000
-YGAPEXT=60.000 -FCAPOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=011g0 -TRANS=human40.0d1 -LIST=45 -DOCALIGN=200
-THR_SCORE=quality -THR_MIN=1 -ALIGN=15 :MODE=LOCAL -OUTEMT=pfs
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=10.000000
-USER-US08973363_e(CRIL_1_186 -NCPU=6 -ICPD=3 -LONGLOG
-USCRE-US08973363_e(CRIL_1_186 -NCPU=6 -ICPD=3 -LONGLOG
-DEV_TIMEOUT=120 -WARR_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                            uery length: 88
                                                                                                                                                                                                                                                                                                                                                                             XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP=60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT=60.000
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                                     1.7e-6
0.0121
10.80
                     alignment_block:
US-08-973-363-11 x AAT42752
                                                                        alignment_scores
                                                                                                   Align seg 1/1 to: AAT42752
                                                Percent Similarity:
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AAX02996 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:ABL15140 + /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AAX02303 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAX03377 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAL03377 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAL03377 - /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAL03379 - /SIDS1/gcgdata/hold-geneseq/genes
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ID AAT42752 standard; cDNA; 265 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                             A composite nucleotide sequence (AAT42752) and putative translation (AAW08144) sequence are provided of a motif that is found spliced to a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the complete motif. There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of the CHD-W clone CC14 (see also AAT42753).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avian chromodomain-helicase-DNA binding genes determine sex in birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers misc_difference 52
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                                                                                                                                                                                                                                                                                                                        Sequence 265 BP; 158 A; 16 C; 61 G; 30 T; 0 other;
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/note= "base 52 disrupts the reading frame for
the translated amino acid sequence given
in Fig 7"
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0.852
98.876
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639.
648.
648.
914.
914.
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from: 1

to:

Length: 89
Gaps: 1
Percent Identity: 98.876

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seq_documentation_block:
ID AAT42753 standard; cD
XX
AC AAT42753;
XX
AC AAT42753;
XX
DT 12-MAR-1997 (first e
XX
DT 12-MAR-1997 (first e
XX
Chicken CHD-W clone C
XX
W Bird; sex determinati
KW CHD-W; chromodomain-H
XX
Gallus sp.
XX
Key Locat
FT misc_difference 52
FT //note
FT
XX
VO9639505-A1.
XX
PN W09639505-A1.
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PD 12-DEC-1996.
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PN W09639505
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                             A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CC14 (see also AAT42754). There are no splice donor or acceptor sites within the motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicken CHD-W clone CC14 3'
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                                                                                                                                                                                                              chromodomain-helicase-DNA binding genes determine sex - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex determination; chromodomain-Helicase-DNA binding 1 chromodomain-Helicase-DNA binding on the W chromosome;
                                                                                                                                                                Fig 7; 76pp;
                                                                                                                                                                                                                                                                                                                                                                                                                               INNOVATION LTD
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the translated amino
in Fig 7"
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US-08-973-363-11
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                               The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA ilbraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             splicing.
(see also
                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                        Claim 1; SEQ ID 8910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 137 BP;
                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                Dumas Milne Edwards
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Sequence

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alignment_block:
US-08-973-363-11 x AAH70996
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                                                                                                                                  alignment_scores:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                 Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-199; 99US-0169681.
21-DEC-1999; 99US-0171350.
14-MAR-2000; 2000US-0189315.
12-MAY-2000; 2000US-02189315.
09-UUN-2000; 2000US-021660.
21-JUL-2000; 2000US-0220114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic actios and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 480; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlegel R, Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-2000; 2000WO-US33312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200142467-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cervical cancer marker nucleic acid 2270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH70996;
                                                                                                                                                                                                 Sequence 271 BP; 98 A; 56 C; 75 G; 41 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH70996 standard; cDNA; 271 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berger A, Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                    seq_documentation_block: ID ABA74794 standard.
                                                                                                                                alignment_block:
US-08-973-363-11 x ABA74794
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                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                         Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                      Align seg 1/1 to: ABA74794 from: 1
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                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. For this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                  Sequence 287 BP; 139 A; 5 C; 138 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 23099; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for
analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; foetal liver; gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human foetal liver single exon nucleic acid probe #23099.
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16 AAAAGGGAGAAGAAGGAGGAG 39
                    49 LysArgGluLysLysGluLysGlu 56
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Gaps: 0
Percent Identity: 100.000
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seq_documentation_block:
ID ABA39495 standard; DN
AC ABA39495;
XX ABA39495;
XX ABA39495;
XX Probe #17961 for gene
XX Probe #17961 for gene
XX Probe #17961 for gene
XX Human; gene expressic
XX Human; gene expressic
XX Homo sapiens.
XX W0200157274-A2.
XX W0200005-C
PR W04-FEB-2000; 2000US-C
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Percent Similarity:
                                                                                                                                                   US-08-973-363-11 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       measuring human gene expression in a sample derived from human heart present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples deri from the human heart via microarrays. By measuring gene expression, probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular se.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not specification, but was obtained in electronic for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probe measuring human gene expression in a sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; SEQ ID No 17961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
  16
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/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:ABA39495
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2000US-0207456.
2000US-0608408.
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seq_documentation_block:
ID AAK23286 standard; DN
AC AAK23286;
XX AAK23286;
XX O5-NOV-2001 (first e
XX Human brain expressed
XX Human; brain expressed
XX Human; brain expressed
XX Human; brain expressed
XX Homo sapiens.
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US-08-973-363-11 x AAK23286
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                                                                       seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAK49450
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AAK49450 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
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                                                                                                                        16
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                                                                                                                      LysArgGluLysLysGluLysGlu
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alignment_block:
US-08-973-363-11 x AAK49450
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ID AAi26561 standard:
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26-MAX-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEB-2000; 2000US-0234687.

27-SEB-2000; 2000US-023559.

04-OCT-2000; 2000GB-0024263.
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26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00668
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             cervical cancer; ss.
                                                                                                                            AAI26561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 287 BP; 139 A; 5 C; 138 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG,
                           Probe; human; microarray; gene expression; cervical epithelial cell;
                                                         Probe #16494 for gene expression analysis in human cervical cell sample.
                                                                                           12-OCT-2001 (first entry)
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                                                                                                                                                          AAi26561 standard; DNA; 287 BP
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Percent Identity: 100.000
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alignment_block:
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26-MAY-2000; 2000US-0608408.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe from the SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the ...
                                WO200157272-A2
                                                                                                                                                                        genetic disorder;
                                                                                                                                                                                                         Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                 17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           AAI55319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 287 BP; 139 A; 5 C; 138 G; 5 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
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                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                           Probe #24005 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488901/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAI55319 standard; DNA; 287 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
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    Ratio:
    Percent Similarity:
  alignment_block:
US-08-973-363-11 x
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                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                      _documentation_block:
AAH72066 standard; cDNA;
08-DEC-1999;
21-DEC-1999;
14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
21-JUL-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one subset. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                       Cervical cancer;
                                                                                                                                                                          Human cervical cancer marker nucleic acid 3340
                                                                                                                                                                                                                   AAH72066;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 287
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                                                                                                              WO200142467-A2
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7-SEP-2000;
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                                                                                                                                   sapiens
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; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
 2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
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                                                                       2000WO-US33312
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99US-0171350.
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                                                                                                                                                      cytostatic;
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n human placenta –
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                                                                                                                                                     pre-malignant condition;
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                                                                                                                                                     gene therapy;
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAH69191
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    Quality:
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US-08-973-363-11 x
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                                                                             14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is affilicted with cervical cancer or has a per-malignant condition; to monitor the progression of cervical cancer or a pre-malignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                      08-DEC-1999;
21-DEC-1999;
                                      Schlegel
                                                                                                                                                    08-DEC-2000;
                                                                                                                                                                         14-JUN-2001
                                                                                                                                                                                             WO200142467-A2
                                                                                                                                                                                                                                    Cervical cancer;
                                                                                                                                                                                                                                                          Human
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                                                                                                                                                                                                                                                                                                 ААН69191;
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                                                          (MILL-)
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                                                                                                                                                                                                                                                                                                                                                                                  20 GluGluLysProGluProAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolated nucleic acid for diagnosing and treating cervical cancer
                                                                                                                                                                                                                                                        cervical cancer marker
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                                                          MILLENNIUM PREDICTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               assessing and detecting compounds for treating the cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 BP;
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                                                                             2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
                                                                                                                                                                                                                                                                             (first entry)
                                      Deeds
                                                                                                                                                     2000WO-US33312
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99US-0171350.
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                                     J,
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                                      Berger
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                                                                                                                                                                                                                                    pre-malignant condition;
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                                                                                                                                                                                                                                                        nucleic acid
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                                                          MEDICINE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal
                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human foetal liver single exon nucleic acid probe #10563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and for assessing and detecting compounds for treating the cancer -
measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting.
                                                                Claim 1; SEQ ID NO 10563; 639pp + sequence listing; English.
                                                                                                                                                 WPI; 2001-483447/52.
                                                                                                                                                                                 Penn
                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; foetal liver; gene expression; single exon nucleic acid probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA62258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:ABA62258
                                                                                                 genome-derived single exon nucleic acid probes useful for
sing gene expression in human fetal liver -
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Ratio:
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2000US-0207456.
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US-08-973-363-11 x ABA62258
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26-MAX-2000; 2000US-0207456.

30-UUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEB-2000; 2000US-0234687.

27-SEB-2000; 2000US-023639.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                             The present invention relates to single exon nucleic acid probes for
                                                                                                                                              Claim 1; SEQ ID No 8070; 530pp; English.
                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                      WPI; 2001-488899/53.
                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #8070 for gene expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABA29604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 575 BP; 223 A; 93 C; 188 G; 71 T; 0 other;
                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABA29604 standard; DNA; 575 BP
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Percent Identity: 100.000
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Note: The sequence data for this patent did not form specification, but was obtained in electronic format

part of the printed directly from WIPO

and

e.g. cardiovascular disease, hypertension, cardiac arrhythmias congenital heart disease.

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seq_documentation_block:
ID AAK10591 standard; DN
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AC AAK10591;
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Human; brain expressed
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Human; brain expressed
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Human; brain expressed
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Human; brain expressed
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WO200157275-A2.
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OS HOMO sapiens.
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VO9-AUG-2001.
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VO9-AUG-2001; 2001WO-U
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O9-AUG-2001; 2000US-O
PR 26-MAY-2000; 2000US-O
PR 26-MAY-2000; 2000US-O
PR 27-SEP-2000; 2000US-O
PR 30-JUN-2000; 2000US-O
PR 21-SEP-2000; 2000US-O
PR 30-JUN-2000; 2000US-O
PR 30-JUN-2000; 2000US-O
PR 21-SEP-2000; 2000US-O
PR 21-SEP-2000; 2000US-O
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PR 21-SEP-2000; 2000US-O
PR 21-SEP-2000; 2000US-O
PR 21-SEP-2000; 2000US-O
PR 30-JUN-2000; 2000US-O
PR 30-JUN-2000; 2000US-O
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US-08-973-363-11 x ABA29604
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Ratio: 1.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          at
                                                   The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure general pression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human brain expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK10591 standard; DNA; 575 BP
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                                                                                                                                                                                                                                                       Example 4; SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                      exon nucleic acid
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2000US-0207456.
2000US-0608408.
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Query length: 88
Database: EST:*
Database: sequences: 13736207
Database: length: -1841457050
Search time (sec): 4311.510000
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9b_gss:AG286520
9b_esst:AG286520
9b_esst:AT284831
9b_esst:BT101081
9b_esst:BT101081
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9b_gss:AC518181
9b_gss:AC518181
9b_gss:AC518181
9b_esst:AM0207742
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9b_esst2:BF338481

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gb_est2:BM015597
gb_est1:AU053734
gb_est2:BG611198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est1:AU053344
gb_est1:AW790096
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gb_est2:BI038399
gb_est2:R0602323
gb_gss:AQ602323
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KEYWORDS
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US-08-973-363-11 x BM015597
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LOCUS AU053734
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                               gb_est1:AU053734
AUU53/34 290 bp mRNA linear
AUU53734 Dictyostelium discoideum SL (H.Urushihara)
discoideum cDNA clone SLJ576, mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 677)
1 (bases 1 to 677)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12066 row: g column: 08
High quality sequence stop: 674.
Location/Qualifiers
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603641828F1 NIH_MGC_87 Homo sapiens
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Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert St
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//db_xref="taxon:9606"
//db_xref="taxon:9606"
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//nab_host="DHIDB (phage-resistant)"
//nab="Organ: breast; Vector: pCMV-SPORT6; Site_1: Not1;
//note="Organ: breast; Vector: pCMV-SPORT6; Site_1: No
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D73021 CELK112G6R Yuji Kohar
i A1551990 vd60b04 yl Knowles
i BE247224 TCBAP1E3832 Pediatr
B1038399 RC5-YT0266-180101-0
1 AQ603223 HS 214 AQ2.A(1.77C
I A1197098 ud57d08.rl Soares_N
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LOCUS BG611108
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                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                    Ammmalia; Eutheria; Primates; Ca
1 (Dases 1 to 413)
1 (Dases 1 to 413)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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BG611198.1 GI:13662569
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                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG611198 413 bp mRNA linear EST 18-APR-2001 602612177F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4737522 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project in Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y. Developmental CDNA in Dictyostelium discoideum
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                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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           Plate: LLCM1605 row: j column: 19 High quality sequence stop: 230.
                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
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/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
/dev_stage="slug"
/dev_stage="slug"
28 c 55 g 47 t 2 others
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LOCUS BI508663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAAGGAAAAAGAAGACAAGAAAGAG
                                                                                                                                                                    Email: generobielife.uiuc.edu
Email: generobielife.uiuc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Research Infunctional Genomics to G.E. Robinson and an NSF
Award in Functional Genomics to G.E. Robinson and an NSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac; ; Apoidea; Apidae; Apis.

1 (bases 1 to 447)

Mhitfield, C.W., Soares, B., Robertson, H.M., Pardinas, J., Liu, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB170001B10E08 Bee Brain Normalized/Subtracted Library, BB17 Apis mellifera cDNA clone BB170001B10E08 5', mRNA sequence. B1508663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Smoller,D. and Robinson,G. An Expressed Sequence Tag Behavior in the Honey Bee Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST.
                                                                        FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCTCACTAAAG
                                                                                                                                                                                                                                                                                                                                                                                        Tel: 217 265 0309
Fax: 217 244 3499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apis mellifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI508663.1
Insert Length: 447
Plate: BB170001B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  honeybee.
                                                                                                                                                    PCR PRimers
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/clone_lib="NIH_MGC_50"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                þ
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77 c 104 g 56 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:4737522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:15359037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from:
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Gaps: 0
Percent Identity: 100.000
Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Resource for Studies of Brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robertson, H.M., Pardinas, J., Liu, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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FEATURES

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alignment_scores: 9.00
Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-973-363-11 x BI508663/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AZ257993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_gss:AZ257993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: BI508663
                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 AAAGAAAGTACACAAAAGGAAAAAGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 LysGluSerThrGlnLysGluLysGlu 83
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library avallability, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                     Unpublished (1999)
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPCI-23-120M12.TV RPCI-23 Mus musculus genomic clone RPCI-23-120M12 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: AGCGGATAACAATTTCACACAGGA High quality sequence stop: 447.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           , B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 469)
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ257993.1 GI:9463121
                                                                                                                                                                                                                                                                                                                                  Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nouse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127
                                                                                                                                                                                                                                                                                                                                                                                                             Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-*Organ: brain; Vector: pT773-Pac; Site_1: EcoR1; Site_2: Not1; This BB17 cDNA library was generated by subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by t soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "strain="mixed strains of European bees, predominantly
A.m. ligustica"
/db.xref="taxon:7460"
/clone="BB170001B10E08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Apis mellifera"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from:
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JOURNAL
COMMENT
                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est1:AU053344
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LOCUS AU053344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 GAAACAAAAGAGAAAGAGAACAAGAGG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 GluThrLysGluLysGluAsnLysArg 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU053344 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium discoideum CDNA clone SL1432, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum
Eukaryota: Mycetozoa: Dictyosteliida; Dictyostelium.

1 (bases 1 to 510)
Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M.,
Yoshino, R., Mitta, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H.,
Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.
Developmental cONA in Dictyostelium discoideum
Unpublished (1998)
Contact: Hideko Urushihara
Tonititto, G. Biologica (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: 120 row: M column: 12
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
                                                                                                                                                                                                                                                                                                                PROJECT -
                                                                                                                                                                                                                                                                                                                                                          3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU053344.1 GI:4701826
                                                                                                                                                                                                                                                                                                                                                                                     University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                 Institute of Biological Sciences
                                                                              263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 a
                                                                                                                                                                                                                                                                               d402hnl@sakura.cc.tsukuba.ac.jp
77 - Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/GJ mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
a 93 c
                                                                           /db_xref="taxon:44689"
/clone="5L1432"
/clone="1b="Dictyostelium discoideum SL (H.Urushihara)"
/dev_stage="slug"
/dev_stage="slug"
64 c 63 g 120 t
                                                                                                                                                                                                      /organism="Dictyostelium discoideum"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RPCI-23-120M12"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Female"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Gaps: 0
Percent Identity: 100.000
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EST 28-APR-1999

COMMENT

TITLE

REFERENCE

KEYWORDS

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REFERENCE
AUTHORS
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-973-363-11 x AU053344
                                                                                                                                                                                                               alignment_block:
US-08-973-363-11 x AW790096/rev
                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                  seq_documentation_block:
LOCUS AZ879168
                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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LOCUS AW790096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est1:AW790096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
     DEFINITION
                                                                    seq_name: gb_gss:AZ879168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                   Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                              Align seg 1/1 to reverse of: AW790096
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                                                                                                          451 AGGGAAAAGAAGGAAAAGGAAGATAAG 425
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                                                                                                                           50 ArgGluLysLysGluLysGluAspLys 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW790096 518 bp mRNA linear EST 01-MAY-2001 C01520-F Lambda Zap, Stratagene Blumeria graminis f. sp. hordei cDNA clone C01520 similar to 101 kd malaria antigen, mRNA sequence. AW790096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blumeria graminis f. sp. hordei.
Blumeria graminis f. sp. hordei
Blumeria graminis f. sp. hordei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
1 (bases 1 to 518)
 RPCI-23-194A5.TJ RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Rasmussen, S.W.
Department of Yeast Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed sequence tag analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: swr@crc.dk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sberg Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            il. Carlsbergvej, DK-2500, Copenhagen, Denmark
45 3327 5230
45 3327 4766
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                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Blumeria graminis f. sp.
/db_xref="taxon:62688"
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/clone_lib="Lambda Zap, Stratagene"
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/cell_type="conidia"
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99 c 84 g 204 t
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Percent Identity:
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Gaps: 0
Percent Identity: 100.000
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542 bp DNA linear GSS 05-MAR-2001 Mus musculus genomic clone RPCI-23-194A5,
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AUTHORS
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LOCUS BF338481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
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                  KEYWORDS
                                                                                        DEFINITION
                                                                                                                                                          seq_name: gb_est2:BF338481
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                                                       BF338481
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Class: BAC ends.
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alignment_block:
US-08-973-363-11 x AZ879168/rev
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                     522 GAGAAAGAGAACAAGAGAGAGCTAAAA 496
                                                                                                                                                                                                                                                                                     41 GluLysGluAsnLysArgGluLeuLys 49
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Eukaryota; Metazoa; Chordata;
Eukheria; Rodentia;
                                                                  BE338481 791 bp 602034145F2 NCI_CGAP_Brn64 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 194 row: A column: 5
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Contact: Shaying Zhao
Department of Eukaryotic Genomics
BF338481.1 GI:11284884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao, S., Nierman, W., Feldblyum, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse BAC End Sequences from Library RPCI-23
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                                                     , mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). " 97 c 84 g 212 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-194A5"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism≔"Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
Percent Identity:
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                                                                       nRNA
sapiens
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100.000
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; Murinae; Mus
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REFERENCE
AUTHORS
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Quality:
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US-08-973-363-11 x BF338481
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LOCUS BG533957
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Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONNTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 817)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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plate: LLAM9496 row: i column: 12
High quality sequence stop: 304.
                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BG533957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602553058F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4662854 5',
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 791).
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                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally, Primer: Oligo dT.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 104 c 160 g 115 t
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/db_xref="taxon:9606"
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AUTHORS
TITLE
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KEYWORDS
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alignment_block:
US-08-973-363-11 x BG533957
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Ratio: 1.000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 817)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
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Plate: LLCM1464 row: c column: 15
                                                                                                                                                                                     High quality sequence stop: 565.
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                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
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//db_xref="taxon:9606"
//db_xref="taxon:9606"
//clone=lib="NAGE:4662854"
//clone_lib="NAGE:4662854"
//clone_lib="NHH_MGC_77"
//lab_host="pHIOB (TI phage-resistant)"
//lab_host="pHIOB (TI phage-resistant)"
//lab_host="pHIOB (TI phage-resistant)"
//sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAAGGCCGAGCAGCGCGCGCACATG-dT(30)BN-3' (where B = A, C, G or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
251 a .139 c 193 g 233 t 1 others
                                                                                                                               Location/Qualifiers
1. .817
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4739191"
/clone_lib="NIH_MGC_60"
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alignment_block:
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LOCUS BF161157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF161157 908 bp 601769402F1 NCI_CGAP_Lu29 Mus mu
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Plate: LLAM9197 row: d column: 02
High quality sequence stop: 620.
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 Colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                          /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
                                                                                                                                           Stem cell origin.
providing samples: Gilbert
                                                                                                           /lab_host="DH10B"
                                                                                                                                                                  /clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:3988561"
                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="CZECH II (feral)"
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Quality: 9.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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Clone distribution: MGC clone distribution information can
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(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched if
full-length clones and was constructed by Contech
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206 c
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/lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-08-973-363-11 x BG435095
seq_name: gb_gss:AG178168
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: BG537228
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                                                                                                                                                                                        32 GluAlaGluGluLysArgGluThrLys 40
                                                                                                                                      GAAGCAGAGAGAAGCGAGAGACAAAG 485
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Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1149) 11 (bases 1 to 1149) 11 (bases) 1 (bases)
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BG537228
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Plate: LLCM1506 row: b column:
High quality sequence stop: 255.
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Homo sapiens
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/clone_lib="NIH_MGC.77"
/clone_lib="NIH_MGC.77"
/lab_host="PHIDB (T1 phage-resistant)"
/lab_host="PHIDB (T1 phage-resistant)
/lab_host="PHIDB (T1 phage-resistant)"
/lab_host="PHIDB (T1 phage-resistant)
/lab_host="PHIDB (T1 phage-resistant)"
/lab_host="PHIDB (T1 phage-resistant)
/lab_host="PHIDB (T1 p
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/db_xref="taxon:9606"
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TITLE
JOURNAL
REFERENCE
AUTHORS
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AUTHORS
                                                                                                                           alignment_block:
US-08-973-363-11 x AG178168/rev
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VERSION.
KEYWORDS
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Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AG178168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                    Quality: 9.00
Ratio: 1.00
Percent Similarity: 100.000
                                                                                      Align seg 1/1 to reverse of: AG178168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsutumi ku, Yokhama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
AG178168
AG178168.1 GI:16707848
AG178168.1 GS:(genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-050A23.T7.
Pan troglodytes
BUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG178168 1310 bp DNA linear GSS 09
Pan troglodytes DNA, clone: RP43-050A23.T7, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY
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R.Site 2
                                                                                                                                                                                                                                                                                                                                               37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing: T7
                                                                                                                                                                                                                                                                                                                                     /sex="male"
/cell_type="lymphocytes"
/cll_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-050A23.T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : pBACe3.6
: EcoRI
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Gaps:
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Title:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                   Query
Score Match Length DB ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenEmbl:*
1: gb_htg
2: gb_htg
3: gb_in:*
4: gb_ow:*
5: gb_ow:*
5: gb_pt:*
7: gb_ph:*
9: gb_pt:*
9: gb_pt:*
10: gb_ro:
10: gb_ro:
10: gb_ro:
10: gb_ro:
11: gb_st:
12: gb_un
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Gapop 60.0 , Gapext 60.0
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265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1797656 seqs, 10463268293 residues
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGAGATTGTTTCAGTGAA.....AAGAAGTGAAGGAAGAAG 265
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em_htg_inv:*
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                               Description
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AUTHORS
TITLE
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A58693
LOCUS
DEFINITION
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FEATURES
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                                                                                                                              source
                                                                                                                          Patent: WO 9639505-A 12 12-DEC-1996;
ISIS INNOVATION (GB)
Other publication AU 5906996 961224.
Location/Qualifiers
1. .265
                                                                                                                                                                                                                                                                                                                                 unclassified.

1 (bases 1 to 265)
Griffiths,R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A58693 265 bp
Sequence 12 from Patent W09639505.
A58693
A58693.1 GI:3714251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unidentified.
unidentified
                                   158 a
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9.8 172705

9.8 237405

9.8 237405

9.1 101223

9.1 101223

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2 (bases
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A CHD1 gene is Z chromosome linked Gene 197 (1-2), 225-229 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus
                                                                                                                                                                                                                                                                                           Glasgow
                                                                                                                                                                                                                                                                                                        Submitted (16-MAY-1997) Zoology,
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Griffiths,R. and Korn,R.M.
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                                                                                                                                                                                                                                                                                             G12 8QQ, UK
                                              DDDEDYDKRGSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTEEDEFETIEKFMD
SRIGRKGATGASTTIYAVEADGDPNAGFEKSKELGEIQYLIKWKGWSHIHNTWETEET
                           DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKRQLDSSEEEE
                                                                                                                                        /function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain
/codon_start=1
                                                                                                                                                                                               /gene="CHD-Z"
228. .5654
                                        LKKQQQQQKAASSDSGSEEDSSSSEDSADDSSSETKKKKHKDEDWQMSGSGSVSGTGS
                                                                                                                          /product="chromo-helicase-DNA-binding on
                                                                                                                                                                                                                                    /organism="Gallus gallus"
/db_xref="taxon:9031"
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                                                                                                                                                                                 /gene="CHD-2"
                                                                                                                                                                                                                                                                             Location/Qualifiers
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Neognathae; Galliformes; Phasianidae;
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Pred. No. 1.3e-106;
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on the Z chromosome
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218; Conserv
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Barown,A., Camarata,J., Campopiano,A., Chang,J., Chaz
                                                                                                             Eukaryota; Metazoa; Chordata; Cri
Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 154919)
Birren,B., Linton,L., Nusbaum,C.
Mus musculus, clone RP24-312H21
                                                                                                                                                                                                                                                                          AC100733.1 GI:17048100
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                    unordered pieces.
AC100733
                                                                                                                                                                                                                                                                                                                                                         AC100733 154919 bp
Mus musculus clone RP24-312H21,
                                                                                     Unpublished
                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                   house mouse.
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LFKEPBGEEQEPQEMOIDEILKRAETFENETGPLTVGDELLSGFKVANFSNMDEDDIE
LEPERNSRWEELIPESQRRIEEEEERQKELEETYMLPRMRNCAKQISFNGSEGRESR
SRRYSGSDSDSITERKRPKKRGRPTIPRENIKGFSDAEIRRIKSYKKEFGGELERLD
AVARDAELVDKSETDLRRLGELVHNGCIKALKDNSSGQERAGGRLGKVKGPTFRISGV
QVNAKLVISHEEELAPLHKSIPSDPERKRYVIPCHTRAAHFDIDMGKEDDSHLLVGI
YEYGYGSWEMIKMDPDLSLTGLIEDEPKKFQAKQIQTRADYLIKLLNKDLARKEAQ
RLAGAGNSKRRTRNKKMKMASKIKELKENSSPQDESEKSDEDDEEDDKSDEIVSVK
HLHKKIKTEKENEEKPEDDIGIKEAEEKRETKEKENKRELKREKEKEKEKEKEKEKEK
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LHKELEPFLLRRVKKUVEKSLPAKVEQIIRMEKSALOKOYYKWILTRNYKALSKOSKG
STSGFLNIMMELKKCCNHCYLIKPDDINEFYNKQEALQHLIRSSGKLILLDKLLIRLR
ERGNRVLIFSQWYMLDILAEYLKYRQFFFQRLDGSIKGELRKQALDHFWAEGSEDFC
FLLSTRAGGLGINLASADTYVLFDSDWAPPONDLQARAHRIGQKKQVNIYRLVTKGS
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CKYLKOPFYYALKKOPSYIGGHESLELFDYOLMGLMVLAHGWCKGNSCILADEWGLG
KYLOTISFLNYLFHEHGLYGFPLLFUPLSTIFWOREEJOTMAPOMNAVYUGDITSKU
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KEYTNPEQIKQWRKNLWIFVSKFTEFDARKLHKLYKHAIKKRQESQQHNDQNISSNVN
THVIRNPDVERLKETTNHDDSSRDSYSSDRHLSQYHDHHKDRHQGDAYKKSDSRKRPY
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Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
MacCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J.,
Mcneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Morbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phinkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Retta, R., Roy, A., Santos, R., Schuer, S., Schupback, R.,
Koman, J., Rosetti, M., Roy, A., Santos, R., Schuer, S., Schupback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Straugs, N., Subramanian, A., Talamas, J., Tesfaye, S., Thodore, J.,
Topham, K., Travers, M., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-NOY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big-Dye; 100% of reads
Assembly program: Phrap; version 0,960731
Consensus quality: 14930 bases at least 040
Consensus quality: 151798 bases at least 030
Consensus quality: 152705 bases at least 020
Insert size: 151000; agarose-fp
Insert size: 151000; agarose-fp
Ouality coverage: 7.0 in 020 bases; sum-of-contigs
Ouality coverage: 6.8 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
               23835: contig of 23835 bp in length
23836 23935: gap of 100 bp
23936 25171: contig of 107 bp in length
25172 25271: gap of 100 bp
26349 26448: gap of 107 bp in length
26449 29041: gap of 100 bp
26449 2741: gap of 100 bp
26449 31763: contig of 2593 bp in length
26149 31763: contig of 2622 bp in length
26149 31763: contig of 2622 bp in length
26149 31763: contig of 2622 bp in length
26149 31763: contig of 100 bp
31561 31951: contig of 1188 bp in length
3164 31831: gap of 100 bp
31513 3512: contig of 2361 bp in length
35513 3512: gap of 100 bp
35513 3512: gap of 100 bp
35513 35612: gap of 100 bp
37677 37676: gap of 100 bp
37678 40817: gap of 100 bp
37678 40818 43884: contig of 3167 bp in length
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43985 44084: gap of

    Genome Center

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                              RESULT
AC068141
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                                                                                                                                                                                                                                                                                        9.8%; Score 26; DB 2; Length 154919; ilarity 100.0%; Pred. No. 0.14; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
29142, ;31763
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29885 c 29043 g 45353 t
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48276. .53706
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37677. .40717
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23936. .25171
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/clone_lib="RPCI-24 Male Mouse BAC"
1. .23835
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/db_xref="taxon:10090"
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   192079 bp
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be preserved.

1608 others

0; Gaps

0;

HTG 29-APR-2000

COMMENT

Web site:

JOURNAL

Direct Submission

0;

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-APR-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 192079)
Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W.
Bouffard,G.G., Dietrich,N.L., Eagle,W.O., Gupta,J., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus chromosome 5 clone RP23-326E9 strain C57BL6/J, WORKING DRAFT SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                               149814
                                                                                                                                               115184
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Insert size: 186000; pulse-field-gel
Insert size: 192079; sum-of-contigs
Quality coverage: 8.09x in 020 bases; pulse-field-gel
Quality coverage: 7.45x in Q20 bases; sum-of-contigs
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Center clone name: 326E09
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/organism="Mus musculus"
/strain="C57BL6/J"
                                                                    Location/Qualifiers
                                               .192079
                                                                                               192079:
                                                                                                                                                                                        gap of unknown length
81567: contig of 23058 bp in length
gap of unknown length
115183: contig of 33616 bp in length
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RESULT 5
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 121716 AAAAAATAAAAACAGAAAAAAGAAAA 121741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AAAAAATAAAAACAGAAAAAAAGAAAA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Dietrich, N.L., Eagle, W.O., Gupta, J., Ho.S.-L., Huang, M.C., Idol, J., Lee-Lin, S.-Q., Maduro, Q.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C., Morse, E., Ojodu, M.A., Pearson, R., Stantripop, S., Summers, T.J., Thomas, J.W., Thomas, P.J., Tiongson, E.E., Touchman, J.W., Tran, J.T., Vogt, J.L., Walker, M.A., Wetherby, K.D. and Green, E.D.
NISC Mouse Sequencing Initiative
Unpublished
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-APR-2000) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 237405)
Beckstrom-Sternberg, S.M., Benj
Bouffard, G.G., Dietrich, N.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus chi
DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC068142.1 GI:7670126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC068142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC068142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58560 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 237405)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.99319
Consensus quality: 230333 bases at least Q40
Consensus quality: 232224 bases at least Q30
Consensus quality: 232224 bases at least Q30
Consensus quality: 232239 bases at least Q20
Insert size: 212000; garose-fp
Insert size: 249000; pulse-field-gel
Insert size: 237405; sum-of-contigs
                                                                                                                                                                                                            Quality coverage: 7.28x in Q20 bases; agarose-fp Quality coverage: 6.20x in Q20 bases; pulse-field-ge Quality coverage: 6.50x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: yt
Center clone name: 053F18
Center clone name: 053F18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: plasmid; n/a; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: nisc_mouse@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- Project Information
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/clone_lib="RPCI mouse BAC library
a 36452 c 35882 g 61161 t 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237405 bp DNA linear HTG 29-APR-2000
le 5 clone RP23-53F18 strain C57BL6/J, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                       pulse-field-gel
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others
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Db 173891 AAAAAATAAAAACAGAAAAAAGAAAA 173866
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Sirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Salren, B., Linton, L., Bastlen, V., BoguslavKly, L., Boukhgalter, B., Anderson, S., Barna, M., Bastlen, V., BoguslavKly, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chang, J., Cook, A., Cook, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferrelra, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Goide, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagoo, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Merphy, T., Naylor, J., Negura, C., McCarthy, M., McBwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Minoya, Y., Murphy, T., Naylor, J., Naylor, J., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC101977 52433 bp DNA linear HTG 23-NOV-2001 Mus musculus clone RP24-333M7, LOW-PASS SEQUENCE SAMPLING. AC101977 AC101977.1 GI:17060753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 52433)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Birren,B., Linton,L., Nusbaum,C. and Lander,E. Mus musculus, clone RP24-333M7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
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/chromosome="5"
/clone="RP23-53F18"
/clone="RP23-53F18"
/clone=Lib="RPCI mouse BAC library 23"
/clone_Lib="RPCI mouse BAC library 23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 52433)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.8%;
llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4718: contig of 4718 bp in length
gap of unknown length
11420: contig of 6702 bp in length
gap of unknown length
128006: contig of 16586 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
gap of unknown length
275969: contig of 27758 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
110435: contig of 34466 bp in length
gap of unknown length
145778: contig of 35343 bp in length
gap of unknown length
180307: contig of 55343 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .237405
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 237405; 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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RESULT AC101977

LOCUS DEFINITION ACCESSION EYWORDS ERSION

BASE COUNT ORIGIN

Matches Query Match Best Local : FEATURES

source

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS

SOURCE ORGANISM

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* NOTE: This record contains 67 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

the record is updated, the accession number will

* however.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-NOY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ffp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigliio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved.
13146 13245: gap of 100 bp 1346 13245: gap of 100 bp 13931: contig of 686 bp in length 13932 14031: gap of 100 bp 14704 14803: gap of 100 bp 14804 15467: contig of 667 bp in length 15468 15567: gap of 100 bp 15568 16269: contig of 702 bp in length 16370 16369: gap of 100 bp 16270 16369: gap of 100 bp 16270 16369: gap of 100 bp in length 16370 16369: contig of 702 bp in length 16370 17042: contig of 673 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.9 37.4: contig of 706 bp
3775 3874: gap of 100 bp
3875 4524: contig of 650 bp
4525 4624: gap of 100 bp
4525 4624: gap of 100 bp
4525 4624: gap of 5301: contig of 677 hp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The event of 754 contig of 754 bp in length 1855 1486; contig of 632 bp in length 187 1586; gap of 100 bp 1687 1687; contig of 637 bp in length 1687 1686; contig of 577 bp in length 2164 2263; gap of 100 bp 2264 2968; contig of 705 bp in length 1969 3068; gap of 100 hp 175 38774; contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
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10795 10894: gap of 100 bp
10895 11583: contig of 689 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6865 6964: yur
7634:
                                                                                                                                                                                                                                                                                                      11584 11683: gap of 100 bp
11684 12362: contig of 679 bp in length
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8538 9
                                                                                                                                                                                                                                                                                    12363 12462:
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101: gap of 100 bp

6084: contig of 683 bp

14: gap of 100 bp

6864: contig of 680 bp

1: gap of 100 bp

1: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                       77; gap of 100 bp 10 length 236; contig of 699 bp in length 36; gap of 100 bp 10 length 994; contig of 658 bp in length 904; gap of 100 bp 10 length 10794; contig of 700 bp in length
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13145: contig of 683
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6437: contig of 703 bp

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35923 36022; gap or 100 bp in legacian service of 688 bp in legacian service of 684 bp in legacian service of 689 bp in legacian service of 688 bp in legacian service of 687 bp in legacian service of 689 bp in legacian service service of 689 bp in legacian service service of 689 bp in legacian service servi
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26000: contig of 700 bp in length
2601
26700: gap of 100 bp
26701
27379: contig of 679 bp in length
27380
27479: gap of 100 bp
27480
28151: contig of 672 bp in length
28152
28251: gap of 100 bp
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28840: contig of 589 bp in length
28841
28940: gap of 100 bp
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28940: gap of 589 bp in length
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28940: gap of 589 bp in length
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32746: contig of 695 bp in le
32847
32846: gap of
32847
33549: contig of 703 bp in le
33550
33649: gap of
34355: contig of 706 bp in le
34550
34455: gap of
100 bp in le
34356
34456: gap of
100 bp in le
34456
35169: contig of 714 bp in le
35170
35269: gap of
100 bp
35270
35922: contig of 635 bp in le
36703
36707: contig of 685 bp in le
43078 43760: contig of 683 by
43761 43861: gap of 100 bp
43861 44557: contig of 697 by
44558 44657: gap of 100 bp
4458 45283: contig of 626 by
45284 45383: gap of 100 bp
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24212: contig of 714 bp in length
24312: gap of 100 bp
24975: contig of 663 bp in length
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25000: contig of 725 bp in length
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                                                                                                                                                                                                                                                                             Quality: Phrap Quality >=40 100% of Sequence; Estimated Total Number of Errors is 0.
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Submitted (07-DEC-2001) DOE Joint Genome Institute, 2800 M
Drive, Walnut Creek, CA 94598, USA
On Dec 7, 2001 this sequence version replaced gi:15290448.
Draft Sequence Produced by DOE Joint Genome Institute
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                                                                                                                                                                            E: This insert is not the entire sequence of the clone (entiuence is 146.7kb). It is clipped at the overlap with AC012624 number of bases overlapped is 90404.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 AAAAGAAAAAGAGATAAGAAAGA 180
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Submitted (31-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 13435)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 134365)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 21, 2001 this sequence version replaced gi:14277267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 134365)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOE Joint Genome Institute.
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AC012624.6 GI:14993679
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                                                                                                                                                                                                       ACO21449 143079 bp DNA linear HTG 10-SEP-2000 Homo sapiens clone RP11-58M12, WORKING DRAFT SEQUENCE, 10 unordered
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Homo sapiens
                                                                  AC021449
AC021449.3 GI:10047806
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.1%; Score 24; DB 9; Length 134365; Similarity 100.0%; Pred. No. 1.1; 104els 024; Conservative 0; Mismatches 0; Indels 024; Conservative 0; Mismatches 0; Mismatches 0; Indels 024; Conservative 0; Mismatches 0; Mismatches 0; Mismatches 04; Conservative 05; Mismatches 05; Mismatches 04; Mismatches 05; Mismatches 04; Mismatches 05; Mismatches 04; Mismatches 05;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40414 a
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Conservative 0; Mismatches
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2082I17"
/clone="CTD-2082I17"
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1. .134365
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Bouldanter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collynore, A., Cooke, P., Dearle, N., Demain, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Handers, T., Lehczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macqonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Macqonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McCheeterson, R., Morrow, J., Naylor, J., Norman, C., H., O'Connor, T., O'Donnell, P., Olivar, T., M., Peterson, K., Pierre, N., Fisani, C., Pollara, V., Raymond, C., Kiley, R., Rothman, D., Fisani, C., Sovery, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Paddy, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Timera, A., and Tody, M., and A., a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1 (bases 1 to 143079)
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38820: contig of 38920 bp in length
38821 38920: gap of 1491 bp in length
40411 40511: gap of 100 bp
43280 443279: contig of 2768 bp in length
43280 443279: contig of 2768 bp in length
43280 44505: contig of 3536 bp in length
46906 47005: gap of 100 bp
47006 51830: contig of 4825 bp in length
51831 51930: gap of 100 bp
51931 62619: contig of 10689 bp in length
62620 62719: gap of 100 bp
62720 75408: contig of 12689 bp in length
62620 62719: gap of 100 bp
62730 75408: gap of 100 bp
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Insert size: 142779; sum-of-contigs
Quality coverage: 4.6 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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Center clone name: 58_M_12
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ACCESSION
VERSION
KEYWORDS
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AC008531
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                                         Direct Submission Squencing Facility, DOE Joint Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US. On Feb 14, 2001 this sequence version replaced gi:7528342.
                                                                                                                                                     Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Primates; (1 (Dases 1 to 145659)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome
                                                                                                          2 (bases 1 to 145659)
DOE Joint Genome Institute.
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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92517 92616: gap of
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Code: JGI
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43380. .46905
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clone_end:SP6
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106510. .143079
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75509. .92516
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62720. .75408
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/db_xref="taxon:9606"
/clone="RP11-58M12"
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92617. .106409
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Consensus quality: 142556 bases at least Q30
Consensus quality: 143744 bases at least Q20
Estimated insert size: 148000; pulse field gel estimation
Estimated insert size: 148000; pulse field gel estimation
Quality coverage: 6.27 in Q20 bases; pulse field gel estimation
Quality coverage: 6.4 in Q20 bases; pulse field gel estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession as the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submittor of the property of the submitter                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * the accession number will be preserved.

* 1 56174 contig of 56174 bp in length

* 56175 56274 gap of unknown length

* 100875 100874 contig of 44600 bp in length

* 100875 100974 gap of unknown length

* 113128 113127: contig of 12153 bp in length

* 113128 113127: gap of unknown length

* 113128 113129: gap of unknown length

* 118191 118290: contig of 4963 bp in length

* 118191 118290: gap of unknown length

* 118291 119694: contig of 1404 bp in length

* 119795 113794: gap of unknown length

* 119795 123397: contig of 3503 bp in length

* 123398 123397: gap of unknown length

* 123398 123397: gap of unknown length
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Trypanosoma
IN PROGRESS
1 (bases 1 to 145830)
1 (bases 1 to 145830)
1 (bases 1 to 145830)
1 (chases 1 to 145830)
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Center clone name: CIT-HSPC_480B11
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTC-480B11"
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Direct Submission

Direct Submission

Direct Submission

Submitted (11-APR-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasskieabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:gl-298-38-7469)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is seven and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced to be replaced with the replaced by the submitter will be preserved.
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Mon Cot 4, 2001 this sequence version replaced gi:15789236.
NOTE: This is a 'working draft' sequence. It currently
consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
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Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Only in DataBase (2001) In press 2 (bases 1 to 154157) Sasaki, T., Matsumoto, T. and Yamamoto, K.
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, M., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Locke, K., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., McMendald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McMetters, R., Meldrim, J., Meneus, L., Morrow, J., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Ráymond, C., Riley, R., Rothman, D., Ford, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfâye, S., Theodore, J., Timper, A., and John M., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A., and John M., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A., and John M., Stojanovic, N., Stojanovic, N., Stojanovic, N., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A., and John M., Stojanovic, N., Stojanovic, N., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A., and John M., Stojanovic, N., St
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 157625)
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/db_xref="taxon:4530"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa"
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repeat_region 53635669 AT_rich" repeat_region /rpt_family="Aluy" repeat_region /rpt_family="MER83-internal" repeat_region /rpt_family="MER83-internal" repeat_region /rpt_family="Alusp" repeat_region 62646564 /rpt_family="Alusq" repeat_region 65656598 /rpt_family="AT_rich" repeat_region 65996777	All repeats were identified using RepeatMasker: Smit, A. F. A. Goren, P. (1996-1997) http://frb.genome.washIngton.edu/RW/RepeatMasker.html	TITLE Direct Submission JOURNAL Submitted (21-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA COMMENT On Jan 20, 2000 this sequence version replaced 91:6532078.
repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region	patregion patregion	repeat_region
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Db 28698 AAAAATAAAAACAGAAAAAAAAAAA 28721
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                                                                                                                                                                                                                                                                                                                    Consensus quality: 157767 bases at least 040
Consensus quality: 180759 bases at least 020
Consensus quality: 184175 bases at least 020
Consensus quality: 184175 bases at least 020
Consensus quality: 184275 bases at least 020
Estimated insert size: 204590; agarose-fp estimation
Estimated insert size: 190246; sum-of-contigs estimation
Quality coverage: 5.79 in 020 bases; sum-of-contigs estimation
Quality coverage: 5.79 in 020 bases; sum-of-contigs estimation.
**NOTE: This is a 'working draft' sequence. It currently
**consists of 31 contigs. The true order of the pieces
**is not known and their order in this sequence record is
**arbitrary Gaps between the contigs are represented as
**runs of N, but the exact sizes of the gaps are unknown.
**This record will be updated with the finished sequence
**as soon as it is available and the accession number will
**be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Project Information
Center Project Name: 544799
Center clone name: RPCI-11_36012
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-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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1 (bases 1 to 193446)

DOE Joint Genome Institute.

Sequencing of Human Chromosome 5
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Submitted (09-JUN-2001) Production Sequencing Facility, DOE Joint
Submitted Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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DOE Joint Genome Institute.
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/rpt_family="L1M1"
25955. .26103
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1458: gap of unknown length
2667: contig of 1209 bp in length
2767: gap of unknown length
3823: contig of 1056 bp in length
3923: gap of unknown length
5920: contig of 1997 bp in length
6020: gap of unknown length
6020: gap of unknown length
7494: contig of 1474 bp in length
7594: gap of unknown length
9096: contig of 1502 bp in length
9096: contig of 1064 bp in length
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, *** SEQUENCING IN
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/35252 c 37061 g 60360 t 3202 others
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/db_xref="taxon:9606"
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1. .193446
                                                                                                                                                                              100.0%; F
tive 0;
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Si contig of 4978 bp in length

Si gap of unknown length

Contig of 5982 bp in length

Contig of 5915 bp in length

Contig of 5916 bp in length

Contig of 6151 bp in length

Contig of 6563 bp in length

Contig of 7616 bp in length

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JOURNAL REFERENCE AUTHORS REFERENCE AUTHORS TITLE

COMMENT

JOURNAL

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ORGANISM

VERSION ACCESSION RESULT 14 AC091946

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DEFINITION

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Submitted (30-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Aug 30, 2001 this sequence version replaced gi:15148108.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
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4 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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WI-5811 G04974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finishing Completed at Stanford Human Genome Center www-shyc.stanford.edu Quality: Phrap Quality >=40 99.8% of Sequence; Estimated Total Number of Errors is 0.4.
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DOE Joint Genome Institute.
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 219258)
DOE Joint Genome Institute and Stanford Human Genome Center.
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/chromsome="5"
/clone="CTD-2007H13"
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Copyright (c) 1993 - 2000 Compugen Ltd
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479.060 Million cell updates/sec
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Human nervous syst
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Rifin 3198 gene.
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ALIGNMENTS

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ID AAT42752 standard; cDNA; 265 BP.

XX
AC AAT42752;

XX
AC AAT42752;

XX
DT 12-MAR-1997 (first entry)

XX
Chicken CHD-1A insert motif.

XX
Bird; sex determination; chromodomain-Helicase-DNA binding 1 Avian;

XX
CHD-W; chromodomain-Helicase-DNA binding on the W chromosome; ss.

XX
OS Gallus sp.

XX
YX
FH Key Location/Qualifiers
FT misc_difference 52
FT misc_difference 52
FT base 52 disrupts the reading frame for the translated amino acid sequence given in Fig 7"

XX
PN W09639505-A1.

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PD 12-DEC-1996.

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PF 05-JUN-1996; 96WO-GB01341.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                   Gallus
                                                                                                                                       CHD-W;
                                                                                                                                                                                           12-MAR-1997
                                                                                                                                                                                                                                   AAT42753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                              AAT42753;
 12-DEC-1996
                      WO9639505-A1.
                                                                                    misc_difference
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                                                                                                                                      chromodomain-Helicase-DNA binding on
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                                                                                                                                                                                                                                   standard;
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                                                                                                                                                 determination; chromodomain-Helicase-DNA binding
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                                                                                  Location/Qualifiers 52
                                                              /note=
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                                          "base 52 disrupts the
the translated amino
in Fig 7"
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Pred. No. 1.6e-101;
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31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000;

2000US-0184664. 2000US-0186350.

2000US-0180628

17-JAN-2001; 16-AUG-2001. WO200159063-A2

2001WO-US01334.

18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000;

2000US-0189874. 2000US-0190076. 2000US-0198123. 2000US-0205515. 2000US-0209467. 2000US-0214886.

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Best Local S
Matches 33
                                                                                                                                                                                                              Human; nootropic; neuroprotective; cytostatic; dermatological; viriamunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulni antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHD-W clone CC14 (see also AAT42754). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found as an insert in some CHD-1A clones (see also AAT42752).
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birds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
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                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                      neurological
                                                                                                                                                                                                                                                                                           Human nervous
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33; Conser
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                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                      disease;
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                                                                                                                                                                                                      infection; nephrotropic;
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                                                                                                                                                                                                     therapy;
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20-CCT 2000

20-CCT 2000

20-CCT 2000

20-CCT 2000

01-NOV 2000

08-NOV 2000

17-NOV he invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (antipagonists are useful in the diagnosis, treatment and prevention of; (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone
                                                                                                                                                                                       Nucleic acids encoding 3224 human useful for preventing, diagnosing cancers and metastases -
                                                                                                                                                      Disclosure;
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                                                                                                                                                  SEQ ID NO 13769; 1701pp + Sequence Listing; English.
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2000US-0241808

2000US-0241826

2000US-0246476

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2000US-0246477

2000US-0246523

2000US-0246526

2000US-0246526

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2000US-0249216

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2000US-02511869

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2000US-0215135 2000US-0211680 2000US-02117487 2000US-022963 2000US-0229513 2000US-0225266 2000US-0225266 2000US-0225277 2000US-0225277 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-0225344 2000US-0225344 2000US-0225344 2000US-0233431 2000US-0233431 2000US-0233431 2000US-0233431 2000US-0233431 2000US-0233484 2000US-0233497 2000US-0234274 2000US-0234274 2000US-0234274 2000US-0233636 2000US-0233636 2000US-0233636 2000US-0235834 2000US-0235834 2000US-0235834 2000US-0235836 2000US-0235834 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0237039 2000US-0235836 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237036 2000US-0237036 2000US-0237036 2000US-0237039 2000US-0237036 2000US-0237036 2000US-0237036 2000US-0237036 2000US-0236967 2000US-023696

14-AUG-2000
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RESULT
AAZ29250
ID AAZ2
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XX Rifj
KW Stag
KW Manman
KW MANMAN
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                        selected ORF from chromosome 2 using genomic DNA to the mammalian expression purified amplified products were cloned into the mammalian expression plasmid VR1050 to produce DNA vaccines for immunisation. Blood and sera obtained from groups of mice immunised with doses of vaccine was used to identify stage specific expression of Rifin protein by immunofluorescent antibody testing. The method is useful for determination of subcellular localisation of proteins and for the development of antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epliepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rifin 3192 gene; P.falciparum chromosome 2; Rifin protein; mammalian expression plasmid VR1050; DNA vaccine; immunisation; stage specific protein expression; antimicrobial vaccine; antimicrobial drug; IAF; immunofluorescent antibody testing; ds
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                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Page 16; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1998;
23-APR-1999;
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                                                                                                                                                                                                                                The present sequence is the Rifin 3192 gene of chromosome 2. Rifin were used to characterise the protein expression from various life stages of P.falciparum. Oligonocleotide primers were used to amplisely selected ORF from chromosome 2 using genomic DNA as template. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hoffman
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                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       of microbial, animal and/or human genomic data for identification vaccine, drug or diagnostic products -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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99US-0082947
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tronic format directly
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                                                                                                                                                                                                                                                                                            various life
                                                                                                                                                                                                                                                        2. Rifin genes ious life cycle to amplify each
                                                                                                                                                                                                                                                                                                                    2. Rifin
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                                                                                              The present sequence is the Rifin 3194 gene of chromosome 2. Rifin genes were used to characterise the protein expression from various life cycle stages of p.falciparum. Oligonucleotide primers were used to amplify each selected ORF from chromosome 2 using genomic DNA as template. The purified amplified products were cloned into the mammalian expression plasmid VR1050 to produce DNA vaccines for immunisation. Blood and sera obtained from groups of mice immunised with doses of vaccine was used to identify stage specific expression of Rifin protein by immunofluorescent antibody testing. The method is useful for determination of subcellular localisation of proteins and for the development of antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rifin 3194 gene; P.falciparum chromosome 2; Rifin protein; mammalian expression plasmid VR1050; Accine; immunisation; stage specific protein expression; antimicrobial vaccine; antimicrobial drug; IAF; immunofluorescent antibody testing; ds
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23-APR-1999;
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                                   Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rifin 3198 gene; P.falciparum chromosome 2; Rifin protein; mammalian expression plasmid VR1050; DNA vaccine; immunisation; stage specific protein expression; antinicrobial vaccine; antimicrobial drug; IAF; immunofluorescent antibody testing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of microbial, animal and/or human genomic data for identification of vaccine, drug or diagnostic products \, -
Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine. antimalaria; malaria; protozoacide; infection; insecticide; ds.
                                               Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:419
                                                                                07-NOV-2000
                                                                                                                 AAA70286;
                                                                                                                                                                                                                                                                                                                                                             Sequence 978 BP; 357 A; 152 C; 208 G; 261 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 16; Page 17; 23pp; English.
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                                                                                                                                            AAA70286 standard; DNA; 984 BP
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                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                    Similarity
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                                                                              (first entry)
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99US-0082947.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes proteins and their fragments (I) encoded C by chromosome 2 of the human malarial parasite, plasmodium falciparum. CC Also described are: (I) nucleotide sequences (II) encoding (I); and (2) CC vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against P. falciparum infection comprising the sequences of (I), are cc useful in the detection of infection with P. falciparum Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC P. falciparum. Sequencing of the Plasmodium chromosome 2 and the cum derivation of proteins encoded by the complexity of the parasite biology, a process hampered by the CC complexity of the parasite biology, and provide new targets for complexity of the parasite resistance to drugs and mosquito CC resistance to insecticides have led to a resuturence of malaria in many CC parts of the world, and there is a pressing need for vaccines and new CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide cand protein sequences given in the present invention, but which are not vaccines and content of the world, and there is a present invention, but which are not vaccines and content of the world, and there is a present invention, but which are not vaccines and content of the world within the specification.
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                  Plasmodium falciparum; chromosome 2; human malaria parasite; antimalarial; malaria; protozoacide; infection; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum, useful as an diagnosis of P.falciparum infection
                                                                              Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:417
                                                                                                                         07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 575; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-365347/31.
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                                                                                                                                                                 AAA70284;
                                                                                                                                                                                                     AAA70284 standard; DNA; 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 984 BP; 360 A; 145 C; 183 G; 296 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoffman S, Carucci D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200025728-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (VENT/) VENTER J C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
                                                                                                                                                                                                                                                                                                        931 agaaaaaagaaaatgaagaaaa 952
                                                                                                                                                                                                                                                                                                                         45 AGAAAAAAGAAAATGAAGAAAA 66
                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 100. les 22; Conservative
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                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                           8.3%; 500
100.0%; Pro
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 22; DB 21; Length 984; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    0;
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Plasmodium falciparum

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RESULT
AAA7029
ID AAA7
XX AAA7
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                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes proteins and their fragments (I) encoded CC by chromosome 2 of the human malarial parasite, Plasmodium falciparum. CC Also described are: (1) nucleotide sequences (II) encoding (I); and (2) CC vaccines against P. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against CC P. falciparum infection. (I) and polyclonal antisera or a monoclonal CC antibody raised to immunogens comprising the sequences of (I), are CC useful in the detection of infection with P. falciparum. Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent P. falciparum CC infection, or they can be used to identify drug resistance in CC p. falciparum. Sequencing of the Plasmodium chromosome 2 and the CC subsequent identification of proteins encoded by it will help to expand CC complexity of the parasite biology, a process hampered by the CC complexity of the parasite lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito CC resistance to insecticides have led to a resurgence of malaria in many CC parts of the world, and there is a pressing need for vaccines and new CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not constituted to the constitution of the parasity of the world and the present invention, but which are not constituted to the present invention, but which are not constituted to the constitution of the present invention, but which are not constituted to the present invention.
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Best Local :
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins encoded by chromosome 2 of the human plasmodium falciparum, useful as antimalarial diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-365347/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1998;
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Plasmodium falciparum
                                     antimalarial; malaria;
                                                                                                                                   07-NOV-2000
                                                                                                                                                                                                              AAA70279 standard; DNA; 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1038 BP; 379 A; 157 C; 209 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specifically mentioned within the specification.
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                                                     Plasmodium falciparum;
                                                                                            Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:412
                                                                                                                                                                          AAA70279;
                                                                                                                                                                                                                                                                                                          985
                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                           45 AGAAAAAAGAAAATGAAGAAAA 66
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                                                                                                                                                                                                                                                                                                        agaaaaaagaaaatgaagaaaa 1006
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22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 574-575;
                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                  8.3%;
                                     chromosome 2; human malaria parasite;
protozoacide; infection; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             577pp;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 T;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
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L vaccines
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and in the
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                                                        vaccine;
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Matches :
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(CARU/)
(GARD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines diagnosis of P.falciparum infection -
                                         pharmaceutical;
                                                                                    Drosophila
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Also described are: (1) nucleotide sequences (II) encoding (I); and (2) vaccines against P. falciparum infection comprising (I) or (II).
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                                                     Drosophila;
                                                                                                                 26-MAR-2002
                                                                                                                                               ABL18816;
                                                                                                                                                                          ABL18816 standard; DNA; 29783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VENT/)
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CARUCCI D.
GARDNER M.
                                                                                                                                                                                                                                                                                                           . Similarity
22; Conser
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                                                                                                                                                                                                                                                                                                                                                                                    1047
                                                                                   melanogaster genomic polynucleotide SEQ ID NO 7921
                                       developmental biology; cell signalling; insecticide;
cal; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carucci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 573;
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0107131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the human malarial parasite,
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                                                                                                                                                                                                                                                                                                                        8.3%;
                                                                                                                                                                                                                                                                                                                                                                                    A; 163 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            describes proteins and their fragments (I) encoded
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                                                                                                                                                                                                                                                                                                                         Score 22; pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                    290 T;
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                                                                                                                                                                                                                                                                                                                                                                                     other;
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Drosophila melanogaster

WO200171042-A2

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RESULT 11
AAA18181
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AC AA1818
AC AA1818
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG10511), expressed DNA sequences (ABLIG10511), expressed DNA sequences (ABLIG105131), and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 7921; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                  Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tlssue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI81813 standard; cDNA; 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                   28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                  07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 1873.
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                             (HYSE-) HYSEQ INC
                                                                                                                                                                      26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                          WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Pred. No.
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Best Local Similarity 100.0%; I
Matches 21; Conservative 0;
                                                                                                                                                                                                     04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-UUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0532366.

21-SEB-2000; 2000US-0234687.

27-SEB-2000; 2000US-023659.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immundisorders -
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genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 471 BP; 121 A; 123 C; 126 G; 97 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probe #13075 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAI44389 standard; DNA; 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not specification, but was obtained in electronic fo
                              WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
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DB; AAO01882.
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Best Local Similarity
                                               The present sequence is the Rifin 3201 gene of chromosome 2. Rifin genes were used to characterise the protein expression from various life cycle stages of p.falciparum. Oligonucleotide primers were used to amplify each selected ORF from chromosome 2 using genomic DNA as template. The purified amplified products were cloned into the mammalian expression plasmid VR1050 to produce DNA vaccines for immunisation. Blood and sera obtained from groups of mice immunised with doses of vaccine was used to identify stage specific expression of Rifin protein by immunofluorescent antibody testing. The method is useful for determination of subcellular localisation of proteins and for the development of antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 17; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                   of vaccine,
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23-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USNA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            of microbial, animal and/or human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF NAVY
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99US-0082947.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   or diagnostic products
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immunisation;
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Query Match Best Local S Matches 21

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Best Local
                                                                          inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagno and treatment of colorectal carcinomas and cancers. AAH37196 to AAH372 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                         expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing
                                                                                                                                                                                              cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P
                        present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                  AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                      useful
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03-NOV-1999;
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 Sequence
                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                    Nucleic
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DB; AAG73720.
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arcinoma; chromosome 16; ss.
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99US-0163280.
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RESULT 15
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                                                                                                                     The present invention describes proteins and their fragments (I) encoded CC by chromosome 2 of the human malarial parasite, plasmodium falciparum. CC Also described are: (I) nucleotide sequences (II) encoding (I); and (2) CC vaccines against p. falciparum infection comprising (I) or (II). CC (I) and (II) are useful for the development of vaccines against p. falciparum infection. (I) and polyclonal antisers or a monoclonal CC antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with p. falciparum. Furthermore, CC (I) (especially when they are rifins or secreted or membrane proteins) CC can aid the identification of drugs to treat or prevent p. falciparum CC infection, or they can be used to identify drug resistance in CC subsequent identification of proteins encoded by the will help to expand CC our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito CC resistance to insecticides have led to a resurgence of malaria in many CC parts of the world, and there is a pressing need for vaccines and new CC drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide CC and protein sequences given in the present invention, but which are not xx
  Ouery Match 7.9%; Score 21; DB 21; Length 1005; Best Local Similarity 100.0%; Pred. No. 11; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOFF/) HOFFMAN S.
(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum; chromosome 2; human malaria parasite; vaccine; antimalarial; malaria; protozoacide; infection; insecticide; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 448-449; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1999;
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                                                                                             Sequence 1005 BP; 381 A; 145 C; 196 G;
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A748563 oa57c9.s. A7148563 oa57c9.s. A7213624 Sheared D A7221363 gh81602.x AA699918 z161f12.s. A664293 RPC133 -pp A0500417 v40B12 mr A0952151 Sheared D AZ508184 1M0350618 BM015597 603641826 BF239967 601905170 A1039357 A1053257 A1039357 A1653205 A1653305 B1640191 SD23001.5 B1640191 SD23001.5 B1640191 SD23001.5	Description AZ184391 SP_1002_B	score of the result being printed, otal score distribution.	by chance to have a					27472414				.AAGAAGTGAAGGAAGAGAAG 265	earch time 7016.61 Seconds (without alignments) 509.747 million cell updates/sec		en Ltd.
FEATURES SOUICE	JOURNAL MEDLINE COMMENT	AUTHORS TITLE	KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 AZ184391 LOCUS DEFINITION ACCESSION		45		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		C 36		c 29 31 32	C 25 25 28	c 22 23 24	c 18 c 19 20
Californii Pasadena Tel: (626 Fax: (626 Email: ac Plate: 10 Seq prime Class: BA	additional resources Proc. Natl. Acad. Sc 20402566 Contact: Cameron, RA	Cameron,R. Swartzell, ,G.A., Ett Hood,L. A sea urch	GSS. Strongyloce Strongyloce Strongyloce Eukaryota; Echinoidea, Strongyloce 1 (bases:	AZ184391 SP_1002_B2 , sperm ge clone plat AZ184391			¹ .7.7.						22 8.3 22 8.3 8.3		
mia Institute of Tech a California 91125, U 326) 395-841 326) 793-3047 a cameronecatech.edu 1002 row: N column: mer: T BAC ends ality sequence stop: Location/Qualifiers 1. 882 /organism="Strongyl /db_xref="taxon:766 /clone="plate=1002 /clone=11b="Strongyl	l resources l. Acad. Sci Cameron, RA,	A., Mahai S., Walla Sensohn,C.	sentrotus pur sentrotus pur Metazoa; Ec (; Euechinoid sentrotidae; 1 to 882)	2_G05_T7A			254 9 273 12						518 12 520 10 554 10 560 10		826 12 867 12 920 12
91125, USA 91125, USA 1125, USA 125, USA 126, USA 127, USA 128, US	•	Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R. Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wrz,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. Hood,L. A sea urchin genome project: Sequence scan, virtual map, and	GSS. Strongylocentrotus purpuratus. Strongylocentrotus purpuratus. Strongylocentrotus purpuratus. Strongylocentrotus punguratus Ebukaryota; Metazoa; Echinodermata; Eleutherozoa; Ebhinoidea; Euchinoidea; Echinoder; Echinoida; Strongylocentrotidae; Strongylocentrotus. 1 (bases 1 to 882)	oppo	ALTGNMENTS	AA305433		AW368791		2 CNS045OL	AU067771 2 CNS01SN3			⊳	2 AQ912123 2 AZ668023 2 AZ674814 2 AG059567
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Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bbac_ends/mouse/bac_end_intro.html
plate: 27 row: F column: 16
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Unpublished (1999)
Other_GSSs: RPCI-23-27F16.TJ
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,B., Levins,M., Mcgann,S., Tsegaye
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Mammalia; Eutheria;
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301 838 0208
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                                                                                           /lab_host="PH10B"
//lab_host="PH10B"
//lab_host="PH10B"
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
a 130 c 94 g 140 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="RPCI-23-27F16"
                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                /sex="Female"
                                                                                                                                                                                                                                                                                               /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                   . 590
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9.8%;
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Rodentia;
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Tsegaye, G., Geer, K.,
  . No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 t
DB 12;
9.2;
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                      590;
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REFERENCE
AUTHORS
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AA748563/c
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52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
CDNA Library Preparation: M. Bento Soares, Ph.D.,
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AA748563
AA748563
AA7609.S1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1309072 3' similar to SW:CHDD_MOUSE P40201 CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN CHD-1. [1] ;contains element L1 repetitive element ;, mRNA
                                                                          . Similarity
24; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1312 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 282.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA748563.1 GI:2788521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40ml3 fwd. ET from Amersham
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                                                                        9.1%; Score 24; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                    j. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

1 69 c 35 g 177 t
                                                                                                                                                                                                                                                                                               /clone="IMAGE:1309072"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   David Allman,
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RESULT 4
AZ213624/c
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KEYWORDS
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AI242163/c
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                                                                                                                                                                                                                                                                                                                                                      172 TAAGAAAGAATTAAAAGAAAAAGA 195
                                                                                                                                                                                                                                                                                                                         308 TAAGAAAGAATTAAAAGAAAAAGA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: nelsayed@tigr.org Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through Research Genetics, Alabama, USA. Sheared DNA end sequences search page: http://www.tigr.org/tdb/mdb/tbdb/.seq.primer: M13-Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Najib M. El-Sayed
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ213624 375 bp DNA linear GSS 09-JUN-2000 Sheared DNA-113F9.TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-113F9, DNA sequence.
                                                                                              A1242163 430 bp mRNA linear EST 01-DEC-1998 qh816102 x1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:1851099 3' similar to contains element LTR5 repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., MelVille, S., Donelson, J., Fraser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat
AI242163
AI242163.1 GI:3837560
                                                              element ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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301 838 0208
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//db_xref="txxxx; 59"
//clone="Sheared_DNA-11389"
//clone="Sheared_DNA-11389"
//clone="lib="Sheared_DNA"
//c
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/strain="TREU927/4 GUTat 10.1"
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100.0%; Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AAAAGAAAAAGAGGATAAGAAAGA 28
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 456)

RS Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project

Unpublished (1997)

Contact: Wilson RK
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA699918 456 bp mRNA linear EST 19-DEC: zi61f12.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:435311 3 , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1274 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
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/clone="IMAGE:1851099"
/clone_lib="Soares_fetal_liver_spleen_lNFLS_S1"
/sex="male"
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library for gene discovery and sequence-ready map construction unpublished (1999)
Other_GSSs: RPC193-DpnII-28K15.TJ
Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                             El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
Fraser,C. and Adams,M.
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AQ642393
RPCI93-DpnII-28K15.TV RPCI93-DpnII Trypanosoma brucei genomic clone RPCI93-DpnII-28K15, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emmail: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq_primer: -40ml3 fwd. ET from Amersham
                                                                             Email: nelsayed@tigr.org
Clones and high density filters may be purchased from BACPAC
Resources (http://bacpac.med.buffalo.edu. BAC end sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei
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Location/Qualifiers
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                      Class: BAC ends.
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                                     e: http://www.tigr.org/tdb/mdb/tbdb/.
primer: T?
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/note-*Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Sit-1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. 1st strand cDNA was primed
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95 c 57 g 185 t
Location/Qualifiers
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/clone="IMAGE:435311"
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/db_xref="GDB:1335080"
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Matches 24
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                                                                                                                                                                                                                                                                                                                                                                                              P.O. Box 208103, New Haven, CT 06520-8103, USA
Tel: 203 432 9949
Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kumar A
Michael Snyder, Dept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Cheung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Saccharomyces cerevisiae
Eukaryota; fungi; Ascomyo
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V40B12 mTn-3xHA/lacZ Insertion Library Saccharomyces
genomic 5', DNA sequence.
AQ500417
                                                                                                                                                                                                                                                                                                                                               Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yale University
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                                                                                                                                                                                                                                                                                                 primer: GGCCTTCTTTCTTTGGAAGTAC
ss: transposon-tagged.
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/strain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Ibb="RPCL93-DpNII"
/clone=lib="RPCL93-DpNII"
/clone=lib="RPCL93-DpNII"
/clone=lib="RPCL93-DpNII"
/constructed for The Institute for Genomic Research by
Bohui Zhao in Pieter de Jong's laboratory (Roswell Park
Cancer Institute, Buffalo, NY). Briefly, Trypanosoma
brucei TREU927/4 GUTat 10.1 agarose embedded DNA was
partially digested with a combination of Eco RI and Eco RI
methylase (RPCL93-EcoRI segment) or Dpn II (RPCL93-DpNII
segment). High molecular weight fragments were ligated in
pBACe3.6 vector digested with Eco RI or Bam H1,
respectively, The average insert size is 141 Kb. Total
non-minichromosomal genome."
153 t lothers
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                  /lab_host="E. coli"
/lab_host="E. coli"
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
/note="Vector: pHSS6-Sal; A yeast genomic DNA library
/note="Vector: pHSS6-Sal; A yeast genomic DNA was size-fractionated (DNA of roughly 2-3 kb
in length) prior to cloning. This library was
subsequently mutagenized with a mTn 3xHA/lacZ
                                                                                                                                                                  /organism="Saccharomyces cerevisiae"
/db_xref="taxon:4932"
/clone_lib="mTn-3xHA/lacZ Insertion Library"
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GSS 05-OCT-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 GAAAAGGGAGAAAAAAGAAAAAGA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelsayedetigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sheared DNA-42C8, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sheared DNA-42C8.TF Sheared DNA Trypanosoma brucei genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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301 838 0200
301 838 0208
                        Conservative
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                                                                                                                                                                                                               /organism="Trypanosoma brucei"
/ostrain="TREU927/4 GUTat 10.1"
/db_xref="taxon:5691"
/db_xref="taxon:5691"
/clone="Sheared DNA-42C8"
/clone="Sheared DNA-42C8"
/clone="Vector: pUC18: Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert librarles for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Praces 1000 v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cocation/Qualifiers
                                         9.1%; Score 24; DB 12; 100.0%; Pred. No. 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longare,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 657)
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Seq primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0350 row: G column: 18
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                                                                                                                                                  182 a
Conservative
                                                                                                                                       was blunt end-repaired with TM DNA polymerase and TM
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4733114(gblAF129072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XLIO-Gold (Stratagene) cells
and selected for amplicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through 0.005 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Male"
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                   9.1%; Score 24; DB 12; Length 657; 100.0%; Pred. No. 46;
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COMMENT

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FEATURES

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                                                                                                                                                                                       601905170F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                      Homo sapiens
                                                                                                                          EST
                                                                                                                                          BF239967.1 GI:11153890
                                                                                                                                                            BF239967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12066 row: g column: 08
High quality sequence stop: 674.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
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 National Institutes
                NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                          numan
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                    (bases 1 to 821)
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                                                                                                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="IMAGE:5417887"
//clone_lib="NIH_MGC_87"
//tissue_type="mammary adenocarcinoma, cell line"
//lab_host="PH10B (phage-resistant)"
//note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
05 a 92 c 153 g 127 t
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100.0%; Pred. No. 46
Live 0; Mismatches
                                                  Chordata;
Primates;
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Primates;
of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                           821 bp
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                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                    Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'.
                                                                                                                                Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                                                                                                                                                                                      DNA Res. 5 (6), 335-340 (1998)
99156227
                                                                                                                                                                                                                                                                                                                                 Yoshino,R., Mitra,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H., Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum Eukaryota; Mycetozoa; Dictyostelium. 1 (bases 1 to 372)
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AU039357
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Tissue Procurement: ATCC
                                                                                                                                                                                                                         Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                       development
                                                                                                                                                                                                                                                                                                                                                                                                                                             Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345
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/clone_lib="NHH_MGC_34"
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/lab_host="DH10B (TI phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
); Double-stranded cDNA was prepared from cell line RNA.
); Double-stranded cDNA was prepared from cell line RNA.
); and 3' adaptors were used in cloning as follows: 5',
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-APTCTAAAGGCCGGCGGCGCGCACATC-dT(30)BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                Location/Qualifiers
/organism="Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4133129"
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/db_xref="taxon:9606"
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone SLH629, mRNA sequence.
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. 44;
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Matches 23
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.
Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/lmage/image.html
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 393)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AA658426 AA658426 GI:2594580 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                         121
                                                                                                                                                                    //dev_stage="45 years old"
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/db_xref="taxon:9606"
/clone="MAGE:1208396"
/clone_lib="NCI_CGAP_Pr2"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="AX4"
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/db_one="516629"
/clone_lib="Dictyostelium discoideum SL (H.Urushihara)"
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/dev_stage="slug"
/dev_stage="slug"
/dev_stage="slug"
8.7%;
100.0%;
Score 23;
Pred. No.
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DB 9; Length 393;
1.2e+02;
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Search completed: August Job time: 30176 sec

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                   35 AAATAAAAACAGAAAAAAAGAAAA 57
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1 (bases 1 to 683)
Huckle, E. Taylor, R., Ashurst, J.L., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
Contact: Huckle E
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western clawed frog.
western clawed frog.
Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.-
AL653205
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                                                                   l Similarity
23; Conserv
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Email: trop@sanger.ac.uk
Sanger Xenopus troplcalis EST project 2001
TROPICALIS_SEQUENCE_ID: TGas049n16.sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL653205 XGC-gastrula Silurana tropicalis cDNA clone TGas049n16 5',
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This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
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llarity 100.0%;
Conservative
                                                                                                                                                                                   /dev_stage="gastrula (stages 10.5-13 mixed)"
/lab_host="secherichia coli xL1-blue"
/note="wector: pCS107; Site_1: EcoR1; Site_2: NotI; cDNA
/note="wector: pCS107; Site_1: EcoR1; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from stages
10-13 gastrulae. EcoRI-NotI cut cDNA was then ligated
into pCS107 with EcoRI at the 5' end and NotI at the 3'
end."
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linear

PAT 06-MAR-1998

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9b_P1: ATFICI2
9b_P1: ACC9461
9b_D1: ATCHRIV52
9b_Htg: ACO93916
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gb_pat:A58694
gb_pat:A58693
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gb_htg:AC108422
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Query: US-08-973-363-14
Query length: 45
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Database sequences: 1797656
Database length: 187333701
Search time (sec): 4908.870000
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                                gb_pr:HS438G17
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I J04169 Mouse Cas NS-1 retrovir
I U10414 Caenorhabditis elegans
I Z54270 Caenorhabditis elegans
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I AC033012 Homo sapiens chromos
I AC03112 Homo sapiens thaliana
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I AC033017 Homo sapiens thaliana
I AD010074 Arabidopsis thaliana
I AD010074 Arabidopsis thaliana
APO00617 Homo Sapiens genomi
AC094039 Rattus norvegicus of Continuation (3 of 22) of LM
AC094583 Rattus norvegicus of ALM
AC094583 Rattus norvegicus of ALM
AC094582 Danio rerio chromos
AC044908 Homo sapiens genomi
AC107323 Felis catus clone H
AC107323 Felis catus clone H
AC096870 Rattus norvegicus of AC107324 Felis catus clone H
AC078802 Homo sapiens chromod
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LOCUS A58693
DEFINITION Sequence 12 fr
ACCESSION A58693
VERSION A58693.1 GI:3
KEYWORDS Unidentified
ORGANISM unidentified
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Griffiths.R. and Tiwari,B.
AVIAN GHD GENES AND THEIR USE IN METHODS
BIRDS
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Location/Qualifiers
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Sequence 13 from Patent WO9639505.
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Sequence 12 from Patent WO9639505.
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Griffiths, R. and Tiwari, B.
AVIAN GHD GENES AND THEIR USE IN METHODS FOR SEX IDENTIFICATION
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    Patent: WO 9639505-A 12 12-DEC-1996 ISIS INNOVATION (GB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 GAAAAAAGAGAGACAAAAGAGAAAGGAAAATAAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluLysArgGluThrLysGluLysGluAsnLys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glasgow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Griffiths,R. and Korn,R.M.
A CHD1 gene is Z chromosome linked
Gene 197 (1-2), 225-229 (1997)
97473516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF004397 6872 bp mRNA Gallus gallus chromo-helicase-DNA-binding protein, variant with hydrophilic domain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other publication AU 5906996 961224.
Location/Qualifiers
1. .265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 6872)
Griffiths, R. and Korn, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-MAY-1997) Zoology, Molecular Lab, Glasgow University.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chicken.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF004397.1 GI:2501845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: A58693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G12 8QQ, UK
                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Gallus gallus"
/db_xref="taxon:9031"
1..6872
                                      DDDEDYDKRGSRRQATVNVSYKEAEETKTDSDDLLEVCGEDVPQTĒEDEFETIEKFMD
SRIGKRGATGASTIYAVEADGEDPNAGFEKSKELGEIQYLIKWRGWSH.HNITWFTEET
LKQQNVKGHNKLDNYKKYQETKRWLKNASPEDVEYVNCQDELTDDLHKQVQIVERIL
AHSNQKSAAGYPDYYCKWQGLPYSECSWEDGALIAKKPQARIDEYFSRNQSKTTPFKD
                                                                                                                        /translation="MNGHSDEESVRNSSGESSRDDDSGSASGSGSGSSSGSSSDGSS
SQSGSSDSESGSEGGSESBSDTSREKKQVQAKPFRADGSEFWKSSPSILAVQRSAV
LKKQQQQQKAASSDGSEEDDSSSSBDSADDSSSETIKKKHQDEDWQMSGSSGVSGTGS
DSESAEDGDKSSCEESEDSSSSBDSADDSSSETIKKKKHQDEDWQMSGSGVSGTGS
DSESAEDGDKSSCEESESDYEPKNKVKSRKPPSRIKPKSGKKSTGQKKKQLDSSEEEE
CKVLKQRPRFVALKKQPSYIGGHESLELRDYQLNGLNWLAHSWCKGNSCILADEMGLG
KTIQTISFLNYLFHEHQLYGPFLLRVPLSTLTSWQREIQTWAPQMNAVVYLGDITSRN
                                                                                                                                                                                                                                                     protein"
                                                                                                                                                                                                                                                                                        /function="role in chromatin architecture"
/note="CHD protein with hydrophilic domain"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .6872
                                                                                                                                                                                                        /protein_id="AAC60282.1"
/db_xref="GI:2501846"
                                                                                                                                                                                                                                                                  /product="chromo-helicase-DNA-binding on the Z chromosome
                                                                                                                                                                                                                                                                                                                                                      /gene="CHD-Z"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 to 6872)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                           /gene="CHD-Z"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear VRT 08-OC on the Z chromosome (CHD-Z) mRNA, compl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRT 08-OCT-1997
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 11.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-973-363-14 x AF004397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4443 GAAAAAAGAGAGACAAAAGAGAAAGGAAAATAAA 4475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 GluLysArgGluThrLysGluLysGluAsnLys 45
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
MacGewan, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 62575)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
mus musculus, clone RP23-438D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus clone RP23-438D3, LOW-PASS SEQUENCE SAMPLING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC108422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
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AVARDAELVDKSETDLERLGELVHNGCIKALKONSSGQERAGGRLGKVKGFFFRISGV
QVAKLVISHEEELAPLHKSIPSDPEERKRYVIPCHTKAAHFDIDWGKEDDSNLLVGI
YEYGYGSWEMIKMDPDLSLTQRILPDDPDKRPQAKOLOTRADYLIKLLNKDLARKEAQ
RLAGAGNSKRRKTRNKKNKMKASKIKEEIKSDSSPQPSEKSDEDDEEEDNKDEIVSVK
HLHKKIKTEKENEEKPEDIGIKKEAEEKRETKEKKEKKEKEDKKELKEKD
NEEKRENKVRESTQKKEEVKEEKVDENKUMKSENKEKSKKILDTPVHTTATSEPVPISE
ESEELHQKTFSVCKERMRPVKAALKQLDRPEKGLSERDLEHTRQCLIKIGDHITECL
KEYTNDEQIKOMINIFOSOFTETDARKLHKLYKHAIKKRQESQUHDQNISSNVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="short
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SAFSNGKDHRDWDHYKQDSRYYSDSKHRKLDDHRSRDHRSNLEGNLKDSRGHSDHRSH
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LFKEPEGEEQEPQEMDIDEILKRAETRENEPGPLTVGDELLSQFKVANFSNMDEDDIE
LEPERNSRNWEEIIPESQRRRIEEEERQKELEEIYMLPRMRNCAKQISFNGSEGRRSR
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ERGNRVLIFSQMVRMLDILAEYLKYRQFPFQRLDGSIKGELRKQALDHFNAEGSEDFC
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RTLIDFKSNHRLLITGTPLQNSLKELWSLLHFIMPEKFSSWEDFEEEHGKGREYGYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDHRIHSDHRSTSEYSHHKSSRDYRYHSDWQMDHRASGSGPRSPLDQRSPYGSRSPLG
HRSPFEHSSDHKSTPEHTWSSRKT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1223 c
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1520 g 1683
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100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murinae; Mus
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REFERENCE

AUTHORS JOURNAL REFERENCE

AUTHORS TITLE

KEYWORDS VERSION

JOURNAL

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Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Plerre,N., Pollara,V., Raymond,C., Retta,R., Riaback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schuer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Triglio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., WuX., Wyman,D., Ye,W.J., Young,G., Zandoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-JAN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This record contains 77 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be generich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preserved.
                                                                                                                                 12106 12205:
12206 128
12868 12967:
12968 136
                                                                                                                                                                                                                                                                                                                                                                                                                                 8068 8167: gar
8168
                         14495 14594: gap of
14595 15328: con
                                                                          13667 13766: gap of
13767 14494: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            728: contig of 728 bp in length
729 828: gap of 100 bp
829 1553: contig of 725 bp in length
1554 1653: gap of 100 bp
1654 2373: contig of 725 bp in length
3374 2473
                                                                                                                                                                                                                                                    11301 11400:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2374 2373: contig of 720 bp in length 2374 2473: gap of 100 bp 2474 2473: gap of 100 bp 3176: contic ~ 3177 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7239 7338:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp in length 6414: contig of 707 bp in length 6514: gap of 100 bp 17328: contig of 7730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4098: ga
4821
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1604 28337: contig of 705 bp in length
1604 28337: contig of 734 bp in length
138 28161: contig of 724 bp in length
162 29261: gap of 100 bp
15 29984: contig of 723 bp in length
15 30084: gap of 100 bp
16 30084: gap of 100 bp
17 30804: gap of 100 bp
1804: gap of 100 bp
1809: contig of 625 bp in length
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112 43740: contig of 729 bp
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2350: gap of 100 bp
24284: contig of 724 bp in 24284: gap of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in 25099: contig of 724 bp in length
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144: gap of 100 bp

34766: contig of 722 bp in length

166: gap of 100 bp

35551: contig of 685 bp in length
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                                                   EU Arabidopsis sequencing, project.

Direct Submission

Submitted (20-SEP-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael bevanebbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                     Bevan, M., Terryn, N., Ardiles, W., Buysshaert, C., Dasseville, R. Clerck, R., De Keyser, A., Neyt, P., Rouze, P., Van Den Daele, H., Villaroel, R., Gielen, J., Van Montagu, M., Bancroft, I., Mewes, H. Mayer, K.F.X., Lemcke, K. and Schueller, C.
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                               On Apr 18, 1998 this sequence version replaced gi:2982425
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on performance of analysis and a more detailed
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47029: contig of 730 bp
7129: gap of 100 bp
47847: contig of 718 bp
7947: gap of 100 bp
48664: contig of 777 bp
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49486: contig of 722 bp in
586: gap of 100 bp
50310: contig of 724 bp in
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52708: contig of 699 bp in
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GLIPK SLADLGNLÖTLDISÄNNLITGEI PEEFWANSOLLDLVAANNHLSGSIPKSICSN
NTNLEQULUSGTOLSGEI PVELSKCOSI KOLDLSNNSLÄGSI PEALFELVELTELY ENKFSGEI FO
NTLEGTLSPSI SNLTMLÖWLYLYHNNLEGKLEKEI SALRKLEVLFLYENKFSGEI FO
EIGNOTSLKMI DMFONHFEGE I PPSI GRIKELNLLHLRONELVGGLEAGNICHOLNI
LDLADNQLSGSI PSSFGFLKGLEQLMLY NISHONLHGKI KERLYGELYGEL PWILGKI RE
TI HPLCGSSSY LSFDVTNNGFEDEI PPLELGNSONLDRLÆLGKNOLTGK I EWILGKI RE
LSLLDMSSNALTGT I PLQLYLCKKLTHI DLNNFLSGFI PPWLGKLSQLGELKLSSNO
FVESILPTELFKOTKLLVISLDGNSLNGSI PQEIGNLGALMVLNILDKNQFSGSSLPOAMG
KLSKLY ELTRLSKNSLITGEI PVEIGOLODLOSALDLSVNNFTGDI FST IGTLSKLETLD
LSHNOLTGEVGSVGDMKSLGY LNVSFNNLGGKLKKQFSRWPADSFLGNTGLGSPLFR
RCNRVRT I SALTA I GLMILVI ALFFKORHDFSKKVGHGFSKAYTSSSSSGATHKDLFR
RCNRVRT I SALTA I GLMILVI ALFFKORHDFSKKVGHGFSKAYTSSSSSGATHKDLFR
                                                                                                                                            /note="predicted contains EST gb:T21779, AA042326, Aa712523, Aa7
                                                                                                                                                                                                                                            complement(join(19211.
/gene="F1C12.70"
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/gene="F1C12.70"
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/gene="F1C12.70"
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pimpinellifolium, PIR:T10515
contains EST gb:Z38045, Z46532"
                         /product="putative protein"
/protein_id="CAA18240.1"
/db_xref="GI:2982432"
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/gene="F1C12.60"
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/gene="F1C12.60"
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/db_xref="GI:2982431"
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/protein_id="CAA18239.1"
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/gene="F1C12.60"
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/chromosome="4"
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/variety="Columbia"
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12771, AA605387, F13839"
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VSLESNKSKEVEDGAI KPQGVTTQADSCLERKPALEEKVLDETTYKSDLKKPTEKESSRE
ERELEEESTS ING JAEKVRUMRISKEKKURERAMERGKGKTEGKALTETINELLOGASR
RISHVETSHAERSLOTSHITVK VYVGDRV IMDKREKSGETTRSAELGGGALTETINELLOGASRA
KSKUV IEDKAHRSLOTSHITVK VYVGDRV IMDKREKSGGETTRSAELGGGASVEA
KSKUV IEDKAHRSLOTSHITVK VYVGDRV IMDKREKSGGETTSLERKSGTKE EERPKYGE
EKSYSHGREKKHSKAGODDETTSTHAHRNINKGLEEDEDEEKKKVEREETTGERVEEASVETVUDW
DGNEMEEEEEEEYGDY FNGDDDWITHDISRPRSYMEDLIKKERYLEYLNTESEKKDICNL
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TSSM6SNALENSESLESVKESQMLQP I EECHNEEEEEE IECAPPPLESGEKDREGVRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="similarity to mature-parasite-infected erythrocyte surface antigen MESA, Plasmodium falciparum, PIR2:A45605"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Juin(21131. .22045,22134. .22261,22328. .24208,24317. .24665,
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FGV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IERRTVSSNF17SDLROK1DNLM1TRVQSH1GVFLNQ1EGGDEVEESHEVEGSARNEES
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24974. .25119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
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alignment_block:
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Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhbay, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Charzos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Douthwaite, K.J., Davis, C., Davy-Carroll, L., Dederich, D.A., Dolthwaite, K.J., Davager, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hahes, A., Hernandez, J., Harris, K., Hart, M., Halloway, C., Holliows, M., Holloway, C., Holliows, M., Hollows, M., Hollows, M., Hollows, M., Hollows, M., Hollows, C., Harris, C., Holliows, M., Hollows, M
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AC094613
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Ratio:
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Eukaryota; Metazo
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Arabidopsis thaliana
contains EST gb:237280, Z37281"
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/note="36bp_TTC tandem repeat"
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KWMFFFDVDEFLHVPVKETISSVMESLEEYSQFTIEQMPMSSRICYSGDGPARTYRKW
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VLTEPPKSVDFDLYNSTKKTKKYDYLYCGSSLYGNLSPQRVREWIAYHVRFFGERSHF
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Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
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Weinstock, G., and Glbbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ma.J., Manesuwati, m., Mayhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nugyen, Nugyen, N., Nugyen,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15624448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Mahashwari, M., Mapua, P., Martin, R., Martindae, A., Martin, R., M
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                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus quality: 130278 bases at least Q40 Consensus quality: 139554 bases at least Q30 Consensus quality: 147493 bases at least Q20 Estimated insert size: 137875; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation quality coverage: 1.9x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
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Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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1 (bases 67424 to 179368)

Terryn.N., Ardiles,W., Buysshaert,C., Dasseville,R., De Clerck,R.,

Terryn.N., Ardiles,W., Buysshaert,C., Dasseville,R., Villaroel,R.,

Gielen,J., Van Montagu,W., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
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Volckaert, G., Grymonprez,
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Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Lemcke@mips.biochem.mpg de, mayer@mips.biochem.mpg de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevanebbsrc.ac.uk

Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thai/ this fragment has an overlap with ATCHRIV51 at the 5' end and an overlap with ATCHRIV53 at the 3' end.

Source of the sequence of the Max overlap with ATCHRIV51 at the 5' end and an overlap with ATCHRIV51 at the 5' end and an overlap with ATCHRIV53 at the 3' end.
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Pohl,T., Wei Unpublished

Unpublished

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REFERENCE AUTHORS

JOURNAL REFERENCE

AUTHORS

Lemcke, K. a Unpublished

VERSION
KEYWORDS
SOURCE
ORGANISM

DEFINITION ACCESSION

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LOCUS ATCHRIV52

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145411

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KEYWORDS
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US-08-973-363-14 x ATCHRIV52
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Percent Similarity: 100.000
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SEQUENCE, 4 unordered pieces.
AC073916
AC073916 GI:18390150
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1 (bases 1 to 206258)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homsi,F., Howard,S., Huber,J., Hullyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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DADIIMURDPFPREFDDADFQITCDDYNGRPSDKKHWINSGETYVKANNKTSKEYKYW
IRSSRKEPGKHDODVNRIFIKNDLHVERKLGIKMRFEDDTVYFGGETCOPSRDI INVUNTMHA
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HPNCYYLKTTGTDFSGSKLFATPDYLKMMWRRIELLLTQVLZMGYNFIETDADIMWLRD
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MHDQDVFNOIKKALVSEIGIQMRFFDTVYFGGFCQTSRDINLVCTMHANCCVGLAKK
LHDLNLVLDDWRNYLSLSEPVKNTTWSVPMKCT"
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Gaps:
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Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louissged, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Man, J.,
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Peters, L., Pickens, R., Primus, E., Pu, L. L., Oliles, M., Ren, Y.,
Rives, M., Rojas, A., Rojubokan, T., Rolfe, M., Riz, S., Savery, G.,
Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I.,
Sudergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,
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Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R.,
Wang, S., Warden, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K.,
Weinstock, G. and Gibbs, R.,
Direct Submission
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Direct Submission
Submitted (05-JUL-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jan 29, 2002 this sequence version replaced gi:14717253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly p
                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                              be preserved
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help8bcm.tmc.edu
Contact: hgsc-help8bcm.tmc.edu
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Center clone name: HBWU
Center clone name: HBWU
Center clone name: HBWU
Center clone name: HBWU
Sequencing vector: Plasmid; M77789
Sequencing vector: M13; LO8821
Chemistry: Dye-primer Bodipy: 17% of reads
Chemistry: Dye-terminator Big Dye: 83% of reads
Assembly program: Phrap; version 0.990329First call to
dPhraphist
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146379
181316
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                                                                                                                            146278: contig of 146278 bp in length 146378: gap of unknown length 181315: contig of 34937 bp in length 181415: gap of unknown length 201347: contig of 21942 bp in length 2013457: gap of unknown length 201459: contig of 2801 bp in length 201458: contig of 2801 bp in length.
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AUTHORS
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VERSION
KEYWORDS
SOURCE
ORGANISM
alignment_scores:
Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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ORIGIN
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US-08-973-363-14 x AC073916
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LOCUS AF008215
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Ratio: 1.000
Percent Similarity: 100.000
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AF008215.1 GI:2555076
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Vairimorpha necatrix
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NKYLGAIKLKNIPSAPAGIPKIEVTFEADANGIYKVSAQDGISKNKQEIEIVPSSGLN
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EEVKNFIKSKL"
1 274 c 398 g 596 t
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       Percent Identity:
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FEATURES

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139671 AAACGCGAAACCAAGGAGAAGGAGAAT 139697
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Hirt.R.P. and Healy.B.
Direct Submission
Submitted (12-JUN-1997) Zoology,
Cromwell Rd, London SW7 5BD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF008215 2176 bp mRNA linear INV
Vairimorpha necatrix mitochondrial Hsp70 homolog mRNA,
                                                                                                                                                                                                                                                                                                                          Hirt.R.P., Healy, B., Vossbrinck, C.R., Canning, E.U. and I
A mitochondrial Hsp70 orthologue in Vairimorpha necatris
evidence that microsporidia once contained mitochondria
Curr. Biol. 7 (12), 995-998 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Microsporidia; Burenellidae; Vairimorpha. (bases 1 to 2176)
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177. .1910
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58439 c 59259 g 45228 t
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Gaps: 0
Percent Identity: 100.000
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US-08-973-363-14 x AF008215
                                                                                                                                      alignment_scores:
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                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-FEB-2000) Takahiko Hayakawa, Plantech Research Institute, Research Center; 1000 Kamoshida-cho, Aoba-ku, Yok Kanagawa 227-0033, Japan (E-mail:pri0012@cc.m-kagaku.co.jp, Tel:+81-45-963-3520, Fax:+81-45-962-7492)
                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 2637)
Hayakawa,T., Hamada,A. and Tanaka,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophylliales; Chenopodiaceae; Atriplex.

1 (bases 1 to 2637)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Atriplex gmelini cDNA to mRNA. Atriplex gmelini
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Atriplex gmelini AgNHX1 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolation and characterization of a Na+/H+ antiporter gene from the halophyte Atriplex gmelini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Na/H antiporter Nhx1
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                                                                                            Ratio:
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/db_xref="taxon:118074"
682. .2349
                                                                                                                                                                                                                                                                                                                                                                                                                                  Translation="WWSQLSSLLSGKMDALTTSDHASVVSMNLFVALLCGCIVIGHLL EENRWNLESTALLIGLATGVVILLISGGKSSHLLVFSEDLFETYLLFPTIFNAGFQVKKKQFFRNFTITVLFGAVGTLVSFTLISLGALSIFKKLDIGTLELADVLAJIGATFAAT DSVCTLQVLNQDETPLLYSLVFGEGVVNDATSVVLFNAIQSFDLTRIDHRIALQFMGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene=
                                                                                                                                                                                                                         /note="30 a nucleotides"
509 c 530 g 913 t
                                                                                                                                                                                                                                                                                              MRGAVSMALAYNQFTRSGHTQLRGNAIMITSTISVVLFSTMVFGLLTKPLIMFLLPQP
KHFTSCSTVSDVGSPKSYSLPLLEGNQDYEVDVGNGNHEDTTEPRTIVRPSSLRMLLN
APPHTVHHYWRKFDDSFMRPVFGGRGFVPFVPGSPTEQSTNNLVDRT"
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/protein_id="BAB11940.1"
/db_xref="GI:9857314"
                                                                                                                                                                                                                                                                                                                                                                  VSDSPGISVAVSSILLGLVMVGRAAFVFPLSWLMNFAKKSQSEKVTFNQQIVIWWAGI
                                                                                                                                                                                                                                                                                                                                                                                        ILTVFFCGIVMSHYTWHNVTESSRVTTKHAFATLSFVAEVFLFLYVGMDALDIEKWRF
                                                                                                                                                                                                                                                                                                                                                                                                             FLYLFIASTILGAFTGLLSAYIIKKLYFGRHSTDREVALMMLMAYLSYMLAELFYLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="AgNHX1"
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                                                                                                               Length:
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alignment_block:
US-08-973-363-14 x CASNS1
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AAGAGAGAAACAAAGGAAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 bp upstream
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Draft entry and computer-readable sequence for [1] kindly submitted by W.Y.Langdon, 02-MAR-1989. Cas NS-1 is an acutely transforming murine retrovitus that induces pre-B and pro-B cell lymphomas. It was generated from the ecotropic Cas-Br-M virus by sequential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J04169.1 GI:323269
gag:onc fusion protein; viral oncogene.
GAS NS-1 retrovirus DNA, isolated from me
previously infected with Cas-Br-M virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 2711)
Langdon, W.Y., Hartley, J.W., Klinken, S.P., Ruscetti, S.K. and Morse, H.C. III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cas NS-1 murine leukemia virus
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/db_xref="G1:323270"
/db_x
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HMLAELKGIFSGLFKIFGGDTFKITKADAAEFWRKAFGEKTIVPMKSFRQALHEVHFISS
GLEAMALKGTIDLTCUNDYISVFEFDLFTRLFQPWSSLLRNWNSLAVTHFGYMAFLTYD
EVKARLQKFIHKPGSYIFRLSCTRLGQWAIGYVTADGNILQTIPHNKPLFQALIDGFR
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/db_xref="taxon:11793"
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once, or 1
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Submitted (28-JUN-2001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
Louis, MO 63110, USA
7 (bases 1 to 28990)
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemist or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence fromore than one m13 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Direct Submission
Submitted (05-CCT-2001) Department of Genetics, Washington
Submitted (05-CCT-3001) Department of Genetics, Washington
University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (14-SEP-2001) Department of
University, Genome Sequencing Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (19-AUG-1199) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
6 (bases 1 to 28990)
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Submitted (06-JUN-1994)
University, 4444 Forest
5 (bases 1 to 28990)
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The C. elegans Sequencing Consortium.
The C. elegans Sequence of the nematode C. elegans: a platform for Investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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Louis, MO 63110, USA
Submitted by:
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                                                                                                                                                                                                            E: This sequence may not be the entire insert of this clone y be shorter because we only sequence overlapping sections or longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                             Genome Sequencing Center
Department of Genetics, Wasl
St. Louis , MO 63110, USA,
Sanger Centre, Hinkton Hall
Cambridge CB10 IRQ, England
                                                                                                                                                                                          submissions.
                                                                                                                                                                                                                                                                                                                  rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing
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SQSALIIDPNMHQQVSGHQSGHPGMPSTGSFHQLQSLDTHTHPQYSLDANRKMTQY
SSQSALIIDPNMHQQVSGHQSGHPGMPSTGSFHQLQSLDTHTHPQXMMSRSLNMPSSA
FSSPIPSNQPLSHQQPQMSQNTQAHQQQTQVQNQQPYYGGSGMIIPPPDPSISQI
FEQQTTLMELEKSRSMYETRARIFKEHLEELRGDIDGLKRDGNVQNGQHREHDAVHAQ
NVAHGEDKETIRMASMAGTPBQRAQAFBON*
JOIN (5475. .5696,5827. .6042,6389. .6607,6684. .6818,
6866. .7000,7706. .7378,7422. .7571,7673. .7760,8233. .8503,
/gene="F42A10.2"
                                                                                                                                                                                                         /Product="Hypothetical protein F42A10.2a"
/product="Hypothetical protein F42A10.2a"
/product="Hypothetical protein F42A10.2a"
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/translation="MGGFSIFSRNTkPlykaVSTNDADLEKIVIEKTWTGRHLFEAVC
/translation="MGGFSIFSRNTkPlykaVSTNDADLEKIVIEKTWTGRHLFEAVC
/translation="MGGFSIFSRNTkPlykaVSTNDADLEKIVIELEVLEVAVADLEMYGILYKPPDLD
RHLPKSVIDOYDMSADMWRDRIKRWSSNAGOSEREAELEYLKVAVADLEMYGILYKPI
CNNETDLHLGISAQGIGITKGVWRIFTERPFSWSSIKNIQFKNRKHMKTVDKSTIS
RSRETSIDSSILDLGIGTHNLYLRRROPDTERPFSWSTIKNIQFKNAAEQAKVALE
RKEROOMBKEKYEMKOKVWTIELKMAQDENIRAAERANDVALEGKARHSGHETIALYK
OKSEVFAAECNRLSMNNMKSEEALLEMERKAREAEILAKOMSMSLADVSLDANRKMTQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"similar to ezrin (contains a domain found in band 41, ezrin, moesin, radixin and talin); contains similarity to Pfam domain pr00373 (Band_41), Score-234.3, E-value-4.1e-75, N=1; PF00769 (ERM), Score-489.2, E-value-1e-143, N-1; coded for by the following C. elegans CDNAs: yk34h5.3, yk34h5.5, yk52e5.5, yk214b9.3, yk214b9.5, yk406f4.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Mypothetical protein F42A10.3"
/product="G1:15617835"
/protein_id="AAA19074.2"
/protein_id="AAA19074.2"
/protein_id="AAA19074.2"
/db_xref="G1:15617835"
/translation="MSTLIDDTITESSDAQHTVLLPEDYVKKFDDDEYLQFYFSRDAI
/translation="MSTLIDDTITESSDAQHTVLLDIGAGPTVYSALCFRDYAKRWHLSDFY
DRNLDVLRKHIRHEFIDWVFTIKVINNTEGGFTPDQVCIDVEEKARGLVKSGGIHF
ADVHQMDVVPELAGKKYDLUVSIFTLESACRNYEEYCKCYTNMMRHLRSGGRFVLGSV
LEDDEYNSGRKTIFHLLNLSEQMILDALVSVGLDVANAKKYVLDGEGVMFIMATKL"
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/strain="Bristol N2"
/db_xref="taxon:6239"
/chromosome="III"
/clone="F42A10"
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6866. .7000,7076. .7378,7422. .7571,7673. .7760,8233. .8503,
8615. .8789,9889. .9939)
/gene="F42A10.2"
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/gene="F42A10.
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join(5475. .5696
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                                                                                       35 GluLysArgGluThrLysGluLys 42
gb_in:CEF11C1
                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                       1.000
1.000
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYGDGALGTRGMALFFHSHRÖNDICETMDLSNFËLSPPEIËATEVAMEVAÄKOKKSCI VPPTVEBARRNRISSECVHVEHGISMOLFKRKTLNGSSTDLSAKSHNEDCVCCECIP VVEDLCEPGSEDEEDEEDVRTNILISLOLQOMAANLENDEDVPQVTGHGFSVLGGILF IDLSRYHELGRFVEVDSEHKEMLEGSENDARVPIKYDKOSAIFHLDIARKCGILEAVL TSAHIVGLFHELLKEVTVDDLFPNGFGEDENGITADKGQKFCDLEEFGSDLMEIAASEMGDKGAMLYMAHAYETGOHLGPNETTDYKKSIDTVQDKVFGDEEELDSDCKTTFSSE MGDKGAMLTAMAHAYETGOHLGPNGTBYKSTDATONYQDKVFGOEEEELDSDCKTTFSSE FAPLIRHEILAKMAEMYKEGGYGLNQDFERAYGLFNEAAEAMGAKLANKYYEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(10885. .14126)
/gene="F42A10.4"
complement(join(10885. .11149,11747. .11891,12037. .12060,
12115. .12501,12745. .12850,12904. .13980,14067. .14126))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSQSALIIDPNWHQQVSGHQSGHPGMPSTGSFHQLQSLDTHTHPQQMMSRSLNMPSŠA
FSSPIPSNQPLSHQQPQQMSQNTQAHQQQTQVQNQNQPPYYGGSMIIPPPDPSTSQI
FEQQTTLMELKSRSEYETRARIFKEHLEELRGDIDGLKRDGNVQNGQHREHDAVHAQ
NVAHGFDKFTMKMKKSKSASSIGSSGSSDSLELNTVARHVAGRGIPRVSTVSTTSSS
SILSHVMMLHRQQSYDLGNTEMQEADI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MGGFSIFSRNTKPIYAKVSTMDADLEKIVIEKTWTGRHLFEAVC RIIGLEETWYFGLQFTMKKNIPCWLQNDKTICQDIOKDTSDGFNELEFLVKFYVPEDV EPEIILDATRHLFFLQIFREAILSMNLYCSPEASVLLASFAVQAMHGDCTBEEVGPIDL KHLPKSVIDOYDMSADMRWDRIKKRWSSRNAGQSREEABLEYLEVAQDLEWYGILYYPI CNNKETDLHLGISAQGLGIYKGVNRITPRPFFSWSEIKNIQFKNRKFHMKTVDKSTISFRSRETSIDSSILDLCIGTHNLYLRRRQPDTLEVQQNRSQAKEDKQRRAAEQAKVALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIEQNDVVIEKPRMDPLHVRKLMETWRKAARRARTNYIDPWDEFNIHEYPVQRAKRYR
YSAIRKQWTEDIVDVRLHPDSFARGAMRECYRLKKCSKHGTSQDWSSNYVAKRYICQV
DRRVLFDDVRLQMDAKLWAEEYNRYNPPKKIDIVQMCVIEMIDVKGSPLYHLEHFIEG
KYIKYNSNSGFVSNAARLTPQAFSHFTFERSGHQMMVVDIQGVGDLYTDPQIHTVVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"coded for by the following C. elegans cDNAs: yksf11.3, yksf11.5, yk15444.5, yk15442.5, yk15445.5, yk15465.5, yk15465.3, yk193b4.3, CEMSD19F, yk324d1.5, yk408g12.5, yk409g10.5, yk445b7.5, yk522f8.5, yk602g10.3, yk602g10.5, yk681g2.3, yk681g2.5, yk728g6.3, yk735b12.5, yk735b12.3, yk738g6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(17398. .17529,17631. .18093,18144. .18367))
/gene="F42A10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(17398. .18367)
/gene="F42A10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="SL1 trans-splice site;
yk735b12.5 and yk728g6.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKERQOMEKEYKEMKOKVEVMTLELMKAQENIRKAEEANDQLAEKARHSEHETLMLYK
OKSEVEAECNRLSMNNMKSEEALLRMERKAREAEILAKOMSMSLADVSLDANRKMTOY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Hypothetical protein F42A10.2b"
/protein_id="AAK68385.1"
/db_xref="GI:14574194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yk74f7.3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(14143. .14144)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Hypothetical protein F42A10.4"
/protein_id="AAA19075.1"
/db_xref="GI:500737"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yk406f4.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="coded for by the following C. elegans cDNAs:
yk74f7.3, yk74f7.5, yk112g6.3, yk112g6.5, yk158h11.
yk158h11.5, yk370c4.3, yk370c4.5, yk453c7.3, yk513d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F42A10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="coded for by the following C. elegans cDNAs:
yk406f4.5, yk636e12.3, yk636e12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MTIDTTNESDNSPTNSPGLEASARTFSLNASKMVRITDDYADEV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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6
                                                                                                                                                                                                                                                                                                          Identity:
                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                       : 8
: 0
: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yk681g2.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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CDS

CDS

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Seq_documentation_block: LOCUS CEF11C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (29-SEP-1995) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CBIO 15A, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on Sep 22, 1998 this sequence version replaced gi:1001858. Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Palmer, S.
Direct Su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Eukaryota; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the specified clone. It may be shorter be overlapping sections once, or longer because overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For a graphical representation of this sequence and its analysis
see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The C.elegans Sequencing Consortium 2 (bases 1 to 40852)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence AL008868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99069613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z54270.1 GI:3642282
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                                                                                                                                                                                                                                                                            /db_xref="Sptrembl:Q19347"
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/translation="MMISPFLLAYLVLFPTSLRCSESHKVNERFSLADQVQHKLDFVK
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/vsvre"
                                                     join(4336. .4463,5151. .5312,5860. .
6249. .6327.6386. .6513,6562. .6717.
7743. .7816,7965. .8229)
                                                                                                                                                                                 join(4336. .4463,5151. .5312,5860. .5935,5980. .6062,
6249. .6327,6386. .6513,6562. .6717,6800. .6929,7378.
7743. .7816,7965. .8229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ງວະກາ(ສອປ. .1235,1367. .1611)
/gene="F11C1.4"
/ຕວາລາ
                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAA91029.1"
/db_xref="GI:3875725"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(980. .1235,1367. .1611)
/gene="F11C1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
note="contains similarity"
                               /gene="F11C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="F11C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is NOT necessarily the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .40852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               It may be shorter because we only sequence once, or longer because we arrange for a sma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cosmid
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cosmid FllCl,
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      Pfam
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      domain: PF01130 (CD36
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                                                                                           .5935,5980. .6062,
7,6800. .6929,7378.
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gene

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                                                                    25767 GAAAAAAGAGAAACGAAAGAAAAA 25744
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Length: 8
Gaps: 0
Percent Identity: 100.000

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gene

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INMILENREMOLDGRETAKHOK TOELKELSFHFFLEQAKLIAPWSERNANDLIN VYAYNSASTSEREIGTS VERWENDENDENDLIN VYAYNSASTSEREIGTS VERWENDENDLIN VYAYNSASTSEREIGTS VERWENDENDLIN VYAYNSASTSEREIGTS VERWENDENDLIN TYKTESTSEREIGTS VERWENDENDLIN TYKTESTSEREIGTS VERWENDENDLIN TYKTESTSEREIGTS VERWENDENDLIN TYKTESTSEREIGTS VERWENDENDLIN TYKTESTSEREIGTS VERWENDENDLIN TYKTESTSEREIGTS VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLING VERWENDENDLIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS Muzny,D.M., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Barbooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Barbooks,S.L., Amaratunge,H.C., Bornin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,G., Chen,R., Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-FFB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 23, 2001 this sequence version replaced gi:12739654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC090028 50962 bp DNA linear HTG 16-OCT-2001 Homo sapiens chromosome 3q clone RP11-299G2, *** SEQUENCING IN PROGRESS ***, 48 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley,K., Wu,C., Wu,Y., Wu,Y.F., Weinstock,G. and Gibbs,R.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 50962)
                      Sequencing vector: M13; L08821
Chemistry: Dye-terminator Big Dye: 99% of reads
Assembly program: Phrap; version 0.990329
                                                                                                                                                                         Center project name: HDET Center clone name: RP11-299G2
                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
Assembly program: Phrap; version 0.990329 Consensus quality: 27482 bases at least Q40
                                                                                                                                                                                                                                                                                                                     Web site:
                                                                                                                                                                                                                                                                                                                                                              Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                     http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                          this sequence version replaced gi:12739654
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COMMENT

TITLE

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 48 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 35893 bases at least Q30 Consensus quality: 39768 bases at least Q20 Estimated insert size: 18665; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 0.2x in Q20 bases; sum-of-contigs estimation
              19969
20866
20966
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gap of unknown length
contig of 636 bp in length
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ig of 651 bp in length
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g of 1100 bp in length
if unknown length
g of 782 bp in length
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g of 645 bp in length
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of 743 bp in length
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of 716 bp in
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of 683 bp in length
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Ratio: 1.000
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                                                                                                                                                     HSDM723E3 HSQ 2014 APR-2001 HSDM723E3 ON CHYCRE FRI 04-APR-2001 Human DNA sequence from clone RP1-23E3 on chromosome 6q13-15 Contains the gene for a putative secreted protein ZSIG13, ESTs and
                                                              GSSs, complete sequence.
AL121939
AL121939.12 GI:10862831
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Gaps: 0
Percent Identity: 100.000
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gap of unknown length
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contig of 1028 bp in length
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On Oct 17, 2000 this sequence version replaced gi:10732514.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone RP1-23283 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP1-2333 is at 1 in this sequence. The true left end of clone RP1-120N9 is at 59522 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/HGP/Chr6
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPI-228B3 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 5961)
                                                                                /note="L1MC5 1 4513. .47/
                                                                                                                                                                                                                   /note="L1PA10 repeat: matches 5730. .6158 of consensus" 3131. .3443
                                                                                                                                                                                                                                                                                                                                            /note="MER81 repeat: matches 2. .109 of consensus" 1764. .202
                                                                                                                                                                                                                                                                                                                                                                                                              /note="AluSg/x repeat: matches 83. .310 of consensus" 1638. ..1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                          /note="AluJo repeat: matches
                                                                                                                                                                                                                                                                                                               /note="L1MC5 repeat: matches 7306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1M4 repeat: matches 5213. .5269 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MER30 repeat: matches 4. .230 of consensus"
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repeat: matches
                                                                                                                            repeat: matches
                                                                                                                                                                                   matches 1. .312 of
                                                      84. .303 of consensus*
                                                                                                                        7761. .7907 of consensus"
.289 of consensus
                                                                                                                                                                                                                                                                                                           .7740 of consensus"
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ACCESSION VERSION KEYWORDS SOURCE

HTG

seq_documentation_block: LOCUS HSDJ223E3

seq_name: gb_pr:HSDJ223E3

DEFINITION

alignment_scores: Quality: Ratio:

BASE COUNT ORIGIN

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FEATURES Source

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6686. 6788
/note="MLT1-INTERNAL repeat: matches 961. .1046 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5046. .5435

/note-"LIMC2 repeat: matches 5910. .6324 of consensus"

5439. .5813

/note-"ML71B repeat: matches 1. .390 of consensus"

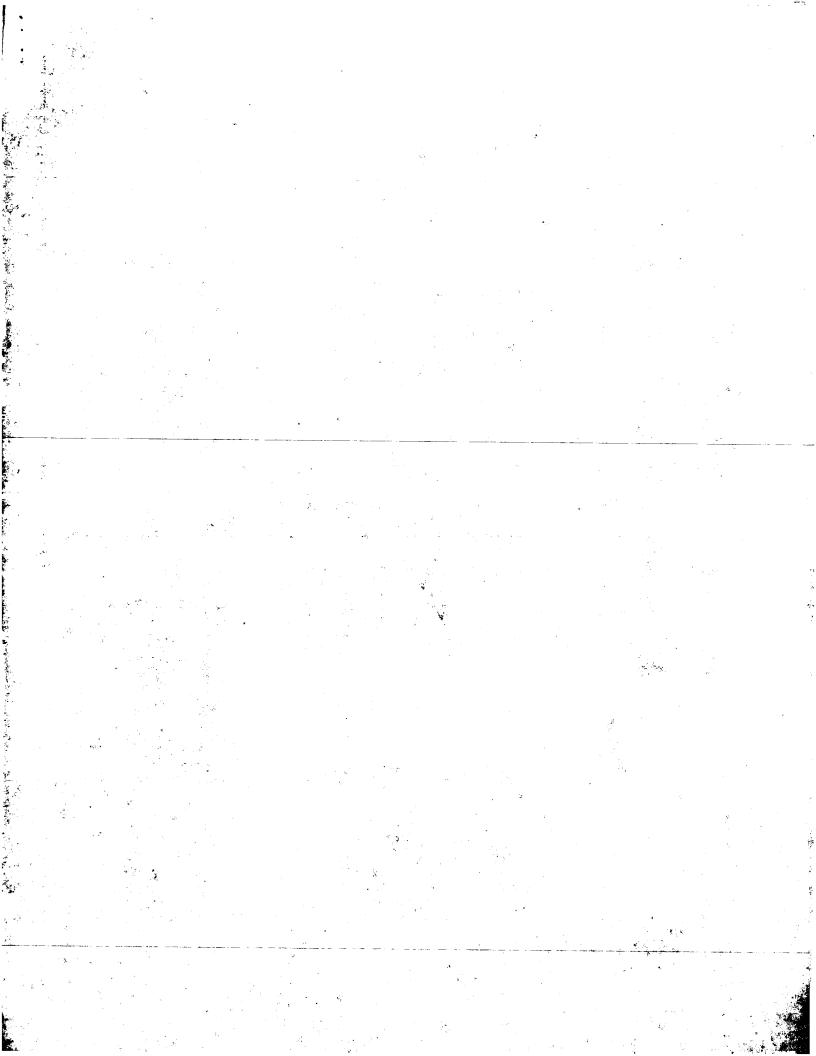
5828. .6022
                                                          /note="29 copies 2 mer at 70% conserved"
23700. .23827
                                                                                                                                                                                                                                                                                                                                                                                                     /note="L1PA5 repeat: matches 11. .6143 of consensus"
18731. .19020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3950. .10223
/note="AluJo repeat: matches 1. .298 of consensus"
10224. .10633
                     /note="L1ME repeat: matches 5678. .5804 of consensus"
23841. .24023
                                                                                                                                                   note="MIR repeat: matches 49. .250 of consensus"
                                                                                                                                                                                        note="MER20 repeat: matches 2.
                                                                                                                                                                                                                            /note="MIR repeat: matches 23. .112 of consensus"
                                                                                                                                                                                                                                                                   note="MLT2FB repeat:
                                                                                                                                                                                                                                                                                                   /note="THE1B repeat: matches 1. .364 of consensus"
                                                                                                                                                                                                                                                                                                                                          'note="match: GSS: Em:AQ521768"
                                                                                                                                                                                                                                                                                                                                                                                 'note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluSg1 repeat: matches 1. .294 of consensus"
12582. .18699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MC2 repeat: matches 3787. .4359 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3300. .9949
/note="L1MC2 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9999. .9299
/note="AluSx repeat: matches 1. .300 of consensus"
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/note="L1MC2 repeat:
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'note="MLT1B repeat: matches 1. .168 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7539. 8133 | note="MLT1B-internal repeat: matches 1. .728 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       392. .6685
/note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5331. .6391
/note="MLT1-INTERNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5828. .6022
/note="MST-INTERNAL repeat: matches 1443. .1637 of
'note="L2 repeat: matches 1904. .2095 of consensus"
                                                                                                                'note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     790. 7091
mote="AluSp repeat: matches 1. .299 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34. .10920
-- "Allusz repeat: matches 12. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :e="L1MC2 repeat:
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                                                                                                                                                                         22805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matches 4787. .5189 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 5189. .5826 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches 5826. .5911 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matches
                                                                                                                                                                                                                                                                   matches 1. .410 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 13.
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alignment_block:
US-08-973-363-14 x HSDJ223E3/rev
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Quali
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/note="MLT1D repeat: matches 396. .505 of consensus"

33204. .33510

/note="Alux repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="59 copies 2 mer cc 65% conserved" complement(29374. .29836)
                                                                                                                                                                                                                                                complement(38574. .39022)
/note="match: GSS: Em:AQ572560"
                                                                                                                                                                                                                                                                                                                                       /note="MER5A repeat: matches 1. .188 of consensus"
38378. .38435
                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 8.
36923. .37001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MLT1D repeat: matches 40.
33990. .34197
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/note="match: GSS: Em:AQ232280"
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/note="MIR repeat: matches 32.
27241. .27530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24642. .24946
/note="Allux repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                     38441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                35679. .35938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1MC5 repeat: matches 7762.
31005. .31642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluJo repeat: matches 1.
28031. .28100
                                                                                                                                                                                                                                                                               /note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                       'note="29 copies 2 mer cc 70% conserved"
18441. .38712
                                                                                                                                                                                                                                                                                                                                                                          'note="AluSc repeat: matches 223. .299 of consensus"
37212. .37407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="AluSx repeat: matches 4. .300 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32407. .32692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match: GSS: Em:B66029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="match: GSS: Em:AQ493139"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER8 repeat: matches 4.
28635. .28670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="L2 repeat: matches 2625. .2693 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="MIR repeat: matches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29412
                                                                                                                                                         Length:
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Database sequences: 1736436
Database length: 858457221
Search time (sec): 521.050000
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Query: US-08-973-363-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Command line parameters:
-MODEL=frame+_p2n.model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -MODEL-frame+_p2n.model -DEV-x1h
-Q-/cgn2_1/USPTO_spool/US08973363/runat_01082002_080123_19849/app_query.fasta_1.638
-DB-M_Geneseq_032802 -OFMT-fastap -SUFFIX-olip2n.rng
-GRPOP-4.500 -GAPEXT-0.050 -MINMATCH-0.100 -LOOPCL-0.000
-LOOPEXT-0.000 -QGAPEXT-0.050 -GAPEXT-0.100 -TGAPOP-60.000
-XGAPEXT-60.000 -FGAPOP-4.500 -GAPEXT-7.000 -YGAPOP-60.000
-XGAPEXT-60.000 -FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-60.000
-XGAPEXT-60.000 -DELOP-6.000 -DELEXT-7.000 -START-1
-MATRIX-olip3 -TRAMS-phumand.odi -LIST-45 -DOCALIGN-20
-MATRIX-OLIP3 -TRAMS-phumand.odi -LIST-45 -DOCALIGN-20
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-20000000
-USER-GS08973353-QCG01_1_186 -NCPU-6 -ICPU-3 -LONGLOG
-USER-GS08973353-QCG01_1 - TRAMS-0 - NORM-C-1-CPU-3 - LONGLOG
-USER-GS08973363-QCG01_1 - TRAMS-0 - NORM-C-1-CPU-3 - LONGLOG
-USER-GS08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of: US-08-973-363-14 to: N_Geneseq_032802:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP=60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                software, version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                out_format : pfs
       8.00 14.33

8.00 13.46

7.00 130.46

7.00 130.46

7.00 127.85

7.00 124.43

7.00 124.43

7.00 124.28

7.00 124.28

7.00 124.28

7.00 124.33

7.00 123.34

7.00 123.34

7.00 123.38

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123.33
                              7 145.81
148.10
148.10
9 161.09
9 172.02
9 224.78
9 225.66
9 265.66
9 275.84
9 281.50
3 300.53
9 366.15
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9 366.15
1 393.53
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1 67.72

1 75.10

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139.33
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0.0043
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Quality:
Ratio:
                                                                                       alignment_block:
US-08-973-363-14 x AAT42753
                                               Align seg 1/1 to:
                                                                                                                                                     Percent Similarity:
       1 AspGlyIleValSerValLysHisProHisLysLysIleLysAlaGlu.L
                                                 AAT42753
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32.00 0.711 97.826

Percent Identity:

97

46 1 .826

from: 1

6

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\(\side \)SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001A_DAT.AAS31233 /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001B_DAT.AAS33499 /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001B_DAT.ABIZ7507 /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001A_DAT.ABIZ7507 /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001A_DAT.ABIZ7507 /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001A_DAT.ABIZ7506 /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001A_DAT.ABIZ7506 /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001B_DAT.ABIZ7506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:AAT42753
                            A composite (incomplete) nucleotide sequence (AAT42753) and putative translation (AAW08145) sequence are provided of a motif that is found spliced to the 3' end of chicken CHP-W clone CCl4 (see also AAT42754). There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found as an insert in some CHD-lA clones (see also AAT42752).
                                                                                                                                                                  Avian chromodomain-helicase-DNA binding genes determine sex birds - used for sex determn. and to control sex of progeny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chicken CHD-W clone CC14 3' motif.
                                                                                                                                        Disclosure; Fig 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex determination; chromodomain-Helicase-DNA binding 1 Avian; chromodomain-Helicase-DNA binding on the W chromosome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
20 52

/*tag= a
/note= "base 52 disrupts the r.
the translated amino a
in Fig 7"
      34
    G; 18
    T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                               reading frame acid sequence
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given
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455
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alignment_block:
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                                                                                          alignment_scores:
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                                      Percent Similarity:
                                                                                                                                                                                                                                                       A composite nucleotide sequence (AAT42752) and putative translation (AAW08144) sequence are provided of a motif that is found spliced to a proportion of chicken CHD-1A clones. The motif is inserted between bases 4327 and 4328 of the CHD-1A composite sequence (AAT42751). None of the 7 CHD-1 clones examined contained the
                                                                                                                                                                                    complete motif. There are no splice donor or acceptor sites within the motif suggesting it is a final rather than an intermediary product of splicing. The motif is also found at the 3' end of the CHD-W clone CC14 (see also AAT42753).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101
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                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 7; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffiths R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHD-W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bird;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicken CHD-1A insert motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT42752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT42752 standard; cDNA;
                                                                                                                                                 Sequence 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-) ISIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAGAAAAAGAGAGACAAAAGAGAAGGAAAATAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysGluAsnGluGluLysAspGluProGluIleGlyIleLysLysGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997-043127/04.
                                                                                                                                                                                                                                                                                                                                                                                                             chromodomain-helicase-DNA binding genes determine sex in used for sex determn, and to control on the sex in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex determination;
                                                       Quality:
Ratio:
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                                                                                                                                                 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                           for sex determn. and to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                 158
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                                                                                                                                                 A; 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "base 52 disrupts the reading frame for
the translated amino acid sequence given
in Fig 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265
                                    Percent Identity: 100.000
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                                                                                                                                                 G;
                                                                                                                                                 30
                                                                                                                                                                                                                                                                                                                                                                                                           control sex of progeny
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                                                                                                                                                 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                     14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
14 - AUG - 2000;
18 - AUG - 2000;
22 - AUG - 2000;
                                                                                                                                                                                                                                                                                                           14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted extracellular matrix protein; ss; immunomodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HIV infection; anaemia; human (managefulariane/autoimmune)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiac arrest; tachycardia; angina; infection; corneal infections;
wound healing; immunogen; gene therapy; antisense; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancers; hyperproliferative disorder; breast neoplasm; melanoma;
Sezary syndrome; Gaucher's disease; neurological diseases;
Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human immunodeficiency virus; rheumatoid arthritis; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding a novel extracellular matrix protein, Seq ID No 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS31339
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14-AUG-2000;
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           healing; immunogen; gene therapy; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; cDNA; 657
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                                                                     2000US-0225266.
2000US-0225267.
2000US-0225268.
2000US-0225276.
2000US-0225447.
2000US-0225757.
2000US-0225759.
2000US-0225759.
2000US-0225759.
2000US-0225759.
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2000US-0217487.
2000US-0217496.
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2000US-0214886.
2000US-0215135.
2000US-0216647.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0205515
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PR 01-SEP 2000; 2000US-0228924, PR 01-SEP 2000; 2000US-022934, PR 01-SEP 2000; 2000US-022934, PR 01-SEP 2000; 2000US-022934, PR 01-SEP 2000; 2000US-022934, PR 01-SEP 2000; 2000US-023124, ```

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Quality:
 The invention relates to isolated nucleic acid molecules encoding convel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased be administered to down regulate expression. The polynucleotides comay be administered to down regulate expression. The polynucleotides comay also be used as DNA probes in diagnostic assays. The SPs may also be used as antigens to produce antibodies and to identify modulators (agonists and antagonists) of the SPs. The anti-(SP) antibodies and cataloguists may also be used to down regulate expression and activity of CS pand as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (e.g. candinac caused by bacteria, viruses cand fungi and ocular disorders (e.g. corneal infections). Other uses cand fungi and ocular disorders (e.g. corneal infections). Other uses cand include wound healing, maintenance of organs before transplantation,
Ratio:
Percent Similarity:
 17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
10-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
 WPI; 200
P-PSDB;
 Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
 Rosen
 Claim
 (HUMA-) HUMAN GENOME SCI INC
 2001-465572/50
DB; AAU19768.
 CA,
 SEQ ID No 153; 577pp;
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 2000US-0249214
2000US-0249215
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 Human; digestive system antigen; ulcerative colitis; infection; Hi
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 17-JAN-2001;
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2000US-0225934.
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 ВP
 42
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 genomic
 to:
 657
 sequence
 SEQ
 ij
 appendicitis; chronic colitis;
 NO:
 20-OCT 2000

20-OCT 2000

20-OCT 2000

20-OCT 2000

20-OCT 2000

20-OCT 2000

20-OCT 2000

01-NOV 2000

08-NOV 2000

01-NOV 2000

08-NOV 2000

09-NOV 2000

017-NOV 2000

17-NOV 2000
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2000US-0249211
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Ratio:
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01-DEC-2000
01-DEC-2000
05-DEC-2000
05-DEC-2000
05-DEC-2000
06-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
08-DEC-2000
 1368 GAAAAAAGGGAAACGAAAGAGAAA 1391
 The present invention provides the protein and coding sequences of a number of human digestive system antiquens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hitschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
 Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
Homo sapiens
 Human; 5' EST; expressed sequence tag; secreted protein;
gene therapy; chromosome mapping; ss.
 Human secreted
 06-OCT-2000
 Disclosure; SEQ ID NO 2962; 986pp; English.
 Sequence 2121 BP; 906 A; 306 C; 407 G; 502 T; 0 other;
 WPI; 2001-502630/55.
 Rosen CA,
 (HUMA-) HUMAN GENÔME SCI INC
 35 GluLysArgGluThrLysGluLys 42
 Barash SC,
 (first entry)
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1.000
100.000
 protein 5' EST, SEQ ID NO: 29917.
 from: 1
 Length: 8
Gaps: 0
Percent Identity: 100.000
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 SM;
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6
 2121
 cDNA isolation;
$\times C C C C C C C C C C C C C C X \times X \
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ID AAK70025 standard; DNA; 312 BP
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US-08-973-363-14 x AAC25842
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 Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
 Align seg 1/1 to: AAC25842 from:
 The present sequence is one of a large number of 5′ ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5′ ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3′ untranslated region (UTR) of the mRNAs because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5′ ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5′ UTR is rarely included. 5′ ESTs are derived from mRNAs with intact 5′ ends and can therefore be used to obtain full length cDNAs with intact 5′ ends and can therefore be used to obtain full length cDNAs with intact 5′ ends and can therefore be a used to obtain upstream regulatory sequences and to design expression and secretion vectors.
 170 ATAAAGAAAGAAGCTGGTGAA 190
 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
 WPI;
 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
 Claim 1; SEQ ID 29917; 71pp + CD-ROM; English.
WO200157182-A2
 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24837
 06-NOV-2001
 Sequence 294 BP; 96 A; 51 C; 72 G; 75 T; 0 other;
 Dumas Milne Edwards J,
 21-FEB-2000; 2000EP-0200610
 06-SEP-2000
 EP1033401-A2
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 29 IleLysLysGluAlaGlyGlu 35
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 (first entry)
 99US-0122487
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Gaps: 0
Percent Identity: 100.000
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 Giordano
 294
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03-DEC-2000
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 2001-483426/52
 acids
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2000US-0241786

2000US-0241809

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2000US-0237040.
2000US-0237040.
2000US-0239935.
encoding human immune/hematopoietic antigen polypeptides,
 GENOME
 MS
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קאר סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סיקים סי

useful for preventing, diagnosing and/or treating cancers and

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ID AAS39061 standard; cDNA; 350 BP
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT:AAS39061
 alignment_block:
 alignment_scores
 CC anks4951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC annino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (I) CP proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CP proteins of the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CP protein. (I) proteins and polynucleotides may be used to provent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC concers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK84942 to AAK84950 and AAK82169 CC represent sequences used in the exemplification of the present invention.
 Align seg 1/1 to: AAK70025 from: 1
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 Percent Similarity: 100.000
 Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Kli
Reinhard C, Randazzo E, Kennedy GC, Pot D, Kassam A, Lam
Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
Leshkowitz D, Kita D, Garcia V, Jones WL, Stache-Crain B;
 09-MAR-2001; 2001WO-US07787
 Human; cancer; breast; lung; colon; prostate; cytostatic; diagnostic;
 Novel human diagnostic and therapeutic gene #2119.
 17-DEC-2001 (first entry)
 AAS39061;
 Sequence 312 BP; 133 A; 40 C; 82 G; 57 T; 0 other;
 Disclosure; SEQ ID NO 24837; 3071pp + Sequence Listing; English.
 metastasis
 WPI; 2001-530177/58.
 09-MAR-2000; 2000US-0188609
 WO200166753-A2
 (HYSE-) HYSEQ INC.
 (CHIR) CHIRON CORP.
 37 ArgGluThrLysGluLysGlu 43
 50 AGGGAGACCAAGGAGAAGGAG 70
 Quality:
 Ratio:
 1.000
 Percent Identity: 100.000
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6
 Length:
 Sudduth-Klinger J; ssam A, Lamson G;
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 alignment_scores:
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 Percent Similarity: 100.000
 -08-973-363-14 x AAS39061/rev
 The invention relates to new polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer. The sequences can be used in detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous. They can also be used to inhibit tumour growth by modulating expression of a gene product. AAS35943 represent novel human diagnostic and therapeutic coding sequences of the invention.
The present invention describes a method for monitoring differential
 Monitoring differential expression of genes in filamentous uses fluorescence-labeled nucleic acids isolated from the c substrate of expressed sequence tags \cdot
 Fusarium venenatum.
 Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
 Fusarium venenatum EST SEQ ID NO:2805.
 13-MAR-2001 (first entry)
 AAF10282
 AAF10282 standard; cDNA; 427 BP.
 260 AAAGAAGCAGGCGAGAAGAGA 240
 Sequence 350 BP; 53 A; 84 C; 60 G; 153 T; 0 other;
 Claim 1; Page 1126; 1193pp; English.
 New polynucleotides and polypeptides, useful for diagnosis and treatment of breast, lung and colon cancer -
 Claim 86; Page 1400; 3161pp; English.
 WPI; 2000-594572/56.
 Berka RM,
 22-MAR-1999;
 28-SEP-2000
 WO200056762-A2
 (NOVO) NOVO NORDISK BIOTECH INC.
 22-MAR-2000; 2000WO-US07781
 31 LysGluAlaGlyGluLysArg 37
 Quality:
Ratio:
 Rey MW, Shuster JR,
 99US-0273623.
 7.00
1.000
 Percent Identity: 100.000
 Kauppinen S,
 from:
 60:
 Clausen IG,
 s fungal cells
cells and a
 Olsen PB;
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seq_documentation_block:
ID AAC00952 standard; cDNA; 468 BF
XX
AC AAC00952;
XX
DT 06-OCT-2000 (first entry)
XX
Human secreted protein 5' EST,
XX
Human; 5' EST; expressed sequen
KW Human; 5' EST; chromosome mappin
XX
Homo sapiens.
XX
PR EP1033401-A2.
XX
PR EP1033401-A2.
XX
PR 21-FEB-2000; 2000EP-0200610.
XX
PF 21-FEB-1999; 99US-0122487.
XX
PR 26-FEB-1999; 99US-0122487.
XX
PR (GEST) GENSET.
XX
PA (GEST) GENSET.
XX
PA (GEST) GENSET.
XX
PR Dumas Milne Edwards J, Duclert
XX
PR P-PSDB; AAG00946.
XX
New nucleic acid that is a 5' e
 alignment_block:
US-08-973-363-14 x AAF10282/rev
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAC00952
 alignment_scores
 Percent Similarity:
 Align seg 1/1
 adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarray based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Aspergillus Pusarium venenatum, AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF148737 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
 expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses filorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be described and account of the microorganisms.
 Human; 5' EST; expressed sequence tag; secreted
gene therapy; chromosome mapping; ss.
 Sequence 427
 monitored.
 165 ACAAAAGAAAAGAAAACAAA 145
 identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells
 ThrLysGluLysGluAsnLys 45
 Quality:
 Ratio:
 to reverse of: AAF10282
 BP;
 100.000
 7.00
 120
 Α
 76
 Duclert
 EST,
 Percent
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 expressed sequence tag (5' EST) for
 97
 SEQ ID
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 <u>ი</u>
 Gaps:
: Identity:
 from:
 Giordano
 134 T; 0 other;
 NO: 950.
 ب
 : 7
: 0
: 100.000
 ţ.
 protein; cDNA isolation;
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seq_documentation_block:
ID AAC00953 standard;
 alignment_block:
 alignment_scores:
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Ratio: 1.000
Percent Similarity: 100.000
 Align seg 1/1 to: AAC00952
 US-08-973-363-14 x AAC00952
 obtaining
 gene
 often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where Long er cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, contains the contains of the contains
 The present sequence is one of a large number mRNAs encoding secreted proteins. An ORF has be sequence. The 5' ESTs were prepared from total
 diagnostic,
 New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
 Dumas Milne Edwards
 Human secreted
 357
 sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNA derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are
 obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
 26-FEB-1999;
 21-FEB-2000; 2000EP-0200610
 06-SEP-2000
 EP1033401-A2
 Homo sapiens
 Human;
 06-OCT-2000
 AAC00953
 Claim 1;
 (GEST) GENSET
 Sequence 468 BP;
 upstream regulatory sequences and to design expression and secretion
 gene therapy and chromosome mapping procedures. They
 13 IleLysAlaGluLysGluAsn
 ATCAAGGCTGAAAAAGAAAAT
 therapy;
 2000-500381/45.
 5' EST;
 AAG00947
 SEQ ID
 forensic,
 (first entry)
 ; expressed chromosome
 99US-0122487
 protein 5' EST,
 950;
 131 A;
 cDNA; 542
 'n
 71pp + CD-ROM; English
 89 C; 116
 Duclert
 mapping;
 sequence
 from:
 19
 Length: 7
Gaps: 0
Percent Identity: 100.000
 377
 therapy
 ВP
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 SEQ ID NO:
 A,
 tag;
 G; 131 T; 1 other;
 .
0
 Giordano
 ORF has been identified
 468
 secreted protein; cDNA isolation,
 951.
 tag (5' EST) for to 5'ESTs and for
 mapping procedures
 are used to obtain
 derived from
 within the polyA+ RNAs
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Claim 1; SEQ ID 951; 71pp + CD-ROM; English

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*888888888888888888
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US-08-973-363-14 x AAC00953
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Ratio: 1.000
Percent Similarity: 100.000
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 Align seg 1/1 to:
 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
 Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
 Arabidopsis thaliana DNA fragment
 431 ATCAAGGCTGAAAAAGAAAAT
 Sequence
 13 IleLysAlaGluLysGluAsn 19
 /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:AAC54696
 542
 BP;
 AAC00953
 151
 ۶,
 105
 from:
 451
 Length: 7
Gaps: 0
Percent Identity: 100.000
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 SEQ ID NO: 78761.
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to:
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 Percent Similarity:
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 Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
 190
 Arabidopsis thaliana DNA fragment
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 26
 GluileGlyileLysLysGlu
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 2000EP-0301439
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990S-0126785

990S-0126785

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: 1.000
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 DNA;
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Gaps:
Percent Identity:
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|-----------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------|-------------------------------------------------------------------|--------------------------------------------------------|--------------------------------------------------------|--------------------------------------------|---------------------|---------------------|---------------------|--------------------------------------------|---------------------|--------------------------------------------|--------------------------------------------|--------------------------------------------------------|--------------------------------------------------------|--------------------------------------------------------|--------------------------------------------------------|------------------------------------------|--------------------------------------------------------|--------------------------------------------------------|--------------------------------------------------------|---------------------------|---------------------------|---------------------|---------------------------|--------------------------------------------------------|-------------------|-------------------|----------------------------------------|------------------------------------|----------------------------------------------------|-----------------------------|-----------------|
| 22200                                                                                                                                         | 2019                                                              | 191                                        | 191                                                               | 4 13 4                                                 | 13                                                     | 98                                         | 200                 | 321                 | 28                  | 29                                         | 40                  | 322                                        | 322                                        | 8 60                                                   | 18                                                     | 18                                                     | 18                                                     | 18                                       | 17                                                     | 16                                                     | 14                                                     | 10                        | 37                        | 20,                 | 28                        | 27                                                     | 24                | 38                | 19                                     | 14                                 | 14                                                 |                             | 96              |
| 0-JUL-<br>1-JUL-<br>1-JUL-                                                                                                                    | -10L-<br>9-JUL-<br>9-JUL-                                         |                                            | -70T-                                                             |                                                        |                                                        | 9-JUL-                                     | 6-JUL-              | )1-JUL-1            | -JUN-               | -JUN-1                                     | -JUN-               | JUN-                                       |                                            |                                                        |                                                        |                                                        |                                                        | JUN-                                     | 3-JUN-1                                                | 9 9                                                    | -JUN-                                                  | -JUN-                     | -NDV-                     | 3-JUN-              | 28 - MAY - 1              | 25 -MAY - 1<br>27 -MAY - 1                             | × S               | 0-MAY-1           | - YAY -                                | 4-MAY-1                            | -MAY-1                                             | 1-MAY-1                     | -MAY-1          |
|                                                                                                                                               | 1555                                                              | 111                                        |                                                                   |                                                        | 1-1                                                    | 55                                         | E-1                 | 366                 | 7 Z                 | N-1                                        |                     | 222                                        | 222                                        |                                                        |                                                        |                                                        |                                                        | Z Z .                                    |                                                        | Z Z                                                    | Z-1                                                    |                           |                           |                     | Y-1                       | Y-1                                                    | Y-1               | Y - 1             |                                        | : Y - 1                            | : 4 - 1                                            | . Y - 1                     | Y-1             |
| -1999<br>-1999<br>-1999                                                                                                                       | 999                                                               | 999                                        | 999                                                               | 999                                                    | .999                                                   | 999                                        | 999                 | 6661                | 999                 | 999                                        | 999                 | 1999                                       | 6661                                       | 1999                                                   | .999                                                   | 6661<br>6661                                           | 999                                                    | 999                                      | 999                                                    | .999                                                   | 999                                                    | 999                       | 999                       | 999                 | 999                       | 999                                                    | 999               | 999               | 999                                    | 999                                | 999                                                | 6661                        | 999             |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   | 7.37.             |                                        |                                    |                                                    |                             |                 |
| 99999                                                                                                                                         | 9999                                                              | ووو                                        | 999                                                               | 9 9                                                    | 9 9                                                    | 9 9                                        | 9 9                 | 9 9 5               | 9 9                 | 9 9                                        | 9 9                 | 9 9 9                                      | 9 9                                        | 9 9                                                    | 9 9                                                    | 99                                                     | 9 9                                                    | 9 9                                      | 9 9                                                    | 9 9                                                    | 9 9                                                    | 9 9                       | 9 9                       | 9 0                 | 90                        | 9 9                                                    | 99                | 99                | 9 9                                    | 9 9                                | 9 9                                                | 9 9 9                       | 9 9             |
| SDES                                                                                                                                          | Suc                                                               | Sugar                                      | Suc                                                               | SDE                                                    | SDE                                                    | SDE                                        | SD                  | Soci                | Sol                 | SOC                                        | S                   | SDC                                        | S                                          | SDCS                                                   | SD                                                     | SD(                                                    | SD                                                     | S. O.                                    | S S                                                    | g ig                                                   | SOS                                                    | S                         | S                         | S                   | Š                         | ġġ.                                                    | SD                | S. S.             | ŭs-                                    | S                                  | S                                                  | S                           | S               |
| 99US-0144632.<br>99US-0144884.<br>99US-0144814.<br>99US-0145086.                                                                              | င်ုင်င်                                                           | 200                                        |                                                                   | 200                                                    | 25                                                     | 200                                        | 01                  | 900                 | 9                   | 92.                                        | 200                 | 200                                        | 200                                        | 200                                                    | 20                                                     | 01                                                     | 00                                                     | 22                                       | 99                                                     | 01                                                     | 22                                                     | 01                        | 200                       | 225                 |                           | 22                                                     | 01                | 22                | 010                                    | 9                                  | Ò                                                  | 200                         | 20              |
| 446                                                                                                                                           | 443                                                               | 443                                        | 140                                                               | 140                                                    | 135                                                    | 128                                        | 23                  | 2121                | 112                 | 904                                        | 6                   | 03                                         | 898                                        | 397                                                    | 394                                                    | 394                                                    | 394                                                    | 94                                       | 94                                                     | 394                                                    | 391                                                    | 85                        | 377                       | 375                 | 3678                      | 636                                                    | 356               | 51                | 3476                                   | 343                                | 342                                                | 3428                        | 224             |
| 86.4.4.8                                                                                                                                      | 55.                                                               | 35.5                                       | 56.                                                               | 25.                                                    | 12.                                                    | 20.                                        | 0.                  | л 4                 | 37.                 | 23.                                        | 55.                 | 33.9                                       | 57.                                        |                                                        | 52.                                                    | 0.                                                     | 57                                                     | 6 6                                      | 4.                                                     | 3 2                                                    | 9.                                                     | 0.4                       |                           | 3 8 6               | 3 8                       | 2 .                                                    |                   | ع. د              | - ĕ                                    | 0 F                                | φα                                                 | 56.                         | 37              |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        | •                 |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        | ٠                         |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        | ٠                         | ٠                         |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            | -                                          |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           | ٠                         |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            | ٠                                          |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        | •                         |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
| ·                                                                                                                                             |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            | ·                   |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     | -                         |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     | -                         |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     |                           |                                                        |                   |                   |                                        |                                    |                                                    |                             |                 |
| PR<br>PR<br>PR                                                                                                                                | PR<br>PR                                                          | ק<br>ק<br>ק                                | אי<br>מי                                                          | PR                                                     | PR                                                     | PR                                         | איז                 | מס                  | PR<br>Rd            | PR                                         | אַק<br>R            | גיי                                        |                                            | PR                                                     | PR                                                     | PR                                                     | PR                                                     | מק                                       | PR                                                     | PR                                                     | PR                                                     | ייי                       | PR                        | מים<br>מים          | פסס                       | PR<br>ਸ਼ਰ                                              | מי                | מסס<br>ייאס       | אַל                                    | ਸ਼ਕ                                | אַק                                                | ק<br>ק                      | PR              |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     | - ,-                      |                                                        | אי                | מם<br>מס          | PR                                     | מ א ש                              | יים אין<br>אין אין אין אין אין אין אין אין אין אין | יי פי זי גע<br>א א גע די גע | PR              |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     | - ,-                      |                                                        | PR 02-            | PR 02-            | PR 27-                                 | PR 27-                             | PR 26-                                             | PR 23-                      | PR 22-          |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     | - ,-                      |                                                        | PR 02-AUG         | PR 02-AUG         | PR 27-JUL                              | PR 27-JUL                          | PR 26-JUL                                          | PR 23-JUL                   | PR 22-JUL       |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     | - ,-                      | 03-AUG-1                                               | PR 02-AUG-19      | PR 02-AUG-19      | PR 27-JUL-19                           | PR 27-JUL-19                       | PR 26-JUL-19                                       | PR 23-JUL-19                | F-1             |
|                                                                                                                                               |                                                                   |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     | - ,-                      | 03-AUG-1                                               | PR 02-AUG-1999;   | PR 02-AUG-1999;   | PR 27-JUL-1999;<br>PR 28-JUL-1999;     | PR 27-JUL-1999;<br>PR 27-JUL-1999; | PR 26-JUL-1999;                                    | PR 23-JUL-1999;             | F-1             |
|                                                                                                                                               | 14-0CT-                                                           |                                            |                                                                   |                                                        |                                                        |                                            |                     |                     |                     |                                            |                     |                                            |                                            |                                                        |                                                        |                                                        |                                                        |                                          |                                                        |                                                        |                                                        |                           |                           |                     | - ,-                      | 03-AUG-1                                               | PR 02-AUG-1999;   | PR 02-AUG-1999;   | PR 27-JUL-1999;<br>PR 28-JUL-1999;     | PR 27-JUL-1999;<br>PR 27-JUL-1999; | PR 26-JUL-1999;                                    | PR 23-JUL-1999;             | F-1             |
| 14-OCT-1999;<br>14-OCT-1999;<br>18-OCT-1999;<br>21-OCT-1999;                                                                                  | 14-OCT-1999;<br>14-OCT-1999;<br>14-OCT-1999;                      | 13-OCT-1999;<br>13-OCT-1999;               | 07-0CT-1999;<br>08-0CT-1999;<br>12-0CT-1999;                      | 05-OCT-1999;<br>06-OCT-1999;                           | 29-SEP-1999;<br>04-OCT-1999;                           | 24-SEP-1999;<br>28-SEP-1999;               | 23-SEP-1999;        | 20-SEP-1999;        | 15-SEP-1999;        | 10-SEP-1999;<br>13-SEP-1999;               | 07-SEP-1999;        | 30-AUG-1999;<br>31-AUG-1999;               | 27-AUG-1999;<br>27-AUG-1999;               | 26-AUG-1999;<br>27-AUG-1999;                           | 23-AUG-1999;<br>25-AUG-1999;                           | 20-AUG-1999;<br>23-AUG-1999;                           | 20-AUG-1999;<br>20-AUG-1999;                           | 17-AUG-1999;<br>18-AUG-1999;             | 13-AUG-1999;<br>16-AUG-1999;                           | 12-AUG-1999;<br>13-AUG-1999;                           | 10-AUG-1999;<br>11-AUG-1999;                           | 09-AUG-1999;              | 06-AUG-1999;              | 05-AUG-1999;        | 04-AUG-1999;              | 03-AUG-1999;<br>04-AUG-1999;                           | 999;              | 999;              | 999;                                   | ,666                               | ,666                                               | 999;                        | UL-1999;        |
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| 14-OCT-1999; 99US-0<br>14-OCT-1999; 99US-0<br>18-OCT-1999; 99US-0<br>21-OCT-1999; 99US-0<br>21-OCT-1999; 99US-0                               | 14-OCT-1999; 99US-0<br>14-OCT-1999; 99US-0<br>14-OCT-1999; 99US-0 | 13-0CT-1999; 99US-0<br>13-0CT-1999; 99US-0 | 07-0CT-1999; 99US-0<br>08-0CT-1999; 99US-0<br>12-0CT-1999; 99US-0 | 05-OCT-1999; 99US-0<br>06-OCT-1999; 99US-0             | 29-SEP-1999; 99US-0<br>04-OCT-1999; 99US-0             | 24-SEP-1999; 99US-0<br>28-SEP-1999; 99US-0 | 23-SEP-1999; 99US-0 | 20-SEP-1999; 99US-0 | 15-SEP-1999; 99US-0 | 10-SEP-1999; 99US-0<br>13-SEP-1999; 99US-0 | 07-SEP-1999; 99US-0 | 30-AUG-1999; 99US-0<br>31-AUG-1999; 99US-0 | 27-AUG-1999; 99US-0<br>27-AUG-1999; 99US-0 | 26-AUG-1999; 99US-0<br>27-AUG-1999; 99US-0             | 23-AUG-1999; 99US-0<br>25-AUG-1999; 99US-0             | 20-AUG-1999; 99US-0<br>23-AUG-1999; 99US-0             | 20-AUG-1999; 99US-0<br>20-AUG-1999; 99US-0             | 17-AUG-1999; 99US-0                      | 13-AUG-1999; 99US-0                                    | 12-AUG-1999; 99US-0<br>13-AUG-1999; 99US-0             | 10-AUG-1999; 99US-0                                    | 09-AUG-1999; 99US-0       | 06-AUG-1999; 99US-0       | 05-AUG-1999; 99US-0 | 04-AUG-1999; 99US-0       | 03-AUG-1999; 99US-0:<br>04-AUG-1999; 99US-0:           | 999; 99US-0       | 99US-0            | 0-SD66<br>0-SD66<br>0-SD66             | 999; 9908-0                        | 999; 99US-0                                        | 999; 99US-0                 | UL-1999; 99US-0 |
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99US-0160770. 99US-0160814. 99US-0160815.

9908-0160980.

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25-CCT-1999
 expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis;
 28-SEP-2000
 Aspergillus oryzae
 metabolic pathway engineering; catabolic pathway engineering; ss
 13-MAR-2001
 26-OCT-1999;
26-OCT-1999;
The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative
 Monitoring differential expression of genes in filamentous fungal uses fluorescence-labeled nucleic acids isolated from the cells a substrate of expressed sequence tags -
 22-MAR-2000; 2000WO-US07781
 AAF11881 standard; cDNA;
 Claim 88; Page 1883-1884; 3161pp; English
 WPI; 2000-594572/56
 Berka RM,
 (NOVO) NOVO NORDISK BIC
 22-MAR-1999;
 WO200056762-A2
 Multiple gene expression; filamentous fungal cell; EST;
 Aspergillus oryzae EST SEQ ID NO:4404
 28-OCT-1999
 26 GluIleGlyIleLysLysGlu
 GAGATTGGGATCAAAAAGGAG
 Rey
 NORDISK BIOTECH INC
 (first entry)
 99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
 99US-0160989.
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: 100.000
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 99US-0161992.
99US-0161993.
 9908-0162142
 99US-0160981.
 Shuster JR,
 710 BP
 from:
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 Percent Identity:
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 Length:
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alignment_scores:
Quality:
 seq_documentation_block:
ID AAI97871 standard; cDNA;
 alignment_block:
US-08-973-363-14 x AAF11881/rev
 seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:AAI97871
 CC expression of the same genes in one or more second filamentous fungal CC cells. The method uses filorescence-labeled nucleic acids isolated from CC the FF cells and a substrate of expressed sequence tags (EST). The ESTS CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring CC potential of the microorganisms to be improved. New genes may be CC discovered, possible functions of unknown open reading frames can be CC discovered, possible functions of unknown open reading frames can be CC discovered. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore CC morphogenesis, recombination, metabolic or catabolic pathway CC engineering. Using ESTs provides several advantages over genomic or CC array equals one gene or open reading frame, and organisation of the CC microarrays based on function of the gene products to facilitate CC analysis of the results. AAF07478 to AAF11247 represents ESTs from CC C AAF14879 to AAF11854 to AAF11878 to AAF11247 represents ESTs from Aspergillus or CC C AAF14879 to AAF11837 represents ESTs from Trichoderma reesei, which are CC all specifically claimed in the present invention.
 Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
 Align seg 1/1 to reverse of: AAF11881
Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker
 233 AAAGAGGCGGGTGAAAAGAGG
 WPI; 2001-565584/63.
 07-MAR-2000; 2000JP-0159195
 02-MAR-2001;
 13-SEP-2001.
 WO200166719-A1
 Homo sapiens.
 Human;
 Human neuroblastoma expressed polynucleotide SEQ ID NO 3946.
 13-NOV-2001
 AAI97871;
 Sequence
 (CHIB-) CHIBA PREFECTURE.
(HISM) HISAMITSU PHARM CO LTD
 31 LysGluAlaGlyGluLysArg
 neuroblastoma;
 710
 BP;
 2001WO-JP01629
 (first entry)
 135 A;
 malignancy; cancer;
 195
 721
 213
 37
 Percent Identity: 100.000
 C; 148
 ВP
 G; 231 T; 1 other;
 from:
 Length:
Gaps:
 tumour marker; N-myc;
 ţo:
 0 7
 from Aspergillus
llus oryzae; and
 TrkA;
 SS
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Claim 1; Page 2902; 2979pp; Japanese

for anti-cancer agents

```
seq_documentation_block:
ID AAH77229 standard; DNA; 729 BP.
XX
AC AAH77229;
XX
Ol-FEB-2002 (first entry)
XX
DE DNA of atRSp41 5'-UTR.
XX
AtRSp41 5'-UTR; thale cress; tran
XX
At atRSp41 5'-UTR; thale cress; tran
XX
W harbidopsis thaliana arginine/ser
XX
Arabidopsis thaliana arginine/ser
XX
Arabidopsis thaliana.
XX
YX
Arabidopsis thaliana
XX
YX
Arabidopsis thaliana
XX
YX
Herbicide tolerance; antibiotic r
XX
Arabidopsis thaliana
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Ratio: 1.000
Percent Similarity: 100.000
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US-08-973-363-14 x AAI97871/rev
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 Align seg 1/1 to reverse of: AAI97871
 The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.
 atRSp41 5'-UTR; thale cress; transgenic plant; virus resistance; ds; altered reproductive capability; insect resistance; disease resistance; Arabidopsis thaliana arginine/serine-type plant splicing factor; atRSp; herbicide tolerance; antibiotic resistance.
 Claim 5; Page 30; 34pp; English.
 DNA sequences comprising atRSp gene promoters, useful for expressing a nucleotide sequence of interest for conferring a desirable phenotypic trait to a plant, e.g. virus, insect or disease resistance, are new.
 Sequence 721 BP; 151 A; 200 C; 176 G; 190 T; 4 other;
 (SYGN) SYNGENTA PARTICIPATIONS AG
 Location/Qualifiers
 Percent Identity: 100.000
 Length:
Gaps:
 from: 1
 .
6
```

```
alignment_block:
US-08-973-363-14 x AAH77229/rev
 CC This polynucleotide sequence represents the DNA of the atRSp41 5'.UTR.

CC The invention relates to novel DNA sequences that function as promoters of the invention of associated nucleotide sequences in plants The CC invention provides a DNA sequence capable of driving expression of an CC associated nucleotide sequence, wherein said DNA sequence is obtainable CC from genes of the atRSp (Arabidopsis thaliana arginine/serine-type plant CC DNA molecules comprising an atRSp41 promoter, the invention also provides CC expression vectors and transgenic plants comprising the promoters of the CC invention. The DNA sequence of the invention is useful for expressing a CC nucleotide sequence of interest. The nucleotide sequences encode proteins CC for conferring a desirable phenotypic trait to a plant transformed with CC the protein, where such traits include antiblotic resistance, virus CC resistance, insect resistance, improved nutritional value, improved CC pests, herbicide tolerance, improved nutritional value, improved capability.
 alignment_scores
 Quality: 7.00
Ratio: 1.000
Percent Similarity: 100.000
 Align seg 1/1 to reverse of: AAH77229
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 Length: 7
Gaps: 0
Percent Identity: 100.000
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 to:
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 gb_est2:BG604006
gb_est2:D73021
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gb_est1:AA728877
gb_est1:AA728877
 WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP-XGAPOP-60.000 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT-60.000
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Database length: -1841457050
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 Query length:
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-USCRES-US08973363_4CGIAL_12938 -NCDP=6 -ICPU=3 -LONGLOG
 Results were produced by Copyright (c) 1993-2000 C
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 y the GenCore software, version 4.5, Compugen Ltd.
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51.08 17
51.08 17
1 94.26 1
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51 123.31
1.88 133.70
135.69
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 Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 143
Seq primer: AATTAACCCTCACTAAAGGG
 Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
 1 (bases 1 to 911)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library Unpublished (2001)
 Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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; Triticeae; Hordeum.
 High quality sequence stop:
 Contact: Wing RA
 On Feb 22,
 BG309136
BG309136.2 GI:16313822
/notes vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
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 AUTHORS
TITLE
 JOURNAL
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 CDNA Library Preparation: Life Technologies, Inc.
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
 1 (bases 1 to 1227)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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 Tissue Procurement: DCTD/DTP
 BG283942.1 GI:13034392
 mRNA sequence.
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 human.
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 BG309136
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/lab_host="DHIOB (phage=resistant)"
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a 208 c 388 g 44 t
 Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30.

(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

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 853
 .
6
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Gaps:
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 911
 03
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 EST 21-FEB-2001
 Site_1: NotI;
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 JOURNAL
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 629
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 Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S.,
 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
 Fax: +55-11-2707001
 Contact: Simpson A.J.G.
 Simpson, {\bf A}.{\bf J}. Shotgun sequencing of the human transcriptome with ORF expressed
 Nagai,M.A., da Silva,W. Jr., 2ago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Homo sapiens
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 MR2-EN0092-110101-006-d03_1 EN0092 Homo sapiens cDNA, mRNA
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&t2=MR2-EN0092-
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 (bases
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 Natl. Acad. Sci. U.S.A.
 reverse of: BI010841
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1.000
100.000
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 Sao
 Briones, M.R.,
 Paulo-SP,
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GluLysArgGluThrLysGluLys 42

33 GAAAAAAGGGAAACGAAAGAGAAA 10

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REFERENCE
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US-08-973-363-14 x BE787833
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 16 GluLysGluAsnGluGluLysAsp 23
 BB416876 RIKEN full-length enriched, 7 days embryo Mus musculus CDNA. clone C430048M07 3', mRNA sequence.
 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
 EST
 mRNA sequence.
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 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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National Institutes of Health, Mammalian Gene Collection (MGC)
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 Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mazuno, Y., Nakamira, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tooninaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamoraka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Oshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Konno, H., et al.)

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9216
 Email genome-res@gsc.riken.go.jp,
URI.http://genome.gsc.riken.go.jp/
URI.http://genome.gsc.riken.go.jp/
Carnincl.P. Nahiyama.y. Westover.A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu.M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
Carninci,P. and Hayashizaki,Y.
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Ratio:
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 Please visit our web site (http://genome.rtc.riken.go.jp) for
 45 a
 contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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 30 LysLysGluAlaGlyGluLysArg 37
 Unpublished (2000)
Contact: Genoscope
Genoscope - Centre National de Sequencage
 Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P.
 Medicago truncatula ESTs from Sinorhizobium meliloti-induced root
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 Medicago truncatula
 MtBB32B09R1 MtBB Medicago truncatula cDNA clone MtBB32B09 T7, mRNA
 http://sequence.toulouse.inra.fr/Mtruncatula.html).
 nodules
 barrel medic
 AL377519.1 GI:9677271
 Medicago.
 (bases 1 to 269)
 б
 104 a
 reverse
 XhoI; Plants were grown in an aeroponic chamber on nitrogen-rich medium for 21 days. Three days before inoculation with Sinorhizobium meliloti, the medium was replaced by N-free medium. Root nodules (+ short adjacent root segments) were harvested 4 days post inoculation. CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing CDNA inserts were
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N8560a
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 relating to organism, clone or library availability. Seq primer: T3
 Email: toxo@watson.wustl.edu
David Sibley at toxoest@borcim.wustl.edu for further information
 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Unpublished (1996)
 Hehl, A., Manger, I., Marra, M., Sibley, L.D., Ajioka, J.A., Dietrich, N., Dubuque, T., Hillier, L., Kucaba, T., Wan, K. Waterston, R. H. and Boothroyd, J. WashU-Merck-Stanford-NIH Toxoplasma EST project
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Zhao,B., Wang,X.M., Zhang,Q., Zhu,Z.M., Zhu,S.J. and Hui,R.T.
Cloning of Genes Responsible for Stroke
Unpublished (2000)
Contact: Bin Zhao
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 Caenorhabditis elegans.
 Genome Biology Lab.
National Institute of Genetics
Natianal Institute, Shizuoka 411,
Yata 1111, Mishima, Shizuoka 411,
Tel: 81-559-81-6854
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Contact: Yuji Kohara
Molecular Medical Center for Cardiovascular Disease
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Kappe,S.H.I., Gardner,M.J., Brown,S.M., Ross,J., Matuschewski,K., Ribeiro,J.M., Adams,J.H., Quackenbush,J., Cho,J., Carucci,D.J., Hoffman,S.L. and Nussenzweig,V.
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Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
 Cardiovascular Institute, CAMS & PUMC 167, Bei Li Shi Lu, 100037, Beijing, P.R. China Tel: 86-10-66314466 ext 8136 Fax: 86-10-68331330
 Exploring the transcriptome of the malaria sporozoite stage Proc. Natl. Acad. Sci. U. S. A. 98 (17), 9895-9900 (2001)
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Genome Biology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411,
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 Unpublished
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 Email: gardner@tigr.org
Request for clones, please contact: Stefan Kappe,
kappes01@popmail.med.nyu.edu Michael Heidelberger Division,
bepartment of Pathology New York University School of Medicine.
 Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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Fax: 81-559-81-6855
 Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T.,
 Fax: 301 838 0208
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 1 (bases 1 to 354)
Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSS: BOHMT14TF
Contact: Chris Town
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Class: sheared ends.
 9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
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 Email: cdtown@tigr.org
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 USA
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REFERENCE
AUTHORS
TITLE
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 VERSION
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 JOURNAL
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 source
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EST.
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 CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lln1.gov/bbrp/lnage/thm1

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 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
The Cole of the Cole of
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Homo sapiens
 Unpublished (1997)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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 Homo sapiens
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 Tumor Gene Index
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AUTHORS
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AUTHORS
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LOCUS AA728877

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 TITLE
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 TITLE
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Nati-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
 CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.lln1.gov/bbrp/image/image.html
Seq primer: M13 Forward.
 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Kristina A. Cole, M.D.,
Ph.D. student, Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buc
 Tumor Gene Index
Unpublished (1997)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 EST.
 Email: cgapbs-remail.nih.gov
Eco RI site shown at the beginning of the sequence
Tissue procurement: Louis M. Staudt, M.D., Ph.D.
 Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 423)
 Homo sapiens
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 human.
cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
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 Percent Identity: 100.000
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 EST 22-JAN-1998
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by Louis

```
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: www-bio.llnl.gov/bbrp/Image/hmage.html
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